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(57) Abstract

The present invention relates to peptides which exhibit potent anti-retroviral activity. The peptides of the invention comprise DP178 (SEQ ID:1) peptide corresponding to amino acids 638 to 673 of the HIV-1_{LAI} gp41 protein, and fragments, analogs and homologs of DP178. The invention further relates to the uses of such peptides as inhibitory of human and non-human retroviral, especially HIV, transmission to uninfected cells.

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METHODS AND COMPOSITIONS FOR INHIBITION OF MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV TRANSMISSION

This is a Continuation-In-Part of Serial No. 08/360,107 filed December 20, 1994, which is a 5 Continuation-In-Part of Serial No. 08/255,208 filed June 7, 1994, which is a Continuation-In-Part of Serial No. 08/073,028 filed June 7, 1993, each of which is incorporated herein by reference in its entirety. This invention was made with Government support under Grant No. AI-30411-02 awarded by the National Institutes of Health. The Government has certain rights in the invention.

1. INTRODUCTION

The present invention relates, first, to DP178 15 (SEQ ID NO:1), a peptide corresponding to amino acids 638 to 673 of the HIV-1_{IAI} transmembrane protein (TM) qp41, and portions or analogs of DP178 (SEQ ID NO:1), which exhibit anti-membrane fusion capability, 20 antiviral activity, such as the ability to inhibit HIV transmission to uninfected CD-4⁺ cells, or an ability to modulate intracellular processes involving coiledcoil peptide structures. Further, the invention relates to the use of DP178 (SEQ ID NO:1) and DP178 portions and/or analogs as antifusogenic or antiviral compounds or as inhibitors of intracellular events involving coiled-coil peptide structures. The present invention also relates to peptides analogous to DP107 (SEQ ID NO:25), a peptide corresponding to amino acids 558 to 595 of the HIV-1_{LAI} transmembrane protein (TM) gp41, having amino acid sequences present in other viruses, such as enveloped viruses, and/or other organisms, and further relates to the uses of such peptides. These peptides exhibit anti-membrane fusion capability, antiviral activity, or the ability to

modulate intracellular processes involving coiled-coil peptide structures. The present invention additionally relates to methods for identifying compounds that disrupt the interaction between DP178 and DP107, and/or between DP107-like and DP178-like peptides. Further, the invention relates to the use of the peptides of the invention as diagnostic agents. For example, a DP178 peptide may be used as an HIV subtype-specific diagnostic. The invention is demonstrated, first, by way of an Example wherein DP178 (SEQ ID:1), and a peptide whose sequence is homologous to DP178 are each shown to be potent, noncytotoxic inhibitors of HIV-1 transfer to uninfected CD-4 cells. The invention is further demonstrated by Examples wherein peptides having structural and/or amino acid motif similarity to DP107 and DP178 are identified in a variety of viral and nonviral organisms, and in examples wherein a number of such identified peptides derived from several different viral systems are demonstrated to exhibit antiviral activity.

2. BACKGROUND OF THE INVENTION

2.1 MEMBRANE FUSION EVENTS

Membrane fusion is a ubiquitous cell biological process (for a review, see White, J.M., 1992, Science 258:917-924). Fusion events which mediate cellular housekeeping functions, such as endocytosis, constitutive secretion, and recycling of membrane components, occur continuously in all eukaryotic cells.

Additional fusion events occur in specialized cells. Intracellularly, for example, fusion events are involved in such processes as occur in regulated exocytosis of hormones, enzymes and neurotransmitters.

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Intercellularly, such fusion events feature prominently in, for example, sperm-egg fusion and myoblast fusion.

Fusion events are also associated with disease states. For example, fusion events are involved in the formation of giant cells during inflammatory reactions, the entry of all enveloped viruses into cells, and, in the case of human immunodeficiency virus (HIV), for example, are responsible for the virally induced cell-cell fusion which leads to cell death.

2.2. THE HUMAN IMMUNODEFICIENCY VIRUS

The human immunodeficiency virus (HIV) has been implicated as the primary cause of the slowly 15 degenerative immune system disease termed acquired immune deficiency syndrome (AIDS) (Barre-Sinoussi, F. et_al., 1983, Science 220:868-870; Gallo, R. et_al., 1984, Science 224:500-503). There are at least two distinct types of HIV: HIV-1 (Barre-Sinoussi, F. et 20 al., 1983, Science 220:868-870; Gallo R. et al., 1984, Science 224:500-503) and HIV-2 (Clavel, F. et al., 1986, Science 233:343-346; Guyader, M. et al., 1987, Nature 326:662-669). Further, a large amount of genetic heterogeneity exists within populations of 25 each of these types. Infection of human CD-4 Tlymphocytes with an HIV virus leads to depletion of the cell type and eventually to opportunistic infections, neurological dysfunctions, neoplastic growth, and ultimately death.

HIV is a member of the lentivirus family of retroviruses (Teich, N. et al., 1984, RNA Tumor Viruses, Weiss, R. et al., eds., CSH-Press, pp. 949-956). Retroviruses are small enveloped viruses that contain a diploid, single-stranded RNA genome, and

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replicate via a DNA intermediate produced by a virally-encoded reverse transcriptase, an RNA-dependent DNA polymerase (Varmus, H., 1988, Science 240:1427-1439). Other retroviruses include, for example, oncogenic viruses such as human T-cell leukemia viruses (HTLV-I,-II,-III), and feline leukemia virus.

The HIV viral particle consists of a viral core, composed of capsid proteins, that contains the viral RNA genome and those enzymes required for early replicative events. Myristylated Gag protein forms an outer viral shell around the viral core, which is, in turn, surrounded by a lipid membrane enveloped derived from the infected cell membrane. The HIV enveloped surface glycoproteins are synthesized as a single 160 Kd precursor protein which is cleaved by a cellular protease during viral budding into two glycoproteins, gp41 and gp120. gp41 is a transmembrane protein and gp120 is an extracellular protein which remains non-covalently associated with gp41, possibly in a trimeric or multimeric form (Hammarskjold, M. and Rekosh, D., 1989, Biochem. Biophys. Acta 989:269-280).

HIV is targeted to CD-4⁺ cells because the CD-4 cell surface protein acts as the cellular receptor for the HIV-1 virus (Dalgleish, A. et al., 1984, Nature 312:763-767; Klatzmann et al., 1984, Nature 312:767-768; Maddon et al., 1986, Cell 47:333-348). Viral entry into cells is dependent upon gp120 binding the cellular CD-4⁺ receptor molecules (McDougal, J.S. et al., 1986, Science 231:382-385; Maddon, P.J. et al., 1986, Cell 47:333-348) and thus explains HIV's tropism for CD-4⁺ cells, while gp41 anchors the enveloped glycoprotein complex in the viral membrane.

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2.3. HIV TREATMENT

HIV infection is pandemic and HIV associated diseases represent a major world health problem. Although considerable effort is being put into the successful design of effective therapeutics, currently no curative anti-retroviral drugs against AIDS exist. In attempts to develop such drugs, several stages of the HIV life cycle have been considered as targets for therapeutic intervention (Mitsuya, H. et al., 1991, FASEB J. 5:2369-2381). For example, virally encoded reverse transcriptase has been one focus of drug development. A number of reverse-transcriptasetargeted drugs, including 2',3'-dideoxynucleoside analogs such as AZT, ddI, ddC, and d4T have been developed which have been shown to been active against HIV (Mitsuya, H. et al., 1991, Science 249:1533-1544). While beneficial, these nucleoside analogs are not curative, probably due to the rapid appearance of drug resistant HIV mutants (Lander, B. et al., 1989, Science 243:1731-1734). In addition, the drugs often exhibit toxic side effects such as bone marrow suppression, vomiting, and liver function abnormalities.

which can inhibit viral entry into the cell, the earliest stage of HIV infection. Here, the focus has thus far been on CD4, the cell surface receptor for HIV. Recombinant soluble CD4, for example, has been shown to inhibit infection of CD-4+ T-cells by some HIV-1 strains (Smith, D.H. et al., 1987, Science 238:1704-1707). Certain primary HIV-1 isolates, however, are relatively less sensitive to inhibition by recombinant CD-4 (Daar, E. et al., 1990, Proc. Natl. Acad. Sci. USA 87:6574-6579). In addition,

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recombinant soluble CD-4 clinical trials have produced inconclusive results (Schooley, R. et al., 1990, Ann. Int. Med. 112:247-253; Kahn, J.O. et al., 1990, Ann. Int. Med. 112:254-261; Yarchoan, R. et al., 1989, Proc. Vth Int. Conf. on AIDS, p. 564, MCP 137).

The late stages of HIV replication, which involve crucial virus-specific secondary processing of certain viral proteins, have also been suggested as possible anti-HIV drug targets. Late stage processing is dependent on the activity of a viral protease, and drugs are being developed which inhibit this protease (Erickson, J., 1990, Science 249:527-533). The clinical outcome of these candidate drugs is still in question.

Attention is also being given to the development 15 of vaccines for the treatment of HIV infection. HIV-1 enveloped proteins (gp160, gp120, gp41) have been shown to be the major antigens for anti-HIV antibodies present in AIDS patients (Barin, et al., 1985, Science 228:1094-1096). Thus far, therefore, 20 these proteins seem to be the most promising candidates to act as antigens for anti-HIV vaccine development. To this end, several groups have begun to use various portions of gp160, gp120, and/or gp41 as immunogenic targets for the host immune system. 25 See for example, Ivanoff, L. et al., U.S. Pat. No. 5,141,867; Saith, G. et al., WO 92/22,654; Shafferman, A., WO 91/09,872; Formoso, C. et al., WO 90/07,119. Clinical results concerning these candidate vaccines, however, still remain far in the future.

Thus, although a great deal of effort is being directed to the design and testing of anti-retroviral drugs, a truly effective, non-toxic treatment is still needed.

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3. SUMMARY OF THE INVENTION

The present invention relates, first, to DP178 (SEQ ID:1), a 36-amino acid synthetic peptide corresponding to amino acids 638 to 673 of the transmembrane protein (TM) gp41 from the HIV-1 isolate LAI (HIV-1_{LAI}), which exhibits potent anti-HIV-1 activity. As evidenced by the Example presented below, in Section 6, the DP178 (SEQ ID:1) antiviral activity is so high that, on a weight basis, no other known anti-HIV agent is effective at concentrations as low as those at which DP178 (SEQ ID:1) exhibits its inhibitory effects.

The invention further relates to those portions and analogs of DP178 which also show such antiviral activity, and/or show anti-membrane fusion capability, or an ability to modulate intracellular processes involving coiled-coil peptide structures. The term "DP178 analog" refers to a peptide which contains an amino acid sequence corresponding to the DP178 peptide sequence present within the gp41 protein of HIV-1141, but found in viruses and/or organisms other than HIV-1LAI. Such DP178 analog peptides may, therefore, correspond to DP178-like amino acid sequences present in other viruses, such as, for example, enveloped viruses, such as retroviruses other than HIV-1LAI, as well as non-enveloped viruses. Further, such analogous DP178 peptides may also correspond to DP178like amino acid sequences present in nonviral organisms.

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The invention further relates to peptides DP107 (SEQ ID NO:25) analogs. DP107 is a peptide corresponding to amino acids 558-595 of the HIV-1_{LAI} transmembrane protein (TM) gp41. The term "DP107 analog" as used herein refers to a peptide which contains an amino acid sequence corresponding to the

DP107 peptide sequence present within the gp41 protein of HIV-1_{LAI}, but found in viruses and organisms other than HIV-1_{LAI}. Such DP107 analog peptides may, therefore, correspond to DP107-like amino acid sequences present in other viruses, such as, for for example, enveloped viruses, such as retroviruses other than HIV-1_{LAI}, as well as non-enveloped viruses. Further, such DP107 analog peptides may also correspond to DP107-like amino acid sequences present in nonviral organisms.

Further, the peptides of the invention include DP107 analog and DP178 analog peptides having amino acid sequences recognized or identified by the 107x178x4, ALLMOTI5 and/or PLZIP search motifs described herein.

The peptides of the invention may, for example, exhibit antifusogenic activity, antiviral activity, and/or may have the ability to modulate intracellular processes which involve coiled-coil peptide structures. With respect to the antiviral activity of the peptides of the invention, such an antiviral activity includes, but is not limited to the inhibition of HIV transmission to uninfected CD-4⁺ cells. Additionally, the antifusogenic capability, antiviral activity or intracellular modulatory activity of the peptides of the invention merely requires the presence of the peptides of the invention, and, specifically, does not require the stimulation of a host immune response directed against such peptides.

The peptides of the invention may be used, for example, as inhibitors of membrane fusion-asociated events, such as, for example, the inhibition of human and non-human retroviral, especially HIV, transmission to uninfected cells. It is further contemplated that

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the peptides of the invention may be used as modulators of intracellular events involving coiled-coil peptide structures.

The peptides of the invention may, alternatively, be used to identify compounds which may themselves exhibit antifusogenic, antiviral, or intracellular modulatory activity. Additional uses include, for example, the use of the peptides of the invention as organism or viral type and/or subtype-specific diagnostic tools.

The terms "antifusogenic" and "anti-membrane fusion", as used herein, refer to an agent's ability to inhibit or reduce the level of membrane fusion events between two or more moieties relative to the level of membrane fusion which occurs between said moieties in the absence of the peptide. The moieties may be, for example, cell membranes or viral structures, such as viral envelopes or pili. "antiviral", as used herein, refers to the compound's ability to inhibit viral infection of cells, via, for example, cell-cell fusion or free virus infection. Such infection may involve membrane fusion, as occurs in the case of enveloped viruses, or some other fusion event involving a viral structure and a cellular structure (e.g., such as the fusion of a viral pilus and bacterial membrane during bacterial conjugation).

It is also contemplated that the peptides of the invention may exhibit the ability to modulate intracellular events involving coiled-coil peptide structures. "Modulate", as used herein, refers to a stimulatory or inhibitory effect on the intracellular process of interest relative to the level or activity of such a process in the absence of a peptide of the invention.

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Embodiments of the invention are demonstrated below wherein an extremely low concentration of DP178 (SEQ ID:1), and very low concentrations of a DP178 homolog (SEQ ID:3) are shown to be potent inhibitors of HIV-1 mediated CD-4* cell-cell fusion (i.e., syncytial formation) and infection of CD-4* cells by cell-free virus. Further, it is shown that DP178 (SEQ ID:1) is not toxic to cells, even at concentrations 3 logs higher than the inhibitory DP-178 (SEQ ID:1) concentration.

The present invention is based, in part, on the surprising discovery that the DP107 and DP178 domains of the HIV gp41 protein non-covalently complex with each other, and that their interaction is required for the normal infectivity of the virus. This discovery is described in the Example presented, below, in Section 8. The invention, therefore, further relates to methods for identifying antifusogenic, including antiviral, compounds that disrupt the interaction between DP107 and DP178, and/or between DP107-like and DP178-like peptides.

Additional embodiments of the invention (specifically, the Examples presents in Sections 9-16 and 19-25, below) are demonstrated, below, wherein peptides, from a variety of viral and nonviral sources, having structural and/or amino acid motif similarity to DP107 and DP178 are identified, and search motifs for their identification are described. Further, Examples (in Sections 17, 18, 25-29) are presented wherein a number of the peptides of the invention are demonstrated exhibit substantial antiviral activity or activity predictive of antiviral activity.

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3.1. DEFINITIONS

Peptides are defined herein as organic compounds comprising two or more amino acids covalently joined by peptide bonds. Peptides may be referred to with respect to the number of constituent amino acids, i.e., a dipeptide contains two amino acid residues, a tripeptide contains three, etc. Peptides containing ten or fewer amino acids may be referred to as oligopeptides, while those with more than ten amino acid residues are polypeptides. Such peptides may also include any of the modifications and additional amino and carboxy groups as are described herein.

Peptide sequences defined herein are represented by one-letter symbols for amino acid residues as follows:

- A (alanine)
- R (arginine)
- N (asparagine)
- D (aspartic acid)
- C (cysteine)
- 20 Q (glutamine)
 - E (glutamic acid)
 - G (glycine)
 - H (histidine)
 - I (isoleucine)
 - L (leucine)
 - K (lysine)
 - M (methionine)
- 25 F (phenylalanine)
 - P (proline)
 - S (serine)
 - T (threonine)
 - W (tryptophan)
 - Y (tyrosine)
 - V (valine)

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4. BRIEF DESCRIPTION OF THE FIGURES

- FIG. 1. Amino acid sequence of DP178 (SEQ ID:1) derived from HIV1AI; DP178 homologs derived from HIV-1sp (DP-185; SEQ ID:3), HIV-1gr (SEQ ID:4), and HIV-1mv (SEQ ID:5); DP178 homologs derived from amino acid sequences of two prototypic HIV-2 isolates, namely, HIV-2_{md} (SEQ ID:6) and HIV-2_{MHZ} (SEQ ID:7); control peptides: DP-180 (SEQ ID:2), a peptide incorporating the amino acid residues of DP178 in a scrambled sequence; DP-118 (SEQ ID:10) unrelated to DP178, which 10 inhibits HIV-1 cell free virus infection; DP-125 (SEQ ID:8), unrelated to DP178, also inhibits HIV-1 cell free virus infection; DP-116 (SEQ ID:9), unrelated to DP178, is negative for inhibition of HIV-1 infection when tested using a cell-free virus infection assay. Throughout the figures, the one letter amino acid code is used.
 - Inhibition of HIV-1 cell-free virus FIG. 2. infection by synthetic peptides. IC50 refers to the concentration of peptide that inhibits RT production from infected cells by 50% compared to the untreated control. Control: the level of RT produced by untreated cell cultures infected with the same level of virus as treated cultures.

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- Inhibition of HIV-1 and HIV-2 cell-free FIG. 3. 25 virus infection by the synthetic peptide DP178 (SEQ ID:1). ICm: concentration of peptide that inhibits RT production by 50% compared to the untreated control. Control: Level of RT produced by untreated cell cultures infected with the same level of virus as 30 treated cultures.
 - FIG. 4A-4B. Fusion Inhibition Assays. FIG 4A: DP178 (SEQ ID:1) inhibition of HIV-1 prototypic isolate-mediated syncytial formation; data represents the number of virus-induced syncytial per cell. FIG.

4B: DP-180 (SEQ ID:2) represents a scrambled control peptide; DP-185 (SEQ ID:3) represents a DP178 homolog derived from HIV-1_{8P2} isolate; Control, refers to the number of syncytial produced in the absence of peptide.

- FIG. 5. Fusion inhibition assay: HIV-1 vs. HIV-2. Data represents the number of virus-induced syncytial per well. ND: not done.
- FIG. 6. Cytotoxicity study of DP178 (SEQ ID:1)
 and DP-116 (SEQ ID:9) on CEM cells. Cell
 proliferation data is shown.
- and maltose binding protein (MBP)-gp41 fusion proteins. DP107 and DP178 are synthetic peptides based on the two putative helices of gp41. The letter P in the DP107 boxes denotes an Ile to Pro mutation at amino acid number 578. Amino acid residues are numbered according to Meyers et al., "Human Retroviruses and AIDS", 1991, Theoret. Biol. and Biophys. Group, Los Alamos Natl. Lab., Los Alamos, NM. The proteins are more fully described, below, in Section 8.1.1.
 - FIG. 8. A point mutation alters the conformation and anti-HIV activity of M41.
- FIG. 9. Abrogation of DP178 anti-HIV activity.

 Cell fusion assays were carried out in the presence of 10 nM DP178 and various concentrations of M41Δ178 or M41PΔ178.
 - FIG. 10. Binding of DP178 to leucine zipper of gp41 analyzed by FAb-D ELISA.
- FIG. 11A-B. Models for a structural transition in the HIV-1 TM protein. Two models are proposed which indicate a structural transition from a native oligomer to a fusogenic state following a trigger event (possibly gp120 binding to CD4). Common

features of both models include (1) the native state is held together by noncovalent protein-protein interactions to form the heterodimer of gp120/41 and other interactions, principally though gp41 interactive sites, to form homo-oligomers on the virus surface of the gp120/41 complexes; (2) shielding of the hydrophobic fusogenic peptide at the N-terminus (F) in the native state; and (3) the leucine zipper domain (DP107) exists as a homo-oligomer coiled coil only in the fusogenic state. The major differences in the two models include the structural state (native or fusogenic) in which the DP107 and DP178 domains are complexed to each other. In the first model (FIG. 11A) this interaction occurs in the native state and in the second (FIG. 11B), it occurs during the fusogenic state. When triggered, the fusion complex in the model depicted in (A) is generated through formation of coiled-coil interactions in homologous DP107 domains resulting in an extended α -helix. This conformational change positions the fusion peptide for interaction with the cell membrane. In the second model (FIG. 11B), the fusogenic complex is stabilized by the association of the DP178 domain with the DP107 coiled-coil.

FIG. 12. Motif design using heptad repeat positioning of amino acids of known coiled-coils.

FIG. 13. Motif design using proposed heptad repeat positioning of amino acids of DP107 and DP178.

FIG. 14. Hybrid motif design crossing GCN4 and DP107.

FIG. 15. Hybrid motif design crossing GCN4 and DP178.

FIG. 16. Hybrid motif design 107x178x4, crossing DP107 and DP178. This motif was found to be

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the most consistent at identifying relevant DP107-like and DP178-like peptide regions.

FIG. 17. Hybrid motif design crossing GCN4, DP107, and DP178.

FIG. 18. Hybrid motif design ALLMOTI5 crossing GCN4, DP107, DP178, c-Fos c-Jun, c-Myc, and Flu Loop 36.

FIG. 19. PLZIP motifs designed to identify N-terminal proline-leucine zipper motifs.

FIG. 20. Search results for HIV-1 (BRU 10 isolate) enveloped protein gp41. Sequence search motif designations: Spades (♠): 107x178x4; Hearts (♥) ALLMOTI5; Clubs (4): PLZIP; Diamonds (4): transmembrane region (the putative transmembrane domains were identified using a PC/Gene program 15 designed to search for such peptide regions). Asterisk (*): Lupas method. The amino acid sequences identified by each motif are bracketed by the respective characters. Representative sequences chosen based on 107x178x4 searches are underlined and 20 in bold. DP107 and DP178 sequences are marked, and additionally double-underlined and italicized.

FIG. 21. Search results for human respiratory syncytial virus (RSV) strain A2 fusion glycoprotein F1. Sequence search motif designations are as in FIG. 20.

FIG. 22. Search results for simian immunodeficiency virus (SIV) enveloped protein gp41 (AGM3 isolate). Sequence search motif designations are as in FIG. 20.

FIG. 23. Search results for canine distemper virus (strain Onderstepoort) fusion glycoprotein 1. Sequence search motif designations are as in FIG. 20.

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FIG. 24. Search results for newcastle disease virus (strain Australia-Victoria/32) fusion glycoprotein F1. Sequence search motif designations are as in FIG. 20.

FIG. 25. Search results for human parainfluenza 3 virus (strain NIH 47885) fusion glycoprotein F1. Sequence search motif designations are as in FIG. 20.

virus (strain A/AICHI/2/68) hemagglutinin precursor

HA2. Seguence search designations are as in FIG. 20.

FIG. 27A-D. Respiratory Syncytial Virus (RSV) peptide antiviral and circular dichroism data. FIG. 27A-B: Peptides derived from the F2 DP178/DP107-like region. Antiviral and CD data. FIG. 27C-D:

Peptides derived from the F1 DP107-like region. Peptide and CD data.

Antiviral activity (AV) is represented by the following qualitative symbols:

"-", negative antiviral activity;

"+/-", antiviral activity at greater than
100μg/ml;

"+", antiviral activity at between $50-100\mu g/ml$; "++", antiviral activity at between $20-50\mu g/ml$; "+++", antiviral activity at between $1-20\mu g/ml$; "++++", antiviral activity at $<1\mu g/ml$.

CD data, referring to the level of helicity is represented by the following qualitative symbol:

"-", no helicity;

"+", 25-50% helicity;

"++", 50-75% helicity;

"+++" 75-100% helicity.

 ${\rm IC}_{50}$ refers to the concentration of peptide necessary to produce only 50% of the number of syncytial relative to infected control cultures

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containing no peptide. IC₅₀ values were obtained using purified peptides only.

FIG. 28A-B. Respiratory Syncytial Virus (RSV) DP178-like region (F1) peptide antiviral and CD data. Antiviral symbols, CD symbols, and IC $_{50}$ are as in FIG. 27A-D. IC $_{50}$ values were obtained using purified peptides only.

FIG. 29A-B. Peptides derived from the HPIV3 F1 DP107-like region. Peptide antiviral and CD data. Antiviral symbols, CD symbols, and IC₅₀ are as in FIG. 27A-D. Purified peptides were used to obtain IC₅₀ values, except where the values are marked by an asterisk (*), in which cases, the IC₅₀ values were obtained using a crude peptide preparation.

FIG. 30A-B. Peptides derived from the HPIV3

F1 DP178-like region. Peptide antiviral and CD data.

Antiviral symbols, CD symbols, and IC₅₀ are as in FIG.

27A-D. Purified peptides were used to obtain IC₅₀

values, except where the values are marked by an

asterisk (*), in which cases, the IC₅₀ values were

obtained using a crude peptide preparation.

FIG. 31. Motif search results for simian immunodeficiency virus (SIV) isolate MM251, enveloped polyprotein gp41. Sequence search designations are as in FIG. 20.

FIG. 32. Motif search results for Epstein-Barr Virus (Strain B95-8), glycoprotein gp110 precursor (designated gp115). BALF4. Sequence search designations are as in FIG. 20.

Barr Virus (Strain B95-8), BZLF1 trans-activator protein (designated EB1 or Zebra). Sequence search designations are as in FIG. 20. Additionally, "@" refers to a well known DNA binding domain and "+" refers to a well known dimerization domain, as defined

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by Flemington and Speck (Flemington, E. and Speck, S.H., 1990, Proc. Natl. Acad. Sci. USA 87:9459-9463).

FIG. 34. Motif search results for measles virus (strain Edmonston), fusion glycoprotein F1. Sequence search designations are as in FIG. 20.

FIG. 35. Motif search results for Hepatitis B Virus (Subtype AYW), major surface antigen precursor S. Sequence search designations are as in FIG. 20.

FIG. 36. Motif search results for simian Mason-Pfizer monkey virus, enveloped (TM) protein qp20. Sequence search designations are as in FIG. 20.

FIG. 37. Motif search results for Pseudomonas aerginosa, fimbrial protein (Pilin). Sequence search designations are as in FIG. 20.

FIG. 38. Motif search results for Neisseria gonorrhoeae fimbrial protein (Pilin). Sequence search designations are as in FIG. 20.

FIG. 39. Motif search results for Hemophilus influenzae fimbrial protein. Sequence search designations are as in FIG. 20.

FIG. 40. Motif search results for Staphylococcus aureus, toxic shock syndrome toxin-1. Sequence search designations are as in FIG. 20.

FIG. 41. Motif search results for Staphylococcus aureus enterotoxin Type E. Sequence search designations are as in FIG. 20.

FIG. 42. Motif search results for Staphylococcus aureus enterotoxin A. Sequence search designations are as in FIG. 20.

FIG. 43. Motif search results for

Escherichia coli, heat labile enterotoxin A. Sequence search designations are as in FIG. 20.

FIG. 44. Motif search results for human cfos proto-oncoprotein. Sequence search designations are as in FIG. 20.

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FIG. 45. Motif search results for human lupus KU autoantigen protein P70. Sequence search designations are as in FIG. 20.

FIG. 46. Motif search results for human zinc finger protein 10. Sequence search designations are as in FIG. 20.

FIG. 47. Measles virus (MeV) fusion protein DP178-like region antiviral and CD data. Antiviral symbols, CD symbols, and IC $_{50}$ are as in FIG. 27A-D. IC $_{50}$ values were obtained using purified peptides.

FIG. 48. Simian immunodeficiency virus (SIV) TM (fusion) protein DP178-like region antiviral data. Antiviral symbols are as in FIG. 27A-D "NT", not tested.

price 49A-C. DP178-derived peptide antiviral data. The peptides listed herein were derived from the region surrounding the HIV-1 BRU isolate DP178 region (e.g., gp41 amino acid residues 615-717).

In instances where peptides contained DP178 point mutations, the mutated amino acid residues are shown with a shaded background. In instances in which the test peptide has had an amino and/or carboxy-terminal group added or removed (apart from the standard amidoand acetyl- blocking groups found on such peptides), such modifications are indicated. FIG. 49A: column to the immediate right of the name of the test peptide indicates the size of the test peptide and points out whether the peptide is derived from a one amino acid peptide "walk" across the DP178 region. The next column to the right indicates whether the test peptide contains a point mutation, while the column to its right indicates whether certain amino acid residues have been added to or removed from the DP178-derived amino acid sequence. FIG 49B: column to the immediate right of the test peptide name

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indicates whether the peptide represents a DP178 truncation, the next column to the right points out whether the peptide contains a point mutation, and the column to its right indicates whether the peptide contains amino acids which have been added to or removed from the DP178 sequence itself. FIG. 49C: The column to the immediate right of the test peptide name indicates whether the test peptide contains a point mutation, while the column to its right indicates whether amino acid residues have been added to or removed from the DP178 sequence itself. IC50 is as defined in FIG. 27A-D, and IC $_{50}$ values were obtained using purified peptides except where marked with an asterisk (*), in which case the IC₅₀ was obtained using a crude peptide preparation. 15

FIG. 50. DP107 and DP107 gp41 region truncated peptide antiviral data. IC_{50} as defined in FIG. 27A-D, and IC_{50} values were obtained using purified peptides except where marked with an asterisk (*), in which case the IC_{50} was obtained using a crude peptide preparation.

FIG. 51A-B. Epstein-Barr virus Strain B95-8 BZLF1 DP178/DP107 analog region peptide walks and electrophoretic mobility shift assay results. The peptides (T-423 to T-446, FIG. 51A; T-447 to T-461, FIG. 51B) represent one amino acid residue "walks" through the EBV Zebra protein region from amino acid residue 173 to 246.

The amino acid residue within this region which corresponds to the first amino acid residue of each peptide is listed to the left of each peptide, while the amino acid residue within this region which corresponds to the last amino acid residue of each peptide is listed to the right of each peptide. The

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length of each test peptide is listed at the far right of each line, under the heading "Res".

"ACT" refers to a test peptide's ability to inhibit Zebra binding to its response element. "+" refers to a visible, but incomplete, abrogation of the response element/Zebra homodimer complex; "+++" refers to a complete abrogation of the complex; and "-" represents a lack of complex disruption.

surface antigen precursor S protein DP178/DP107 analog region and peptide walks. 52A depicts Domain I (S protein amino acid residues 174-220), which contains a potential DP178/DP107 analog region. In addition, peptides are listed which represent one amino acid peptide "walks" through domain I. 52B depicts Domain II (S protein amino acid residues 233-291), which contains a second potential DP178/DP107 analog region. In addition, peptides are listed which represent one amino acid peptide "walks" through domain II.

5. <u>DETAILED DESCRIPTION OF THE INVENTION</u>

Described herein are peptides which may exhibit antifusogenic activity, antiviral capability, and/or the ability to modulate intracellular processes involving coiled-coil peptide structures. The peptides described include, first, DP178 (SEQ ID NO:1), a gp41-derived 36 amino acid peptide and fragments and analogs of DP178.

In addition, the peptides of the invention described herein include peptides which are DP107 analogs. DP107 (SEQ ID NO:25) is a 38 amino acid peptide corresponding to residues 558 to 595 of the HIV-1_{LAI} transmembrane (TM) gp41 protein. Such DP107 analogs may exhibit antifusogenic capability, antiviral activity or an ability to modulate

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intracellular processes involving coiled-coil structures.

Further, peptides of the invention include DP107 and DP178 are described herein having amino acid sequences recognized by the 107x178x4, ALLMOTI5, and PLZIP search motifs. Such motifs are also discussed.

Also described here are antifusogenic, antiviral, intracellular modulatory, and diagnostic uses of the peptides of the invention. Further, procedures are described for the use of the peptides of the invention for the identification of compounds exhibiting antifusogenic, antiviral or intracellular modulatory activity.

While not limited to any theory of operation, the following model is proposed to explain the potent anti-HIV activity of DP178, based, in part, on the 15 experiments described in the Examples, infra. In the HIV protein, gp41, DP178 corresponds to a putative α helix region located in the C-terminal end of the gp41 ectodomain, and appears to associate with a distal site on gp41 whose interactive structure is influenced by the leucine zipper motif, a coiled-coil structure, referred to as DP107. The association of these two domains may reflect a molecular linkage or "molecular clasp" intimately involved in the fusion process. It is of interest that mutations in the C-terminal α helix motif of gp41 (i.e., the D178 domain) tend to enhance the fusion ability of gp41, whereas mutations in the leucine zipper region (i.e., the DP107 domain) decrease or abolish the fusion ability of the viral protein. It may be that the leucine zipper motif is involved in membrane fusion while the C-terminal α helix motif serves as a molecular safety to regulate the availability of the leucine zipper during virusinduced membrane fusion.

On the basis of the foregoing, two models are proposed of gp41-mediated membrane fusion which are schematically shown in FIG. 11A-B. The reason for proposing two models is that the temporal nature of the interaction between the regions defined by DP107 and DP178 cannot, as yet, be pinpointed. Each model envisions two conformations for gp41 - one in a "native" state as it might be found on a resting virion. The other in a "fusogenic" state to reflect conformational changes triggered following binding of 10 gp120 to CD4 and just prior to fusion with the target cell membrane. The strong binding affinity between gp120 and CD4 may actually represent the trigger for the fusion process obviating the need for a pH change such as occurs for viruses that fuse within 15 intracellular vesicles. The two major features of both models are: (1) the leucine zipper sequences (DP107) in each chain of oligomeric enveloped are held apart in the native state and are only allowed access to one another in the fusogenic state so as to form 20 the extremely stable coiled-coils, and (2) association of the DP178 and DP107 sites as they exist in gp41 occur either in the native or fusogenic state. FIG. 11A depicts DP178/DP107 interaction in the native state as a molecular clasp. On the other hand, if one 25 assumes that the most stable form of the enveloped occurs in the fusogenic state, the model in FIG. 11B can be considered.

When synthesized as peptides, both DP107 and DP178 are potent inhibitors of HIV infection and fusion, probably by virtue of their ability to form complexes with viral gp41 and interfere with its fusogenic process; e.g., during the structural transition of the viral protein from the native structure to the fusogenic state, the DP178 and DP107

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> peptides may gain access to their respective binding sites on the viral gp41, and exert a disruptive influence. DP107 peptides which demonstrate anti-HIV activity are described in Applicants' co-pending application Serial No. 08/264,531, filed June 23, 1994, which is incorporated by reference herein in its entirety.

As shown in the Examples, infra, a truncated recombinant gp41 protein corresponding to the ectodomain of gp41 containing both DP107 and DP178 domains (excluding the fusion peptide, transmembrane region and cytoplasmic domain of gp41) did not inhibit HIV-1 induced fusion. However, when a single mutation was introduced to disrupt the coiled-coil structure of the DP107 domain -- a mutation which results in a total loss of biological activity of DP107 peptides -the inactive recombinant protein was transformed to an active inhibitor of HIV-1 induced fusion. This transformation may result from liberation of the potent DP178 domain from a molecular clasp with the 20 leucine zipper, DP107 domain.

For clarity of discussion, the invention will be described primarily for DP178 peptide inhibitors of HIV. However, the principles may be analogously applied to other viruses, both enveloped and nonenveloped, and to other non-viral organisms.

5.1. DP178 AND DP178-LIKE PEPTIDES

The DP178 peptide (SEQ ID:1) of the invention corresponds to amino acid residues 638 to 673 of the transmembrane protein gp41 from the HIV-1LAI isolate, 30 and has the 36 amino acid sequence (reading from amino to carboxy terminus):

 $\mathrm{NH_{2} ext{-}YTSLIHSLIEESQNQQEKNEQELLELDKWASLWNWF-COOH}$ (SEQ ID:1)

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In addition to the full-length DP178 (SEQ ID:1) 36-mer, the peptides of the invention may include truncations of the DP178 (SEQ ID:1) peptide which exhibit antifusogenic activity, antiviral activity and/or the ability to modulate intracellular processes involving coiled-coil peptide structures. Truncations of DP178 (SEQ ID:1) peptides may comprise peptides of between 3 and 36 amino acid residues (i.e., peptides ranging in size from a tripeptide to a 36-mer polypeptide), as shown in Tables I and IA, below. 10 Peptide sequences in these tables are listed from amino (left) to carboxy (right) terminus. "X" may represent an amino group (-NH2) and "Z" may represent a carboxyl (-COOH) group. Alternatively, "X" may represent a hydrophobic group, including but not 15 limited to carbobenzyl, dansyl, or T-butoxycarbonyl; an acetyl group; a 9-fluorenylmethoxy-carbonyl (FMOC) group; or a covalently attached macromolecular group, including but not limited to a lipid-fatty acid conjugate, polyethylene glycol, carbohydrate or 20 peptide group. Further, "2" may represent an amido group; a T-butoxycarbonyl group; or a covalently attached macromolecular group, including but not limited to a lipid-fatty acid conjugate, polyethylene glycol, carbohydrate or peptide group. A preferred 25 "X" or "Z" macromolecular group is a peptide group.

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TABLE I DP178 (SEO ID:1) CARBOXY TRUNCATIONS

X-YTS-Z X-YTSL-Z X-YTSLI-Z X-YTSLIH-Z X-YTSLIHS-Z X-YTSLIHSL-Z X-YTSLIHSLI-Z X-YTSLIHSLIE-Z X-YTSLIHSLIEE-Z X-YTSLIHSLIEES-Z X-YTSLIHSLIEESQ-Z X-YTSLIHSLIEESQN-Z X-YTSLIHSLIEESONO-Z X-YTSLIHSLIEESQNQQ-Z X-YTSLIHSLIEESQNQQE-Z X-YTSLIHSLIEESQNQQEK-Z X-YTSLIHSLIEESONQQEKN-Z X-YTSLIHSLIEESQNQQEKNE-Z X-YTSLIHSLIEESONQOEKNEQ-Z 15 X-YTSLIHSLIEESQNQQEKNEQE-Z X-YTSLIHSLIEESONQQEKNEQEL-Z X-YTSLIHSLIEESQNQQEKNEQELL-Z X-YTSLIHSLIEESQNQQEKNEQELLE-Z X-YTSLIHSLIEESQNQQEKNEQELLEL-Z X-YTSLIHSLIEESQNQQEKNEQELLELD-Z X-YTSLIHSLIEESQNQQEKNEQELLELDK-Z X-YTSLIHSLIEESQNQQEKNEQELLELDKW-Z X-YTSLIHSLIEESQNQQEKNEQELLELDKWA-Z X-YTSLIHSLIEESQNQQEKNEQELLELDKWAS-Z X-YTSLIHSLIEESQNQQEKNEQELLELDKWASL-Z X-YTSLIHSLIEESQNQQEKNEQELLELDKWASLW-Z X-YTSLIHSLIEESQNQQEKNEQELLELDKWASLWN-Z X-YTSLIHSLIEESQNQQEKNEQELLELDKWASLWNW-Z X-YTSLIHSLIEESQNQQEKNEQELLELDKWASLWNWF-Z 25

The one letter amino acid code is used.

Additionally,

"X" may represent an amino group, a hydrophobic group, including but not limited to carbobenzoxyl, dansyl, or T-butyloxycarbonyl; an acetyl group; a 9-fluorenylmethoxy-carbonyl (FMOC) group; a macromolecular carrier group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.

"Z" may represent a carboxyl group; an amido group; a T-butyloxycarbonyl group; a macromolecular carrier group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.

TABLE IA DP178 (SEO ID:1) AMINO TRUNCATIONS

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X-NWF-Z
                                                    X-WNWF-Z
                                                   X-LWNWF-Z
                                                  X-SLWNWF-Z
 5
                                                 X-ASLWNWF-Z
                                                X-WASLWNWF-Z
                                               X-KWASLWNWF-2
                                              X-DKWASLWNWF-Z
                                             X-LDKWASLWNWF-Z
                                            X-ELDKWASLWNWF-Z
                                           X-LELDKWASLWNWF-Z
                                          X-LLELDKWASLWNWF-Z
10
                                         X-ELLELDKWASLWNWF-2
                                        X-QELLELDKWASLWNWF-Z
                                       X-EQELLELDKWASLWNWF-Z
                                      X-NEQELLELDKWASLWNWF-Z
                                     X-KNEQELLELDKWASLWNWF-Z
                                    X-EKNEOELLELDKWASLWNWF-Z
                                  X-OEKNEOELLELDKWASLWNWF-Z
15
                                 X-QQEKNEQELLELDKWASLWNWF-Z
                                X-NQQEKNEQELLELDKWASLWNWF-Z
                               X-QNQQEKNEOELLELDKWASLWNWF-Z
                              X-SQNQQEKNEQELLELDKWASLWNWF-Z
                             X-ESQNQQEKNEQELLELDKWASLWNWF-Z
                            X-EESQNQQEKNEQELLELDKWASLWNWF-Z
                           X-IEESONOOEKNEOELLELDKWASLWNWF-Z
                          X-LIEESQNQQEKNEQELLELDKWASLWNWF-Z
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                         X-SLIEESONOOEKNEOELLELDKWASLWNWF-Z
                        X-HSLIEESQNQOEKNEOELLELDKWASLWNWF-Z
                       X-IHSLIEESONQOEKNEQELLELDKWASLWNWF-Z
                      X-LIHSLIEESQNQOEKNEOELLELDKWASLWNWF-Z
                     X-SLIHSLIEESQNQQEKNEQELLELDKWASLWNWF-Z
                    X-TSLIHSLIEESQNQQEKNEQELLELDKWASLWNWF-Z
                   X-YTSLIHSLIEESQNQQEKNEQELLELDKWASLWNWF-Z
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The one letter amino acid code is used.

Additionally.

"X" may represent an amino group, a hydrophobic group, including but not limited to carbobenzoxyl, dansyl, or T-butyloxycarbonyl; an acetyl group; a 9fluorenylmethoxy-carbonyl group; a macromolecular carrier group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.

"Z" may represent a carboxyl group; an amido group; a T-butyloxycarbonyl group; a macromolecular carrier 35 group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.

The peptides of the invention also include DP178like peptides. "DP178-like", as used herein, refers, first, to DP178 and DP178 truncations which contain one or more amino acid substitutions, insertions and/or deletions. Second, "DP-178-like" refers to peptide sequences identified or recognized by the ALIMOTIS, 107x178x4 and PLZIP search motifs described herein, having structural and/or amino acid motif similarity to DP178. The DP178-like peptides of the invention may exhibit antifusogenic or antiviral activity, or may exhibit the ability to modulate intracellular processes involving coiled-coil peptides. Further, such DP178-like peptides may possess additional advantageous features, such as, for example, increased bioavailability, and/or stability, or reduced host immune recognition.

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HIV-1 and HIV-2 enveloped proteins are structurally distinct, but there exists a striking amino acid conservation within the DP178-corresponding regions of HIV-1 and HIV-2. The amino acid conservation is of a periodic nature, suggesting some conservation of structure and/or function. Therefore, one possible class of amino acid substitutions would include those amino acid changes which are predicted to stabilize the structure of the DP178 peptides of the invention. Utilizing the DP178 and DP178 analog sequences described herein, the skilled artisan can readily compile DP178 consensus sequences and ascertain from these, conserved amino acid residues which would represent preferred amino acid substitutions.

The amino acid substitutions may be of a conserved or non-conserved nature. Conserved amino acid substitutions consist of replacing one or more amino acids of the DP178 (SEQ ID:1) peptide sequence with amino acids of similar charge, size, and/or

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hydrophobicity characteristics, such as, for example, a glutamic acid (E) to aspartic acid (D) amino acid substitution. Non-conserved substitutions consist of replacing one or more amino acids of the DP178 (SEQ ID:1) peptide sequence with amino acids possessing dissimilar charge, size, and/or hydrophobicity characteristics, such as, for example, a glutamic acid (E) to valine (V) substitution.

Amino acid insertions may consist of single amino acid residues or stretches of residues. The insertions may be made at the carboxy or amino terminal end of the DP178 or DP178 truncated peptides, as well as at a position internal to the peptide. Such insertions will generally range from 2 to 15 amino acids in length. It is contemplated that insertions made at either the carboxy or amino terminus of the peptide of interest may be of a broader size range, with about 2 to about 50 amino acids being preferred. One or more such insertions may be introduced into DP178 (SEQ.ID:1) or DP178 truncations, as long as such insertions result in peptides which may still be recognized by the 107x178x4, ALLMOTI5 or PLZIP search motifs described herein, or may, alternatively, exhibit antifusogenic or antiviral activity, or exhibit the ability to modulate intracellular processes involving coiled-coil peptide structures.

Preferred amino or carboxy terminal insertions are peptides ranging from about 2 to about 50 amino acid residues in length, corresponding to gp41 protein regions either amino to or carboxy to the actual DP178 gp41 amino acid sequence, respectively. Thus, a preferred amino terminal or carboxy terminal amino acid insertion would contain gp41 amino acid sequences found immediately amino to or carboxy to the DP178 region of the gp41 protein.

Deletions of DP178 (SEQ ID:1) or DP178 truncations are also within the scope of the invention. Such deletions consist of the removal of one or more amino acids from the DP178 or DP178-like peptide sequence, with the lower limit length of the resulting peptide sequence being 4 to 6 amino acids. Such deletions may involve a single contiguous or greater than one discrete portion of the peptide sequences. One or more such deletions may be introduced into DP178 (SEQ.ID:1) or DP178 truncations, 10 as long as such deletions result in peptides which may still be recognized by the 107x178x4, ALLMOTI5 or PLZIP search motifs described herein, or may, alternatively, exhibit antifusogenic or antiviral activity, or exhibit the ability to modulate 15 intracellular processes involving coiled-coil peptide structures.

DP178 analogs are further described, below, in Section 5.3.

5.2. <u>DP107 AND DP107-LIKE PEPTIDES</u>

Further, the peptides of the invention include peptides having amino acid sequences corresponding to DP107 analogs. DP107 is a 38 amino acid peptide which exhibits potent antiviral activity, and corresponds to residues 558 to 595 of HIV-1_{LAI} transmembrane (TM) gp41 protein, as shown here:

 $NH_2-NNLLRAIEAQQHLLQLTVWQIKQLQARILAVERYLKDQ-COOH$ (SEQ ID:25)

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In addition to the full-length DP107 (SEQ ID:25) 38-mer, the peptides of the invention may include truncations of the DP107 (SEQ ID:25) peptide which exhibit antifusogenic activity, antiviral activity and/or the ability to modulate intracellular processes

involving coiled-coil peptide structures. Truncations of DP107 (SEQ ID:25) peptides may comprise peptides of between 3 and 38 amino acid residues (i.e., peptides ranging in size from a tripeptide to a 38-mer polypeptide), as shown in Tables II and IIA, below. Peptide sequences in these tables are listed from amino (left) to carboxy (right) terminus. "X" may represent an amino group (-NH2) and "Z" may represent a carboxyl (-COOH) group. Alternatively, "X" may represent a hydrophobic group, including but not limited to carbobenzyl, dansyl, or T-butoxycarbonyl; an acetyl group; a 9-fluorenylmethoxy-carbonyl (FMOC) group; or a covalently attached macromolecular group, including but not limited to a lipid-fatty acid conjugate, polyethylene glycol, carbohydrate or peptide group. Further, "Z" may represent an amido group; a T-butoxycarbonyl group; or a covalently attached macromolecular group, including but not limited to a lipid-fatty acid conjugate, polyethylene glycol, carbohydrate or peptide group. A preferred "X" or "Z" macromolecular group is a peptide group.

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TABLE II DP107 (SEO ID:25) CARBOXY TRUNCATIONS

X-NNL-Z X-NNLL-Z X-NNLLR-Z X-NNLLRA-Z X-NNLLRAI-Z X-NNLLRAIE-2 X-NNLLRAIEA-Z X-NNLLRAIEAO-Z X-NNLLRAIEAQQ-Z X-NNLLRAIEAOOH-Z X-NNLLRAIEAQQHL-Z X-NNLLRAIEAQQHLL-Z X-NNLLRAIEAOOHLLO-Z X-NNLLRAIEAOOHLLOL-Z X-NNLLRAIEAOOHLLOLT-Z X-NNLLRAIEAQOHLLOLTV-Z X-NNLLRAIEAQQHLLQLTVW-Z X-NNLLRAIEAQQHLLQLTVWQ-Z 15 X-NNLLRAIEAQQHLLQLTVWQI-Z X-NNLLRAIEAQQHLLQLTVWQIK-Z X-NNLLRAIEAQQHLLQLTVWQIKQ-Z X-NNLLRAIEAQQHLLQLTVWQIKQL-Z X-NNLLRAIEAQOHLLQLTVWQIKQLQ-Z X-NNLLRAIEAOOHLLOLTVWOIKOLOA-Z X-NNLLRAIEAQQHLLQLTVWQIKQLQAR-Z X-NNLLRAIEAOOHLLOLTVWOIKOLOARI-Z X-NNLLRAIEAQQHLLQLTVWQIKQLQARIL-Z X-NNLLRAIEAQQHLLQLTVWQIKQLQARILA-Z X-NNLLRAIEAQQHLLQLTVWQIKQLQARILAV-Z X-NNLLRAIEAQOHLLQLTVWQIKOLOARILAVE-Z X-NNLLRAIEAQQHLLQLTVWQIKQLQARILAVER-Z X-NNLLRAIEAQQHLLQLTVWQIKQLQARILAVERY-Z 149 X-NNLLRAIEAQQHLLQLTVWQIKQLQARILAVERYL-Z 148 25 X-NNLLRAIEAQQHLLQLTVWQIKQLQARILAVERYLK-Z X-NNLLRAIEACOHLLOLTVWOIKOLOARILAVERYLKD-Z 142 X-NNLLRAIEAOOHLLQLTVWQIKQLQARILAVERYLKDQ-Z

The one letter amino acid code is used.

Additionally,

"X" may represent an amino group, a hydrophobic group, including but not limited to carbobenzoxyl, dansyl, or T-butyloxycarbonyl; an acetyl group; a 9-fluorenylmethoxy-carbonyl (FMOC) group; a macromolecular carrier group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.

"Z" may represent a carboxyl group; an amido group; a T-butyloxycarbonyl group; a macromolecular carrier group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.

DP178 (SEO ID:25) AMINO TRUNCATIONS

```
X-KDQ- Z
                                                    X-LKDQ- Z
                                                  X-YLKDO- Z
 5
                                                 X-RYLKDQ-
                                                X-ERYLKDQ-
                                               X-VERYLKDQ- Z
                                              X-AVERYLKDQ- Z
                                             X-LAVERYLKDO- Z
                                            X-ILAVERYLKDQ- Z
                                           X-RILAVERYLKDO- Z
10
                                          X-ARILAVERYLKDO- Z
                                         X-QARILAVERYLKDO- Z
                                        X-LQARILAVERYLKDQ- Z
                                       X-QLQARILAVERYLKDO-.Z
                                      X-KQLQARILAVERYLKDQ- 2
                                     X-IKQLQARILAVERYLKDQ- Z
                                    X-QIKQLQARILAVERYLKDO- Z
                                   X-WQIKQLQARILAVERYLKDQ- Z
15
                                  X-VWQIKQLQARILAVERYLKDO- Z
                                 X-TVWQIKQLQARILAVERYLKDQ- Z
                                X-LTVWQIKQLQARILAVERYLKDQ- Z
                              X-QLTVWQIKQLQARILAVERYLKDQ- 2
                             X-LQLTVWQIKQLQARILAVERYLKDQ- Z
                            X-LLQLTVWQIKQLQARILAVERYLKDQ- Z
                           X-HLLQLTVWQIKQLQARILAVERYLKDQ- Z
                          X-QHLLQLTVWQIKQLQARILAVERYLKDQ- Z
20
                         X-QQHLLQLTVWQIKQLQARILAVERYLKDQ- Z
                        X-AQQHLLQLTVWQIKQLQARILAVERYLKDQ- Z
                       X-EAQQHLLQLTVWQIKQLQARILAVERYLKDQ- Z
                      X-IEAQQHLLQLTVWQIKQLQARILAVERYLKDQ- Z
                     X-AIEAQQHLLQLTVWQIKQLQARILAVERYLKDQ- Z
                    X-RAIEAQQHLLQLTVWQIKQLQARILAVERYLKDQ- Z
       181
                   X-LRAIEAQQHLLQLTVWQIKQLQARILAVERYLKDQ- Z
       180
25
                  X-LLRAIEAQQHLLQLTVWQIKQLQARILAVERYLKDQ- Z
       179
                 X-NLLRAIEAQQHLLQLTVWQIKQLQARILAVERYLKDQ- Z
                X-NNLLRAIEAQQHLLQLTVWQIKQLQARILAVERYLKDQ- Z
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The one letter amino acid code is used.

Additionally,

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"X" may represent an amino group, a hydrophobic group, including but not limited to carbobenzoxyl, dansyl, or T-butyloxycarbonyl; an acetyl group; a 9-fluorenylmethoxy-carbonyl group; a macromolecular carrier group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.

"Z" may represent a carboxyl group; an amido group; a T-butyloxycarbonyl group; a macromolecular carrier group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.

The peptides of the invention also include DP107-"DP107-like", as used herein, refers, like peptides. first, to DP107 and DP107 truncations which contain one or more amino acid substitutions, insertions and/or deletions. Second, "DP-107-like" refers to peptide sequences identified or recognized by the ALLMOTIS, 107x178x4 and PLZIP search motifs described herein, having structural and/or amino acid motif similarity to DP107. The DP107-like peptides of the invention may exhibit antifusogenic or antiviral activity, or may exhibit the ability to modulate intracellular processes involving coiled-coil peptides. Further, such DP107-like peptides may possess additional advantageous features, such as, for example, increased bioavailability, and/or stability, or reduced host immune recognition.

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HIV-1 and HIV-2 enveloped proteins are structurally distinct, but there exists a striking amino acid conservation within the DP107-corresponding regions of HIV-1 and HIV-2. The amino acid 20 conservation is of a periodic nature, suggesting some conservation of structure and/or function. Therefore, one possible class of amino acid substitutions would include those amino acid changes which are predicted to stabilize the structure of the DP107 peptides of 25 the invention. Utilizing the DP107 and DP107 analog sequences described herein, the skilled artisan can readily compile DP107 consensus sequences and ascertain from these, conserved amino acid residues which would represent preferred amino acid 30 substitutions.

The amino acid substitutions may be of a conserved or non-conserved nature. Conserved amino acid substitutions consist of replacing one or more amino acids of the DP107 (SEQ ID:25) peptide sequence with amino acids of similar charge, size, and/or

> hydrophobicity characteristics, such as, for example, a glutamic acid (E) to aspartic acid (D) amino acid substitution. Non-conserved substitutions consist of replacing one or more amino acids of the DP107 (SEQ ID:25) peptide sequence with amino acids possessing dissimilar charge, size, and/or hydrophobicity characteristics, such as, for example, a glutamic acid (E) to valine (V) substitution.

Amino acid insertions may consist of single amino acid residues or stretches of residues. The insertions may be made at the carboxy or amino terminal end of the DP107 or DP107 truncated peptides, as well as at a position internal to the peptide. Such insertions will generally range from 2 to 15 amino acids in length. It is contemplated that 15 insertions made at either the carboxy or amino terminus of the peptide of interest may be of a broader size range, with about 2 to about 50 amino acids being preferred. One or more such insertions may be introduced into DP107 (SEQ.ID:25) or DP107 truncations, as long as such insertions result in peptides which may still be recognized by the 107x178x4, ALLMOTI5 or PLZIP search motifs described herein, or may, alternatively, exhibit antifusogenic or antiviral activity, or exhibit the ability to modulate intracellular processes involving coiled-coil peptide structures.

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Preferred amino or carboxy terminal insertions are peptides ranging from about 2 to about 50 amino acid residues in length, corresponding to gp41 protein regions either amino to or carboxy to the actual DP107 gp41 amino acid sequence, respectively. Thus, a preferred amino terminal or carboxy terminal amino acid insertion would contain gp41 amino acid sequences found immediately amino to or carboxy to the DP107 region of the gp41 protein.

Deletions of DP107 (SEQ ID:25) or DP178 truncations are also within the scope of the invention. Such deletions consist of the removal of one or more amino acids from the DP107 or DP107-like peptide sequence, with the lower limit length of the resulting peptide sequence being 4 to 6 amino acids. Such deletions may involve a single contiguous or greater than one discrete portion of the peptide sequences. One or more such deletions may be introduced into DP107 (SEQ.ID:25) or DP107 truncations, as long as such deletions result in peptides which may still be recognized by the 107x178x4, ALLMOTI5 or PLZIP search motifs described herein, or may, alternatively, exhibit antifusogenic or antiviral activity, or exhibit the ability to modulate intracellular processes involving coiled-coil peptide structures.

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DP107 and DP107 truncations are more fully described in Applicants' co-pending U.S. Patent Application Ser. No. 08/374,666, filed January 27, 1995, and which is incorporated herein by reference in its entirety. DP107 analogs are further described, below, in Section 5.3.

5.3. DP107 and DP178 ANALOGS

Peptides corresponding to analogs of the DP178, DP178 truncations, DP107 and DP107 truncation sequences of the invention, described, above, in Sections 5.1 and 5.2 may be found in other viruses, including, for example, non-HIV-1_{LAI} enveloped viruses, non-enveloped viruses and other non-viral organisms.

The term "analog", as used herein, refers to a peptide which is recognized or identified via the 107x178x4, ALLMOTI5 and/or PLZIP search strategies discussed below. Further, such peptides may exhibit antifusogenic capability, antiviral activity, or the

ability to modulate intracellular processes involving coiled-coil structures.

Such DP178 and DP107 analogs may, for example, correspond to peptide sequences present in TM proteins of enveloped viruses and may, additionally correspond to peptide sequences present in non enveloped and non-viral organisms. Such peptides may exhibit antifusogenic activity, antiviral activity, most particularly antiviral activity which is specific to the virus in which their native sequences are found, or may exhibit an ability to modulate intracellular processes involving coiled-coil peptide structures.

DP178 analogs are peptides whose amino acid sequences are comprised of the amino acid sequences of peptide regions of, for example, other (<u>i.e.</u>, other than HIV-1_{LAI}) viruses that correspond to the gp41 peptide region from which DP178 (SEQ ID:1) was derived. Such viruses may include, but are not limited to, other HIV-1 isolates and HIV-2 isolates.

DP178 analogs derived from the corresponding gp41 peptide region of other (<u>i.e.</u>, non HIV-1_{LAI}) HIV-1 isolates may include, for example, peptide sequences as shown below.

NH₂-YT<u>NT</u>IYTLLEESQNQQEKNEQELLELDKWASLWNWF-COOH (DP-185; SEQ ID:3);

NH2-YTGIIYNLLEESQNQQEKNEQELLELDKWANLWNWF-COOH (SEQ ID:4);

NH2-YTSLIYSLLEKSQIQQEKNEQELLELDKWASLWNWF-COOH (SEQ ID:5).

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SEQ ID:3 (DP-185), SEQ ID:4, and SEQ ID:5 are derived from HIV- $1_{\rm SF2}$, HIV- $1_{\rm RF}$, and HIV- $1_{\rm MN}$ isolates, respectively. Underlined amino acid residues refer to those residues that differ from the corresponding position in the DP178 (SEQ ID:1) peptide. One such

DP178 analog, DP-185 (SEQ ID:3), is described in the Example presented in Section 6, below, where it is demonstrated that DP-185 (SEQ ID:3) exhibits antiviral activity. The DP178 analogs of the invention may also include truncations, as described above. Further, the analogs of the invention modifications such those described for DP178 analogs in Section 5.1., above. It is preferred that the DP178 analogs of the invention represent peptides whose amino acid sequences correspond to the DP178 region of the gp41 protein, it is also contemplated that the peptides of the invention may, additionally, include amino sequences, ranging from about 2 to about 50 amino acid residues in length, corresponding to gp41 protein regions either amino to or carboxy to the actual DP178 15 amino acid sequence.

Striking similarities, as shown in FIG. 1, exist within the regions of HIV-1 and HIV-2 isolates which correspond to the DP178 sequence. A DP178 analog derived from the HIV-2_{NIHZ} isolate has the 36 amino acid sequence (reading from amino to carboxy terminus):

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NH2-LEANISQSLEQAQIQQEKNMYELQKLNSWDVFTNWL-COOH (SEQ ID:7)

of the HIV-2_{NDHZ} DP178 analog, which may comprise peptides of between 3 and 36 amino acid residues (i.e., peptides ranging in size from a tripeptide to a 36-mer polypeptide). Peptide sequences in these tables are listed from amino (left) to carboxy (right) terminus. "X" may represent an amino group (-NH₂) and "Z" may represent a carboxyl (-COOH) group. Alternatively, "X" may represent a hydrophobic group, including but not limited to carbobenzyl, dansyl, or T-butoxycarbonyl; an acetyl group; a 9-fluorenylmethoxy-carbonyl (FMOC) group; or a

covalently attached macromolecular group, including but not limited to a lipid-fatty acid conjugate, polyethylene glycol, carbohydrate or peptide group. Further, "Z" may represent an amido group; a T-butoxycarbonyl group; or a covalently attached macromolecular group, including but not limited to a lipid-fatty acid conjugate, polyethylene glycol, carbohydrate or peptide group. A preferred "X" or "Z" macromolecular group is a peptide group.

TABLE III

HIV-2_{NIHZ} DP178 analog carboxy truncations.

```
X-LEA-Z
   X-LEAN-Z
   X-LEANI-Z
   X-LEANIS-Z
5 X-LEANISQ-Z
   X-LEANISQS-Z
   X-LEANISQSL-Z
   X-LEANISQSLE-Z
   X-LEANISQSLEQ-Z
   X-LEANISQSLEQA-Z
   X-LEANISOSLEQAQ-Z
   X-LEANISQSLEQAQI-Z
   X-LEANISOSLEQAQIQ-Z
   X-LEANISQSLEQAQIQQ-Z
   X-LEANISQSLEQAQIQQE-Z
   X-LEANISQSLEQAQIQQEK-Z
   X-LEANISQSLEQAQIQQEKN-Z
   X-LEANISOSLEQAQIQQEKNM-Z
   X-LEANISQSLEQAQIQQEKNMY-Z
15 X-LEANISQSLEQAQIQQEKNMYE-Z
   X-LEANISQSLEQAQIQQEKNMYEL-Z
   X-LEANISQSLEQAQIQQEKNMYELQ-Z
    X-LEANISQSLEQAQIQQEKNMYELQK-Z
    X-LEANISQSLEQAQIQQEKNMYELQKL-Z
    X-LEANISQSLEQAQIQQEKNMYELQKLN-Z
    X-LEANISQSLEQAQIQQEKNMYELQKLNS-Z
   X-LEANISQSLEQAQIQQEKNMYELQKLNSW-Z
    X-LEANISQSLEQAQIQQEKNMYELQKLNSWD-Z
    X-LEANISQSLEQAQIQQEKNMYELQKLNSWDV-2
    X-LEANISQSLEQAQIQQEKNMYELQKLNSWDVF-Z
    X-LEANISQSLEQAQIQQEKNMYELQKLNSWDVFT-Z
    X-LEANISQSLEQAQIQQEKNMYELQKLNSWDVFTN-Z
    X-LEANISQSLEQAQIQQEKNMYELQKLNSWDVFTNW-Z
    X-LEANISQSLEQAQIQQEKNMYELQKLNSWDVFTNWL-Z
25
```

The one letter amino acid code is used.

Additionally,

"X" may represent an amino group, a hydrophobic group, including but not limited to carbobenzoxyl, dansyl, or T-butyloxycarbonyl; an acetyl group; a 9-fluorenylmethoxy-carbonyl (FMOC) group; a macromolecular carrier group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.

"Z" may represent a carboxyl group; an amido group; a T-butyloxycarbonyl group; a macromolecular carrier group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.

TABLE IV

HIV-2_{NDHZ} DP178 analog amino truncations.

```
X-NWL-Z
                                                    X-TNWL-Z
                                                   X-FTNWL-Z
                                                  X-VFTNWL-Z
 5
                                                 X-DVFTNWL-Z
                                                X-WDVFTNWL-Z
                                               X-SWDVFTNWL-Z
                                              X-NSWDVFTNWL-Z
                                             X-LNSWDVFTNWL-Z
                                            X-KLNSWDVFTNWL-Z
                                           X-OKLNSWDVFTNWL-Z
                                          X-LQKLNSWDVFTNWL-Z
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                                         X-ELQKLNSWDVFTNWL-Z
                                        X-YELQKLNSWDVFTNWL-Z
                                       X-MYELQKLNSWDVFTNWL-Z
                                      X-NMYELOKLNSWDVFTNWL-Z
                                     X-KNMYELOKLNSWDVFTNWL-Z
                                    X-EKNMYELQKLNSWDVFTNWL-Z
                                   X-QEKNMYELQKLNSWDVFTNWL-Z
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                                 X-QQEKNMYELQKLNSWDVFTNWL-Z
                                X-IQQEKNMYELQKLNSWDVFTNWL-Z
                               X-QIQQEKNMYELQKLNSWDVFTNWL-Z
                               X-AQIQQEKNMYELQKLNSWDVFTNWL-Z
                             X-QAQIQQEKNMYELQKLNSWDVFTNWL-2
                            X-EQAQIQQEKNMYELQKLNSWDVFTNWL-Z
                           X-LEQAQIQOEKNMYELOKLNSWDVFTNWL-Z
                          X-SLEQAQIQQEKNMYELQKLNSWDVFTNWL-Z
20
                         X-OSLEOAOIOOEKNMYELOKLNSWDVFTNWL-Z
                        X-SQSLEQAQIQQEKNMYELQKLNSWDVFTNWL-Z
                       X-ISQSLEQAQIQQEKNMYELQKLNSWDVFTNWL-Z
                      X-NISQSLEQAQIQQEKNMYELQKLNSWDVFTNWL-Z
                     X-ANISQSLEQAQIQQEKNMYELQKLNSWDVFTNWL-Z
                    X-EANISQSLEQAQIQQEKNMYELQKLNSWDVFTNWL-Z
                   X-LEANISQSLEQAQIQOEKNMYELOKLNSWDVFTNWL-Z
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```

The one letter amino acid code is used.

Additionally,

"X" may represent an amino group, a hydrophobic group, including but not limited to carbobenzoxyl, dansyl, or T-butyloxycarbonyl; an acetyl group; a 9-fluorenylmethoxy-carbonyl (FMOC) group; a macromolecular carrier group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.

"2" may represent a carboxyl group; an amido group; a T-butyloxycarbonyl group; a macromolecular carrier
group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.

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DP178 and DP107 analogs are recognized or identified, for example, by utilizing one or more of the 107x178x4, ALLMOTI5 or PLZIP computer-assisted search strategies described and demonstrated, below, in the Examples presented in Sections 9 through 16 and 19 through 25. The search strategy identifies additional peptide regions which are predicted to have structural and/or amino acid sequence features similar to those of DP107 and/or DP178.

The search strategies are described fully, below, in the Example presented in Section 9. While this search strategy is based, in part, on a primary amino acid motif deduced from DP107 and DP178, it is not based solely on searching for primary amino acid sequence homologies, as such protein sequence homologies exist within, but not between major groups of viruses. For example, primary amino acid sequence homology is high within the TM protein of different strains of HIV-1 or within the TM protein of different isolates of simian immunodeficiency virus (SIV). Primary amino acid sequence homology between HIV-1 and SIV, however, is low enough so as not to be useful. It is not possible, therefore, to find peptide regions similar to DP107 or DP178 within other viruses, or within non-viral organisms, whether structurally, or

Further, while it would be potentially useful to identify primary sequence arrangements of amino acids based on, for example, the physical chemical characteristics of different classes of amino acids rather than based on the specific amino acids themselves, such search strategies have, until now, proven inadequate. For example, a computer algorithm designed by Lupas et al. to identify coiled-coil propensities of regions within proteins (Lupas, A., et al., 1991 Science 252:1162-1164) is inadequate for

otherwise, based on primary sequence homology, alone.

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identifying protein regions analogous to DP107 or DP178.

Specifically, analysis of HIV-1 gp160 (containing both gp120 and gp41) using the Lupas algorithm does not identify the coiled-coil region within DP107. It does, however, identify a region within DP178 beginning eight amino acids N-terminal to the start of DP178 and ending eight amino acids from the C-terminus. The DP107 peptide has been shown experimentally to form a stable coiled coil. A search based on the Lupas search algorithm, therefore, would not have identified the DP107 coiled-coil region. Conversely, the Lupas algorithm identified the DP178 region as a potential coiled-coil motif. However, the peptide derived from the DP178 region failed to form a coiled coil in solution.

A possible explanation for the inability of the Lupas search algorithm to accurately identify coiled-coil sequences within the HIV-1 TM, is that the Lupas algorithm is based on the structure of coiled coils from proteins that are not structurally or functionally similar to the TM proteins of viruses, antiviral peptides (e.g. DP107 and DP178) of which are an object of this invention.

The computer search strategy of the invention, as demonstrated in the Examples presented below, in Sections 9 through 16 and 19 through 25, successfully identifies regions of proteins similar to DP107 or DP178. This search strategy was designed to be used with a commercially-available sequence database package, preferably PC/Gene.

A series of search motifs, the 107x178x4,
ALLMOTI5 and PLZIP motifs, were designed and
engineered to range in stringency from strict to
broad, as discussed in this Section and in Section 9,
with 107x178x4 being preferred. The sequences

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> identified via such search motifs, such as those listed in Tables V-XIV, below, potentially exhibit antifusogenic, such as antiviral, activity, may additionally be useful in the identification of antifusogenic, such as antiviral, compounds, and are intended to be within the scope of the invention.

Coiled-coiled sequences are thought to consist of heptad amino acid repeats. For ease of description, the amino acid positions within the heptad repeats are sometimes referred to as A through G, with the first position being A, the second B, etc. The motifs used to identify DP107-like and DP178-like sequences herein are designed to specifically search for and identify such heptad repeats. In the descriptions of each of the motifs described, below, amino acids enclosed by brackets , i.e., [], designate the only amino acid residues that are acceptable at the given position, while amino acids enclosed by braces, i.e., {}, designate the only amino acids which are unacceptable at the given heptad position. When a set of bracketed 20 or braced amino acids is followed by a number in parentheses i.e., (), it refers to the number of subsequent amino acid positions for which the designated set of amino acids hold, e.g, a (2) means "for the next two heptad amino acid positions".

25 The ALLMOTI5 is written as follows:

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 $\{CDGHP\}-\{CFP\}(2)-\{CDGHP\}-\{CFP\}(3) \{CDGHP\}-\{CFP\}(2)-\{CDGHP\}-\{CFP\}(3) \{CDGHP\} - \{CFP\} (2) - \{CDGHP\} - \{CFP\} (3) - \{CDGHP\} - \{CDGHP\} - \{CFP\} (3) - \{CDGHP\} - \{CDGHP$ $\{CDGHP\}-\{CFP\}(2)-\{CDGHP\}-\{CFP\}(3) \{CDGHP\}-\{CFP\}(2)-\{CDGHP\}-\{CFP\}(3)-$

Translating this motif, it would read: "at the 30 first (A) position of the heptad, any amino acid residue except C, D, G, H, or P is acceptable, at the next two (B,C) amino acid positions, any amino acid residue except 3, F, or P is acceptable, at the fourth 35 heptad position (D), any amino acid residue except C,

D. G. H. or P is acceptable, at the next three (E, F, G) amino acid positions, any amino acid residue except C, F, or P is acceptable. This motif is designed to search for five consecutive heptad repeats (thus the repeat of the first line five times), meaning that it searches for 35-mer sized peptides. It may also be designed to search for 28-mers, by only repeating the initial motif four times. With respect to the ALLMOTIS motif, a 35-mer search is preferred. Those viral (non-bacteriophage) sequences identified via such an ALLMOTI5 motif are listed in Table V, below, at the end of this Section. The viral sequences listed in Table V potentially exhibit antiviral activity, may be useful in the the identification of antiviral compounds, and are intended to be within the scope of the invention. In those instances wherein a single gene exhibits greater than one sequence recognized by the ALLMOTI5 search motif, the amino a cid residue numbers of these sequences are listed under "Area 2", Area 3", etc. This convention is used for each of the Tables listed, below, at the end of this Section.

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The 107x178x4 motif is written as follows:

[EFIKLNQSTVWY]-{CFMP}(2)-[EFIKLNQSTVWY]-{CFMP}(3)-[EFIKLNQSTVWY]-{CFMP}(2)-[EFIKLNQSTVWY]-{CFMP}(3)-[EFIKLNQSTVWY]-{CFMP}(2)-[EFIKLNQSTVWY]-{CFMP}(3)-[EFIKLNQSTVWY]-{CFMP}(2)-[EFIKLNQSTVWY]-{CFMP}(3)-

Translating this motif, it would read: "at the first (A) position of the heptad, only amino acid residue E, F, I, K, L, N, Q, S, T, V, W, or Y is acceptable, at the next two (B,C) amino acid positions, any amino acid residue except C, F, M or P is acceptable, at the fourth position (D), only amino acid residue E, F, I, K, L, N, Q, S, T, V, W, or Y is acceptable, at the next three (E, F, G) amino acid positions, any amino acid residue except C, F, M or P is acceptable. This motif is designed to search for

four consecutive heptad repeats (thus the repeat of the first line four times), meaning that it searches for 28-mer sized peptides. It may also be designed to search for 35-mers, by repeating the initial motif five times. With respect to the 107x178x4 motif, a 28-mer search is preferred.

Those viral (non-bacteriophage) sequences identified via such a 107x178x4 motif are listed in Table VI, below, at the end of this Section, with those viral (non-bacteriophage) sequences listed in Table VII, below at the end of this Section, being preferred.

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The 107x178x4 search motif was also utilized to identify non-viral procaryotic protein sequences, as listed in Table VIII, below, at the end of this Section. Further, this search motif was used to reveal a number of human proteins. The results of this human protein 107x178x4 search is listed in Table IX, below, at the end of this Section. The sequences listed in Tables VIII and IX, therefore, reveal peptides which may be useful as antifusogenic compounds or in the identification of antifusogenic compounds, and are intended to be within the scope of the invention.

The PLZIP series of motifs are as listed in FIG.

19. These motifs are designed to identify leucine zipper coiled-coil like heptads wherein at least one proline residue is present at some predefined distance N-terminal to the repeat. These PLZIP motifs find regions of proteins with similarities to HIV-1 DP178 generally located just N-terminal to the transmembrane anchor. These motifs may be translated according to the same convention described above. Each line depicted in FIG. 19 represents a single, complete search motif. "X" in these motifs refers to any amino acid residue. In instances wherein a motif contains

two numbers within parentheses, this refers to a variable number of amino acid residues. For example, X (1,12) is translated to "the next one to twelve amino acid residues, inclusive, may be any amino acid".

Tables X through XIV, below, at the end of this Section, list sequences identified via searches conducted with such PLZIP motifs. Specifically, Table X lists viral sequences identified via PCTLZIP. P1CTLZIP and P2CTLZIP search motifs, Table XI lists viral sequences identified via P3CTLZIP, P4CTLZIP, P5CTLZIP and P6CTLZIP search motifs, Table XII lsts viral sequences identified via P7CTLZIP, P8CTLZIP and P9CTLZIP search motifs, Table XIII lists viral sequences identified via P12LZIPC searches and Table XIV lists viral sequences identified via P23TLZIPC search motifs The viral sequences listed in these tables represent peptides which potentially exhibit antiviral activity, may be useful in the identification of antiviral compounds, and are intended to be within the scope of the invention.

The Examples presented in Sections 17, 18, 26 and 27 below, demonstrate that viral sequences identified via the motif searches described herein identify substantial antiviral characteristics. Specifically, the Example presented in Section 17 describes peptides with anti-respiratory syncytial virus activity, the Example presented in Section 18 describes peptides with anti-parainfluenza virus activity, the Example presented in Section 26 describes peptides with anti-measles virus activity and the Example presented in Section 27 describes peptides with anti-simian immunodeficiency virus activity.

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The DP107 and DP178 analogs may, further, contain any of the additional groups described for DP178, above, in Section 5.1. For example, these peptides

may include any of the additional amino-terminal groups as described above for "X" groups, and may also include any of the carboxy-terminal groups as described, above, for "Z" groups.

Additionally, truncations of the identified DP107 and DP178 peptides are among the peptides of the invention. Further, such DP107 and DP178 analogs and DP107/DP178 analog truncations may exhibit one or more amino acid substitutions, insertion, and/or deletions. The DP178 analog amino acid substitutions, insertions and deletions, are as described, above, for DP178-like peptides in Section 5.1. The DP-107 analog amino acid substitutions, insertions and deletions are also as described, above, for DP107-like peptides in Section 5.2.

15 Tables XV through XXII, below, present representative examples of such DP107/DP178 truncations. Specifically, Table XV presents Respiratory Syncytial Virus F1 region DP107 analog carboxy truncations, Table XVI presents Respiratory 20 Syncytial Virus F1 region DP107 analog amino truncations, Table XVII presents Respiratory Syncytial Virus F1 region DP178 analog carboxy truncations, Table XVIII presents Respiratory Syncytial Virus F1 region DP178 analog amino truncations, Table XIX 25 presents Human Parainfluenza Virus 3 F1 region DP178 analog carboxy truncations, Table XX presents Human Parainfluenza Virus 3 F1 region DP178 analog amino truncations, Table XXI presents Human Parainfluenza Virus 3 F1 region DP107 analog carboxy truncations and 30 Table XXII presents Human Parainfluenza Virus 3 F1 region DP107 analog amino truncations. Further, Table XXIII, below, presents DP107/DP178 analogs and analog truncations which exhibit substantial antiviral activity. These antiviral peptides are grouped 35 according to the specific virus which they inhibit,

including respiratory syncytial virus, human parainfluenza virus 3, simian immunodeficiency virus and measles virus.

TABLE V

ALLMOTIS SEARCH RESULTS SUMMARY

FOR ALL VIRAL (NON-BACTERIOPHAGE) PROTEINS

- ^

		AB Virgan (no bacterioghages)	П	П	П		71.00		1000	11111
PCCENE	IALLATORIS	YIRUS		48.52	2	7	1		T. T. Mark	
CHERNIE	PARTIES IN ED PROTEIN	TOBACCO RATTLE VIRUS (STRAIN PSG)	٦		T		1044 1039	1115.1116	411711	10.10.10
PINK IRVES	TOTAL SELECTION OF THE PROPERTY.	TOBACCO PATTLE VIRUS (STRAIN SYLI		214.243	301-446		Т	ī		
PINK TAYSY	MILATINE IN BUT THE STATE OF TH	HERPES SINDLEX VIRUS (TYPE 6/STRAIN UGANDA-1101)	128-262							:
PINCO HSVAD	35 B FU TRUIEIR	HEPATITIS DELTA VIRUS (ISOUATE AMERICAM)		100-144						:
AAMI HDVAN	DELIA ANTONEA	HEPATITIS DELTA VIRUS (ISOLATE DISO)	1-48	100-144						
PAAM KOVOI	DELIA ANIMONA	HEPATITIS DELTA VIRUS (ISOLATE ITALIAN)	1-41	100-144				-		:
PAANT HOVE	DELIA ANTOEN (ALTAN ANTOEN)	INFATITIS DELTA VIRUS (1801.ATE LEBANON-1)	3-48							:
PAAM HOVE	DELTA AMINEN	HEPATITIS DELTA VIRUS (ISOLATE JAPANESE M-1)	3-48	100-144						:
PANT MOVAL	DELTA AMIUEN	REPATITION TA VIRUS (ISOLATE JAPANESE AS-1)	3.48	100-144						:
PAANT HOVAD	DELTA ANTICEN	HERAPITE DELTA VIRGE (ICO) ATÉ NAIMU)	3.41	100-144						
PANT HOWA	DELTA ANTIGEN	THE ATTENDED TO THE MANUAL AND	9:	<u> </u>	<u>.</u>					
PAANT IMVSI	DELTA ANTIGEN	TECH INTO CELL A VINCE (190EA) ATE INDIVINE CELL	99.1	189.144				1		!
PAANT HOVS	DELTA ANTIGEN	INFAILUS DELIA VIXUS (ISOLATE INFAILESE 9-2)		180.144						
PAANT KOVVO	DELTA ANTIGEN	HEPATITIS DELTA VIRUS (ISOLATE WOORKIIDEN)								
PATJH FOWPM	ANTITINGACISTA-III HOMOLOG	FOWLPOX VIXUS (ISOLATE IIP-431)	2	777 05.7	150.63					:
PATH VACEV	SA KD A-TYPE DACLUSION PROTEIN	VACCIMIA VIRUS (STRAIN WR)								:
AND ALL A	IN KD A. TYPE INCLUSION PROTEIN	VANOLA VIRUS	43:30	37:50						- :
1000	AT BUA TRANCINDICING PACTOR	HEAPES SOMPLEX VIRUS (TYPE I)	304-345							
1	A COURT OF ANY PARTITION PARTICING	HEIVES SOULEX VIRUS (TYPE 1)	102-139	304.345			1			!!!!
LATEL ROYE	ALTHOUGH THE COLUMN TATEOUR	FOURTHER RESPECTATION TYPE (STRAIN ABAP)	101-147	260-331						:
PATTI HISVES	ALTIA I KANS-INDOCTIO FACTOR	IVACCINTA VIRUS (STRAIN COPENHAGEM)	79.124	219.263						;
PATI2 VACCE	PUINTING A-1 TPE INCLUSION FROIDER	VACCODA VIBER	79-124				2			
PATTS VACCY	PUTATIVE A-TYPE INCLUSION PROTEIN	VACCINIA CLASS CONTRACTOR OF THE PRINCIPLE	104.14	105.420						_
DATE VZVD	ALPHA TRANS-INDUCING FACTOR	VAUCELLA-ZOSTER VIRUS (STAMIN DUMAS)								
PATU VACCV	PUTATIVE A-TYPE INCLUSION PROTEIN	VACCINIA VINUS	6							
PATTA MENSO	IAL PHA TRANS-DIDUCING PROTEIN (VANGS)	HEAPES SDAPLEX VINUS (TYPE 2)	78-21A	7,						
FLASH NAVE	ALPHA THANS-INDUCING PROTEIN (VANWES)	HERPES SDAPLEX VIRUS (TYPE 2)	17.333	24.3						
20000	AT PHA TRANSLINGING PROTEIN	BOVING HEXPESVIRUS TYPE I	195-236				-	-		
10 CU VII VI	AT PUA TRANS. INDIDEDED PROTEIN	EQUINE HERPESVIRUS TYPE I	241-250	ا						:
	AT BUA TRANSLINGUICING PROTEIN (VARICELLA-ZOSTER VIRUS (STAAIN DUNIAS)	106-252							
A STILL STATE	A TVBR DATE LISTON PROTEIN	COWPOX VIRUS	14-57	436-536	313:300	372.029	ACC-COR	W. 1.00		: :
VEL S PRO	PROTEIN BOL73	EFSTEIN-BARA VIRUS (STRAIN B95-1)	20							
700	TRANSCRIPTION ACTIVATOR BRLF1	EPSTEIN-BARR VIRUS (STRAIN DOS-1)	30-117							1 : 1
1000	JONAT PROTEDLYP!	POLYOMAVITUS BK	103-14							1
200	COAT BEATER UP!	POLYGOLAVIDUS BK	107.143							:
COA! COA!	COAT PROTECTION	HAMSTER POLYONAVIRUS	159.195						Ì	
200	Cost Protein (P)	SINGAN VIRUS 40	109.143	İ						
COAL SVE	COAT PROTEIN VP3	BUDGERIGAR FLEDGLING DISEASE VIRUS	141.213							
200	Covinential VP3	POLYGMAYTRUS BK (STRAIN AS)	14-44	117:34						
202	COAT PROTECT VP3	POLYOMAVIRUS BK	14-64	22.5						;
	COAT BEOTHER VES	BOVINE POLYOMIAVIRUS	35.76	133-216					i	
	COAT PROTEIN VP2	KAMSTER POLYDMAVIRUS	3.46	티크					j	:
	CO. 4 BOOTEON CO.	POLYOMAYTRUS JC	14.64	233-267				-		
2007	COAT PROTECT UP	LYNCHOTROPIC POLYOMAVIRUS	14.79	156-206						-
202	COAT MOTEON VES	MOUSE POLYONIAVIRUS (STRAIN))	5.73	23.		1				
	COAT PROTECTION UP 2	MOUSE POLYOMAVIRUS	5.73	<u>2</u>				-		
	CONTRIBUTION VOT	MOUSE POLYOMANTRUS	5.72	3.13						: : :
100 PON	COAT PROTECT VO.	MOUSE POLYOMAVIRUS	15-56	13.21						
200	CONT PROPERTY OF	SDADAN VIRUS 40	14.62	128.262	318-352					
2007	COALTANTA	ABUTE ON MOSAIC VIRUS (ISOLATE WEST INDIA	180-214							
PCOAT ABANY	COAL TAULEIN	APPLE CHA OROTIC LEAF SPOT VIRUS	184-181							
MOAT ACLE	COAT PACIFICATION	AEDES DENSONUCLEOSIS VIRUS	243-384							i
ACA ACA	CO1+ 9501514	ARTICHOKE MOTTLED CRIMILE VIRUS	2.5	<u>\$</u>						
MOVE VALLY	COAL PROPERTY	BEAN LEAFROLL VIAUS	19.123							
YOY SE										

	SHOT IS	AB Vinter (se betirriepheges)		48541 48	OBEA1 ABEA1	ABEAL	A SEA	45.44	
		[YRUS	14-12	-			-		
	PROTEIN	BROME MOSAIC VIRUS	163-197			1	1		
Ī	COAT PROTEIN	RADI EY YELLOW DWARF VIRUS	1	-				1	i
AUVE PARCE	COATPROTEDY	SALES VELLOW DWARF VIRUS		-		-			
Ī.	COAT PROTEIN	SURFACE CAN DWARF VIRUS	2	+		-	-		
T	POLY BEOTHER	PALLET TELLOW CONTRACTOR	161-191	1	1	-	-		
Ţ		PARLEY YELLOW OW AND ALKAS	26-90	166-333			+		L
٦	COAL PROTEIN	CAULIFLOWER MOSAIC VIRUS 13 I PALIF	18:65	183-334	-	1	-		
	COAT PROTEIN	CALL IL LOWER MOSAIC VIRUS	8,6	184-223		-	+		-
	COAT PROTEIN	CALL IPLOWER MOSAIC VIRUS	1	111,333			-		:
NAT CANON	COAT PROTEIN	CALIFIER OWER MOSAIC VIRUS	2		-	-			; ;
1	COAT PROTEIN	COURTS ALOCAIC VIRUS	5			-			: !-
١	COAT PROTECT	CAULIFLOWER PROSPIC	15.51			-			<u> </u>
ı	TOTAL OF THE PARTY.	CARNATION MOTTLE VINGS	141-173				1		!
1	COAT PROTEIN	COWPEA CHLOROTIC MOTTLE VIRUS	163.334					ļ	!
KOAT COAV	COAT PROTEIN	CARNATION ETCHED AING VIRUS		-			-		: :-
PCOAT CEAV	PROBABLE COAT PROTEIN	BARANECHINE BURSAIUA CHLORELLA VIRUS I		†					-
PONT CAN	NIAJOR CAPSID PROTEIN	SUBJECT APENT VIRUS	162:741	1			-		
3 5 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6	COAT PROTEIN	ALIEN PARKET	161.231				 -		_
1	COAT PROTEIN	CASSAVA LA LEGI, VINOS	153-187		1			<u> </u>	<u>.</u> _
COAT CLVN	CON TRACTOR	CUCUNDER MOSAIC VINUS							
COAT CHIVE	COAT PROTEIN	CUCIAGREA MOSAIC VIRUS						-	:
COAT CLAY	COAT PROTEIN	CONTRACTOR NOTATION VIEWS		1				_ _	
100	COAT PROTEIN	\$1000 CT \$000 CT \$1000	183-187		1		-	-	
	COAT PROTEIN	CUCUMBER PIOSAIC VIEWS	1153-181			+	-	 -	-
COAT CAVA		CUCUMBER MOSAIC VIRUS	1		_				!
COAT CHAME	COALFROIGH	PARTIMER MOSAIC VIRUS		1					+
Wat Day	COAT PROTEIN	A PART OF TOPICS VIRUS	758-103			-	_		_
201	COAT PROTEIN	SECOND STREET MOCALE VIRUS	184-213	1	-				_
33.5	LOAT PROTEIN	CHORD STRAIN MOTOR	79.120					-	
TON LAW	COAT BEOTED	CITAUS TRUSIEZA VIRUS	162-204						
COAT CIVIE		CLOVER YELLOW MOSAIL VIAUS	\$ 20	L					-
PCOAT CYNY	The state of the s	ECGPLANT MOSAIC VIRUS	413.466	366-600		-			1
COAT EPAN	COALTROISIN	FELINE CALICIVIRUS	101.550	209-995		-			+
COAT FOVO	COAT PROTEIN	FILING CALICIVIAUS		149.403	-				+
PCOAT FCV74	COAT PROTEIN	SELING CALICIVIRUS		Τ	46.433	-		-	
DAT PCVF9	COAT PROTEIN	PROMORT MOSAIC VIRUS	100	Ţ					
0.04	PLOBABLE COAT PROTEIN	POSTAN MOCAN VINA	22.330		-				
200	COAT PROTEIN	TOXING TOXING	90-134			+			
	CAPSID PROTEIN	TIPOLA INDESCRIT VINCE	10-134			+		-	-
יייי ואר	CAREE PROTEIN	SIMOLIUM HUDESCENT VINCE	\$1-15					-	-
COAT DIVE	CASILITING COLUMN TO THE COLUM	CHILD PAIDESCENT VIRUS	13.30	355-289		1		1	-
COAT DAYS	CASID PROTEIN	LALY SYNOTON ESS VIRUS	7.1	121-31					+
COAT LSV	COAT PROTEIN	MAIZE STRIPE VIRUS	167.53				1		$\frac{1}{1}$
COAT MITY	COATPROIDUR	MAIZE STREAK VTRUS							1
PCOAT MEWE	COAT PROTEIN	LAAIZE STREAK WIRUS				-			1
PCDAT MSVN	COAT PROTEIN	LAIZE STREAK VIRUS	77.73						-
PONT MEVS	COAT PROTEIN	GOOGLOCK IN LINGSPOT VIRUS	105-138				_		
VALUE OF STATE	COAT PROTEIN	SALES BAROOVIETS	160-414	044-480		-			
CB/4	COAT PROTEIN VP2	STATE OF THE PARTY	497.531						
201	COAT PROTEIN VPI	CAKING PARVOTING	111.0			1		<u> </u>	
NAT IND	COAT PROTEIN	PEA EALT BROWNING TIME	10.00					-	
PCOAT PER	SOLT BOOTEN	POPLAR MOSAIC VIXUS	104-138						T
DOAT POPEY	Nation 1003	PEPPER MILD MOTTLE VINUS	2.5	251-292		-		 	+
PCOAT PPINYS	COALPACIENT	POTATO VIRUS	100.734						+
PCOAT PVSP	COAT PROTEIN	POTATO YELLOW MOSAIC WRUS		140.193				+	+
PCOAT PYNAVY	COAT PROTEIN	EASPBEARY BUSHY DWARF VIRUS							1
PCOAT RUDY	COAT PROTEIN	BED CLOVER NECROTIC MOSAIC VIRUS	8)(-7/2		360.108	-			-
VOOLT ROOM	COAT PROTEIN	A COLUMN VIEWS	74.68			-		L	
1		100 to 10	160.224						
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	JAN MANA	All Virgon (ae bacterlophagns)	I	T		, , , ,	ABTAG	7 7 4 4 7	AREA 7	ARTA *
7.CE.	SECURITY			1000	3	7	Τ	Т	1	
TI STORE A TOWN	COATPROTEIN	CVIRUS	3							
TO THE PARTY OF	COAT BEOTEIN	KOYDEAN CHLOROTIC MOTTLE VIRUS	20 12							
MAN 200	COAT BEOTERA	SATELLITE TOBACCO NECROSIS VIRUS I	9							
TOTAL STANS	COAT PROTEIN	SATELLITE FORACCO NECROSIS VIRUS 2	2							
POAT TANA	GENOME POLYPROTEIN	TAMARIT LO MOSAIC WINUS	6							İ L
PCOAT TAV	COAT PROTEIN	TOWATO ASPERAY VIRUS	Ī	15.7						
PCOAT TBSVB	COAT PROTEIN	TOMATO BUSHY STUNT VIRUS	[2						
PCOAT TBSVC	COAT PROTEIN	TOMATO BUSHY STUNT VIRUS	19.46							
PCOAT TCV	COAT PROTEIN	TUNIT CAINKLE VIRUS	100.330	T						
PCOAT TOMY	COAT PROTEIN	TOMATO COLDEN MOSAIC VIRUS	20.00							: !
PCOAT THOMY	COAT PROTEIN	TOBACCO MILD GREEN MOSAIC VIRUS								
PCOAT TMV	COAT PROTEIN	TOBACCO MOSAIC VIRUS								Ĺ
PCOAT TANOS	COAT PROTEIN	TOBACCO MOSAIC VIRUS	101.101							
PCOAT TANCO	COAT PROTEIN	TOBACCO MOSAIC VIRUS								L
PCDAT TAMBA	COAT PROTEIN	TOBACCO MOSAIC VIRUS	10-101							
PONT TANKE	COAT PROTED	TOBACCO MOSAIC VIRUS	103-137							
- LOS	COAT PROTEIN	TOBACCO MOSAIC VIRUS	103-137							
1004	COAT PROTEIN	TOBACCO MOSAIC VIRUS	10.137							-
70074 1000	COAT PROTEIN	TOBACCO MOSAIC VIRUS	103-137							
TOWN I WOOD	TOTAL PROPERTY.	TOBACCO MOSAIC VIRUS	103-137							1
CONT. INVIO	COAT PROTECT	TOBACCO BATTLE VIRUS	11-100							
SAN 1402	NOT THE PROPERTY OF	TOBACCO BATTLE VIRUS	69-103							1
COAT TAVIC	COATTACTED	TOBACCO YELLOW DWARF VIRUS	1-16							1
2011 TO 2	COVE PROPERTY	TURNER YELLOW MOSAIC VIRUS	61-75							
AND THE	COALTROLEGY	TURNIP YELLOW MOSAIC VIRUS	41.75							 -
WANT I VOL	COAT PROTEIN	WHITE CLOVER MOSAIC VIRUS	163-197							; -
COA!	CONT. PROFESS	GROUND SQUIRREL HEPATITIS VIRUS	94-135							:
2007	COSE ANTICEM	HEPATITIS & VIRUS	111.140							
TOTAL PLANT	CORP. ANTIGEN	WOODCHUCK HEPATITIS VIRUS I	A2:186							<u>:</u> -
TOUR VECTOR	CORE ANTIGEN	WOODCHUCK HEPATITIS VIRUS 8	8	į			-			
POSSO ASTRA	PROTEIN DINGR	AFRICAN SWINE FEVER VIRUS	2			1	-		: :	
PONTE ADECT	EAST, Y E2A DMA-BRYDING PROTEIN	HUMAN ADENOVIRUS TYTE 2	90				-			
PONOT ADEBS	EARLY LIA DAM-BROING PROTEIN	HUNLAN ADENOVIRUS TVPI: 5	40.10				-		:	
Povel Fev	MAJOR DWA-BINDING PROTEIN	EPSTEIN-BARR VIRUS	200	761	114-10	45 L		<u> </u>		
ACAN HOWA	MAJOR DNA-BINDONG PROTEIN	HIGHWAY CYTONEGALOVIRUS	212	W01:00		9,01	! -	-	: [
PONTEL HEVIL	MAJOR DNA-BINDING PROTEIN	HEAPES SOMPLEX VINUS	\$57.393) () ()	100.00	10.00	<u> </u>		!	
PDYB! HSVIP	MAJOR DNA-BINDING PROTEIN	HEAPES SIMMLEX VIRUS			100.00	97	<u> </u>		-	:
PDRSI HSVIK	MAJOR DNA-BINDING PROTEIN	HEAPES SIMPLEX VIAUS		17.00	1		ļ	<u> </u> -	1	
PDNBI HSVB2	MAJOR BNA-BIYDING PROTEIN	BOVING HEAPESVIRUS TYPE 2	20.00				<u> </u>	-	:	
PONSI HSVEI	MAJOR DNA-BINDING PROTEIN	EQUINE HERPESYIRUS TYPE I	1,1,1	102.114				<u> </u>	! -	-
POWER KSVDS	MAJOR DNA-BOIDING PROTEIN	EQUING HERVESVIRUS TYPE.	33,319	110.167	\$06-557	133.007	-	<u> </u>	<u> </u>	
PDKBI MSVSA	MAJOR DWA-BINDING PROTEIN	HELVES VIRUS SALMINI	117.410	3,17,18		 -	ļ		<u> </u>	.
PDINST MOUNT	MAJOR DNA-BINDING PROTEIN	MUMURE CYTOMEGALOVINOS	135.163			-	-			
POWEL SOAM	MAJOR DNA-BRYDING PROTEIN	SDITAN CYTUREUALUVIAUS	57.17	121.153		 -	 -			.
POPEL VZVD	MAJOR DNA-BINDING PROTEIN	VAUCELLA-ZOSTER VIRUS	37.10				<u> </u>			
POPIL! ASDG	DNA LIGASE	AFILICAN SWIME PENER VINUS	104.414							: ! :-
PONG.I VACCC	DNA LIGASE	VACCIMA VIRUS	104 414							<u>:</u> _
PORT VACCV	DNA LIDASE	VACCIMIA VIRUS	301 434							!
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TOPOL ADERS	DNA POLYNGIASE	MUNAN ADENOVIRUS TYPE 2	17.19							 -
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DAM POLYBEAJJE	13-44 50-340 13-44 13-144 14-
DAY FOR THE LAND	11.154 11.154 11.154 11.154 11.155 11.155 11.156 11.157
DAM POLYMENANE CHOCKELLA VILLA V	11:31
DAM POLYMEALMS	DUCK ISOLATE 5) 5-19 DUCK ISOLATE 5) 5-19 DUCK ISOLATE 5) 5-19 S11-159
DAM POLYMEAANS GONDON VILLES 13-11	519 131-1014 519 151-1014 519 151-1014 519 151-101 510-233 151-501 510-233 151-501 510-233 151-501 510-234 170-111 510-234 170-111 510-234 170-111 510-234 170-111 510-234 170-111 510-234 170-111 510-234 170-111 510-234 170-111 510-234 170-111 510-234 170-111 510-234 170-111 510-234 170-231 510-234 170-231 510-234 170-231 510-234 170-234 51
DAM POLYMEANS	DUCK ISOLATE 53 5.39 DUCK ISOLATE 53 5.39 131-349 131-349 131-
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DAY NOLYMENTE DUCK	5.30 5.30 5.30 5.30 5.30 5.30 5.30 5.31 5.31 5.31 5.32 5.32 5.32 5.33 5.34
DIAM POLYMEALS DUCK IEGATITIS S WRUS CHRITE SILVEGIAL DUCK ISOLATE S) 1-39	291-33 5-39 5-39 201-233 201-233 310-233 311-359 3
DRA POLYBEAMS	201-23 201-23 201-23 201-23 201-23 201-23 201-23 211-35
DIA POLYMEIASE HEADTHEE WINUS (SIGNTYE AVEN) 101-219	AIN 17) AIN 17) AIN 17) AIN 185 AIN ANGELOTTI AIN 185 AIN SCIE) AIN SC
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DNA POLYMELASE FEDDES SIBPLES VIRUS (TYRE 15 STALIN SCIO) 111-159	\$11.559 \$11.559 \$11.559 \$11.559 \$11.559 \$11.559 \$11.559 \$11.550 \$11.55
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DRIA PACTYGEASE IGENES SIDPLEX VINUS (TYPE IS STALM SEL) 111-139	111.559 (14.55) (14.55
DRIA POLYNEAASE NEEDEES SIGNES VINUS (TYPE 1/57RAIN 186) 191-150	912-560 912-560 913-560 913-546 913-546 913-546 913-546 913-546 913-546 913-510 913
DIA POLYMERASE ENGINE HEIGHSTALMS TYPE 15TAJN ABRY 194-31	864-538 13-47 13-47 13-43 10-74 10-134 1
DNA POLYMERASE EQUINE HAZESTRIUS CHANGEL CAPTISH VIRUS 1543	13-47 238-366 401-433 708-749 735-46 401-433 708-411 638-62 638-643 708-611 638-62 638-643 708-611 638-62 638-643 708-611 708-611 708-613 708-
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PILE HAME	PROTEIN		Γ							
PENI MEN	ENV POLYPROTEIN PRECUISOR	FREED SPLEEN POLUS-FORMING FINAS	141.171							
PENS FISTV	ENV POLYPROTEIN PRECURSOR	FREND SPLEDY FOCUS-FORMING VIKUS								: i
PENY AVILE	ENV POLYPROTEIN	AVIAN RETICULOENDOTHELIOSIS VIRUS	20000							! !_
PENY AVISN	ENV POLYPROTEIN	AVIAN SPLEEN NECROSIS VIRUS	277 001							: ! !
PNV BARVIA	ENV POLYPROTEIN	BABOON ENDOGENOUS VIRUS (STRATH NT)	2		1	636410	415.491			i
POV BIVOS	ENV POLYPROTEIN PRECURSOR	BOYTHE INGUINODE/ICIENCY VIRUS (ISOLATE 106)				10.31.	110.619	664.724		<u> </u>
PENV BIVAY	ENV POLYPROTEIN PRECURSOR	BOVINE INDICHODEFICIENCY VIRUS (ISOLATE 177)								: !
NOV III.VA	ENV POLYPROTED ^d	BOVINE LEUKEMIA VIRUS (ANERICAN ISOLATE FLK)	304.370							! !
PERO BLVALL	ENV POLYPROTEIN	BOVINE LEUREAITA VIRUS (AUSTRALIAN ISOLATE)	1							;
PENY BLVAV	ENV POLYPROTEIN	BOVINE LEUKEAITA VIRUS (ALIERICAN ISOLATE VIM)	106.37							· -
PENY BLVR2	ENV POLYPROTEIN	BOVINE LEUKEMIA VIRUS (BELGIUM ISOLATE LRINS)	304.379							· • •
PENV N. VIIS	ENV POLYPROTEIN	BOVINE LEUX EAILA VIRUS (DELCIUNI ISOLATE LBSP)	25.73			1				: :
10 A A	SAV POLYPROTEIN	BOYING LEUKENIIA VIRUS (JAPANESE ISOLATE NI.V-1)	2				! !		-	<u>.</u>
TABAL CAR	ENV POLYPROTEIN PRECURSOR	CAPAINE ARTHRITIS ENCEPHALITIS VIRUS (STRAIN CORK)	157.196	13.	21.78	10.00			Ì	:
2000	ENV BOLYPROTEIN PRECIREOR	CAPRINE ARTHUTIS EXCEPTIALITIS VIAUS (STRAIN 043)	1X-13	11.1	749.783					: :
200	ENV POLYTEN PRECINCOR	EQUINE INFECTIOUS ANEMIA VIRUS (CLONE P) 3-1)	39.76	436-525	\$59.593	2				
CAN ELAVI	ENV BOY VAROTE DI PRÉCIDEOR	EQUINE INFECTIOUS ANEAIIA VIRUS (CLONE P3 2-2)	19.76	\$ P = 23	28.50	65E-692				
EN 1 21 2 70	ENV BOX YPROTE DE PRECURSOR	EQUINE INTECTIOUS ANEMIA VIRUS (CLONE P) 3-3)	19.76	<u>~</u>	559.593	658.710	1			!
ENA CITATI	SAV BOX VEROTE IN PRECITE SOR	EQUINE INFECTIOUS ANEMIA VIRUS (CLONE P) 3-5)	38.76	437.526	360.50	639-603				:
ENV KIAVS	SAV BOX YEARTH IN PRECINESOR	EQUINE INFECTIOUS ANEALIA VIRUS (CLONE 1169)	19.76	115.33	530.50	2				;
ENV CIAVE	SAN BO WESTERN PRINCIPLE	EDUTINE INTECTIOUS ANENIA VIRUS (CLONE CL22)	39.76	416-525	559-303	658.714				:
ENV EIAVE	ENV BOY SECTION PRECUISOR	EQUINE INFECTIOUS ANEALIA VIRUS (STRAIN WSUS)	39.76	436-525	200	56.7 5			1	:
20 CT CT CT CT CT CT CT CT CT CT CT CT CT	ENV BOLVETON PRECURSOR	EQUINE INFECTIOUS ANEARA VIRUS (ISOLATE WYONING)	39.76	436-533	3	5				:
1200	ENV BOX VEDOTE IN PLECUASOR	PELINE ENDOGENOUS VIRUS ECE!	503-555	Š						-
PAN FEMA	ENVELORE POLVES OTEN PRECURSOR	FELTINE DOADWOOEFICIENCY VIRUS (ISOLATE PETALUNIA)	610-690	115-758						1
ENV FIVED	ENVELOPE POLYPROTEIN PRECURSOR	FELTINE BOWINGOEFICIENCY VIRUS (ISOLATE SAN DIEGO)	189-09	2.3X						;
ENV FIVE	ENVELOPE POLYPROTEIN PRECURSOR	FELING DOLUNODEFICIENCY VIRUS (ISOLATE TAIS)	2 9	600.68	18-73					1
ENV 7LVG	ENV POLYPROTEIN PLECURSOR	FELTINE LEUKEMBA PROVINUS (CLONE CFE 4)	407-349							
ENV 71 VOL	DIV POLYPROTEIN PLECURSOR	FELINE LEUKEMAN YINUS (STRAIN ANGLASGOW-I)	0.5	242.570						Ĺ
PEW FLYIB	ENV POLYPROTEIN PLECURSOR	FELINE LEUKEMIA VINUS (STRAIN LAMIDA-BI)	200	MC-201						-
POW PLYSA	ENV POLYPROTEIN PRECURSOR	FELING LEUKEANA VIRUS (STRAIN SAIMIA)		164.306	1	(4).40)	100-993			i
PENY FOUNTY	ENV POLYMOTER	HADAAN SPUKARETROVIRUS	55 147	763.684						
PENV FEVOR	ENV POLYPROTEIN PRECURSOR	PELINE SARCOMA VIRUS (STRAIN GALDYEN-AUGUSTES)	471.530	342.576						!
PENV PSVOR	DAY POLYTROTEN PLECURSOR	FELTINE CARCINAL VIRIS (STRAIN SM)	481.524	\$45.579						
POW PSWA	BAY POLYTROIEM PRECURSOR	FELDIE SARCOMA VIRUS (STIAIN SMIDER-THEREN)	496-532							
PERV PANE	ENV POLITICAL PRECURSOR	GIBBON APE LEUKEABA VIRUS	513-575	129-285						
ALL PLANTS	ENV POLYPROTEIN	HIDMAN T-CELL LEUKEMIA VIRUS TYPE I (STRAIN ATK)	321.383							
PENY HTLIC	ENV POLYPROTEIN	3								
KEN HELIX	ENV POLYPROTEIN	HUMAN T-CELL LEUKEMIA VIRUS TYPE I (ISOLATE MT-2)	201:122					1		
PEW HTLYS	ENV POLYPROTEIN PRECURSOR	HUMAN T-CELL LEUXEMIA VIRUS TYPE II			174.041					
PEN JIVIAZ	ENVELOPS POLYPROTEIN GP160 PRECURSOR	HIMAN DOMINOPERCIENCY VIRUS TYPE I (ARVINE 190CA IE 197-39)	741 107	200						
PENY HVIBI	ENVELOPE POLYPROTEIN GP160 PRECURSOR	HUNCAN DOMINIONERICIENCY VINUS 1172 1 (BRIT 1804X18)	8 5	101.101	163.63		 -			
PENY HVIBI	ENVELOPE POLYPROTEIN CP160 PRECURSOR	_		87.15	100,700	763.831				
PENV HVIBN	ENVELOPE POLYPROTEIN GP140 PRECURSOR (COM	MICHAN MORCHOUGH CLENCY VIRUS 1176 (ONCH 130CA LE)	10.50	12.51	773.843					
PENV, HV18R	ENVELOPE POLYPROTEIN GP160 PRECURSOR	HONDAN DEMONDER FOR TABLE 1 (SEC 1500 1500 1500 1500 1500 150 150 150 15		210.606	20,000	77-835				L
PENV HVICA	ENVELOPE POLYTROTEIN GPI60 PRECURSOR	MORAN INCOME INTERNATIONAL VINES TYPE I (EL) SOLATE)		203.591	103.700	768-829				
PEN KVIEL	ENVELOPE FOLTPROTEIN OF IN PAECUASON	MANAM MANAMODESICIENCY VIRUS TYPE I (MXB) ISOLATE)	\$2.5g	610-713	767.036					
WENN HATHE	ENVELOPE FOLITACIEN CHIEG PLECUNSOR	HUMAN BOAUNODEFICIENCY VIRUS TYPE I (HXB) ISOLATE)	503-594	610-712	767-843		i			
PENV MVIE	SALVEL CHE POL VPROTEIN CP 160 PRECURSOR	HIDAAN DOKUNODEFICIENCY VIAUS TYPE I (JA) ISOLATE)	30.37	517.405	22.23	2				
PEN HVID	ENVELOPE POLYPROTEIN CP160 PRECURSOR	HUMAN DIGHUNDDEFICIENCY YIAUS TYPE I (INCSF ISOLATE)	29.762	497.516	403-704	200				

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DEVELORS POLYMOTERN OF 10 PRECURSOR PRINCIPAL BAGINODEFICIENCY VIRUS TYPE 2 (1904.ATE SELISY) 151-331 151-732 151-73		
ENVILORE POLYMOTEN OF DECURSOR VINIAN BAGINODEFICIENCY VIRIS TYTE 2 (1801A TE 51) 151-257		
BOYELOPE POLYMOTEN OF PACCHASOR MOUSE DITACESSENATOLE	 - -	
DEV POLYMOTEN PRECURSOR SHEEP FULMONARY ADERGOMATORS VALUE 1913-33 1913-31		
BNY POLYPROTERN PLECURSOR (COAT POLYPROTE AIRNE CELL FOCUS-FORAING NAUNG LEUKENIA VIRUS (190.) 417-231 117-231		
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ENV POLYMOTEN PACCHASOR FUERO MANAGELEGRENIA VIRUS (1SOLATE 1837) 125-544 174-110 100-114 100-		
DAY POLYPROTEIN PRECURSOR FURENCE AND VIOLE (1904-151) 100-151 100-1		
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1	ENVELOPE POL VPROTEIN OPIGO PRECURSOR		٦	3	247.795	780.00				
1	PANEL COR POLYPROTEIN GP140 PRECURSOR	_		20.00	212.584	207				-
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L	ENVELOPE POLYPROTEIN GP 146 PRECUTSOR	E)	ij	-	243.48				j	<u>.</u>
l.	ENVELOPE POLYPROTEIN OPIN PRECURSOR		\$64.50s	70.0				1	!!!	
1	ENVELOPE POLYPROTEIN GP140 PRECURSOR		64.70							•
Į	ENVELOPE OF YOU YPROTEIN OF 140 PRECURSOR	SINGAN INGRAMODEFICIENCY VIRUS (F236/SNRH ISOLATE)	466.500			117:03				:
ļ	ENVELOPE FOR YPROTEIN GP140 PRECURSOR	SDAAN DAKKODEFICIENCY VIRUS (PRIMCI) ISOLATE)	470-513	200	2				i	••
200	ENV BOY VPROTEIN PRECINSOR		400-466							٠,
	Excellent of the contract		409-475						İ	
A LONG AND A LONg AND A LONG A LONG AND A LONG A L	TOW TOU WHO TEN BRICITATION	(1814)	31-62	184-333	137.140	773.803	İ			-
7 27	ENV POLVED TEN PRECIESOR	VISMA LENTIVIRUS (STRAIN ISIA) CLONE LVI-IKSI)	29-12	181-223	643.346	780.814				_ :.
IN IN ANGE	ENV POLYPROTEIN PRECURSOR	VISNA LENTIVIRUS (STRAIN 1514/CLONE LVI-1K\$2)	21-63	 	17.57	343.5				
PFER AVIER	ERBA ONCOCENE PROTEIN	AVIAH ERYTITADILASTOSIS VIRUS (STILAIN ES4)	106-140							
PETEL FOUR	EALLY TRANSCRIPTION FACTOR TO KD SUBUNIT	FOWLIOX VIAUS (STRAIN FP.1)	20.22	25.53					İ	:
PETEL CEVEA	EARLY TRANSCRIPTION FACTOR TO KD SUBUNIT	SHOPE FIBROXIA VIRUS (STRAIN KASZA)	37.71	\$. \$.	2.0.3					:
NA LEGIS	EARLY TRANSCRIPTION FACTOR TO KO SUBUNIT	VACCIMIA YIRUS (STRAIN COPENIAGEN)	13.71	307.34						
70 X	EARLY THANSCRIPTION PACTOR TO KID SUBUNIT	VACCINIA VIRUS (STRAIN WR)	13.71	107.34					j	· ·
	FARLY TRANSCRIPTION FACTOR \$2 KD SUBUNIT	VACCIMIA VIBUS (STRAIN COPENHAGEN)	12.01	174.768		 -				; ;
7817	SABLY TRANSCRIPTION FACTOR 12 KD SUBUNIT	VAUOLA VIRUS	52.97	174.201						-
1000		HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	111.08						j	: : :
No.	ALE AL PAR REPARET FASE	EOUNE NEW ESVIRUS TYPE 1 (STRAIN ADAP)	15-141							:
TEACH NOVE	AT WAS EXCEPTED FASE	PSEUDORABIES VIRUS (STRAIN NIA-1)	021-21							:
S ACADA	A I KAI DAT EXONAICI EASE	VANCELLA-20STER VIRUS (STRAIN DURIAS)	181-601	(16:516)						:
PETERS ADMAG	AL A KD FIRER PROTEDA	HUNAN ADENOVIRUS TYPE 40	182-237							:
PFIB2 ADE41	41 4 KD PIBER PROTEIN	HUMAN ADENOVIRUS TYPE 41	22				-			:
PFIRP ADEGS	FIBER PROTEIN	HUMAN ADENOVIRUS TYPE 3	26-194			 				!
PTEP ADEOT	FIREA PROTEIN	HUMAN ADEMOVIRUS TYPE 1	176.210							-
PFIRE ADEA	FIREM PROTEIN	HUMAN ADENOVIRUS TYPE 40	201-102			-				!
PERP ADEA!	FIBER PROTEIN	HUMAN ADENOVIRUS TYPE 41	370-308			+				
FEB? ADEB)	FIREM PROTEIN	BOVING ADENOVIACION TOTAL	97.14			-				-
PFOSX MSVFR	V-POSFOX TRANSFORMING PROTEIN	PER PICKERS COLECTIONS TINGS	53,001							
POS AVDAX	PSEV-FOS TRANSFORMING PROTEIN	AVIANTED ROTTO CARONAL VIETS	183.193			1				ڳ. ا
MOS MSVT	PSEVEOS TRANSPOUNTER PROTEIN	AVAN CASCOMA VILLE (CTAIN CTIO)	9:50			_				: !
POACC AVISC	PARCACAL PROTEIN	AVIAN ENDOCENOUS VIRUS EV.1	2.2			-				
POAG AVEVI	CAL POLITICIEN	AVIAN ENDOCEMOUS ROUS.ASSOCIATED VIRUS-0	7							
POAU AVEVE	CALCACA CONCENT	AVIAN MYSLOCYTOMATOSIS VIRUS MC29	27.8							i
MOAU AVIA	CACACA VAROTEN	AVIAN MYELOCYTOMATOSIS VIRUS IBI	57.94			Ц				
MAC AVERE	COURT PROTEIN PLO	AVIAN SARCOALA VIRUS (STRAIN URJ)	53.94							
2010	NET COUNTY TO THE	AVIAN SARCONA VIRUS (STRAIN Y7)	13.94							
PAN PAN	CALO POLYPROTEIN (P.S.)	BOVING INGRINODEFICIENCY VIRUS (ISOLATE 106)	7							
WATE 040	GAG POLYPROTEDY	EQUINE INFECTIOUS ANEMIA VIRUS (CLONE CL11)	9:-19							
200	GAG POLYPROTEIN	FELING DOMINODEFICIENCY VIRUS (ISOLATE PETALUNIA)	76.116							1
POAD PTVSD	DAD POLYPROTEIN	FELINE DOMINODEFICIENCY VIRUS (ISOLATE SAN DIEGO)	36-110							
POAD PINT	DAD POLYPROTEIN	FELINE DARUNODEFICIENCY VIRUS (ISOLATE TAU)	26-130 26-130							
POAD PLV	GAG POLYPROTEIN	FELINE LEUKEMIA VIRUS	-21			100,000				
POAD FOAM	DAD POLYPROTEIN	HUMAN SPUBIALETROVIRUS								
POAD PENAD	OAG POLYPROTEIN	TELING SARCOMA VIRUS (STRAIN MCDONOUGH)	* K-M-							

MINALIN BACKGRAY VIRUS GIBBON AFE LEUKEBIA VIRUS GIBBON AFE LEUKEBIA VIRUS GIBBON AFE LEUKEBIA VIRUS GIBBON AFE LEUKEBIA VIRUS HIJAAN BARINOODETICIENEY VIRUS TYPE I (BINI SIGLATE) HIJAAN BARINOODETICIENEY VIRUS TYPE I (BINI SIGLATE) HIJAAN BARINOODETICIENEY VIRUS TYPE I (BINI SIGLATE) HIJAAN BARINOODETICIENEY VIRUS TYPE I (BINI SIGLATE) HIJAAN BARINOODETICIENEY VIRUS TYPE I (BINI SIGLATE) HIJAAN BARINOODETICIENEY VIRUS TYPE I (BINI SIGLATE) HIJAAN BARINOODETICIENEY VIRUS TYPE I (BINI SIGLATE) HIJAAN BARINOODETICIENEY VIRUS TYPE I (BINI SIGLATE) HIJAAN BARINOODETICIENEY VIRUS TYPE I (BINI SIGLATE) HIJAAN BARINOODETICIENEY VIRUS TYPE I (BINI SIGLATE) HIJAAN BARINOODETICIENEY VIRUS TYPE I (BINI SIGLATE) HIJAAN BARINOODETICIENEY VIRUS TYPE I (BINI SIGLATE) HIJAAN BARINOODETICIENEY VIRUS TYPE I (BYDI SIGLATE) HIJAAN BARINOODETICIENEY VIRUS TYPE I (BYDI SIGLATE) HIJAAN BARINOODETICIENEY VIRUS TYPE I (BYDI SIGLATE) HIJAAN BARINOODETICIENEY VIRUS TYPE I (BYDI SIGLATE) HIJAAN BARINOODETICIENEY VIRUS TYPE I (BYDI SIGLATE) HIJAAN BARINOODETICIENEY VIRUS TYPE I (BYDI SIGLATE) HIJAAN BARINOODETICIENEY VIRUS TYPE I (BYDI SIGLATE) HIJAAN BARINOODETICIENEY VIRUS TYPE I (BYDI SIGLATE) HIJAAN BARINOODETICIENEY VIRUS TYPE I (BYDI SIGLATE) HIJAAN BARINOODETICIENEY VIRUS TYPE I (BYDI SIGLATE) HIJAAN BARINOODETICIENEY VIRUS TYPE I (BYDI SIGLATE) SIGLAN BARINOODETICIENEY VIRUS TYPE I (BYDI SIGLATE) SIGLAN BARINOODETICIENEY VIRUS TYPE I (BYDI SIGLATE) SIGLAN BARINOODETICIENEY VIRUS TYPE I (BYDI SIGLATE) SIGLAN BARINOODETICIENEY VIRUS TYPE I (BYDI SIGLATE) SIGLAN BARINOODETICIENEY VIRUS TYPE I (BYDI SIGLATE) SIGLAN BARINOODETICIENEY VIRUS TYPE I (BYDI SIGLATE) SIGLAN BARINOODETICIENEY VIRUS TYPE I (BYDI SIGLATE) SIGLAN BARINOODETICIENEY VIRUS TYPE I SIGLATE SIGLATE SIGLAN BARINOODETICIENEY VIRUS TYPE I SIGLATE SIGLAN BARINOODETICIENEY VIRUS TYPE I SIGLATE SIGLAN BARINOODETICIENEY VIRUS TYPE I SIGLATE SIGLAN BARINOODETICIENEY VIRUS TYBE I SIGLATE SIGLAN BARINOODETICIENEY VIRUS TYBE I SIGLATE SIGL	XL0XXX.2.2.2.2.2.2.2.2.2.2.2.2.2.2.2.2.2.2		11	1338	+				1
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ADDITIONAL STREETS				100	ļ	<u> </u>			1
GAGO GY PROTTEN WALAN BAGNOGETERS YNUS TYPE (1903 190.47E) 10.11 10.13		_	1	93.38	1	<u> </u>			
			١	200					
Did GOLYMOTER MILALIN PRACTICENCY VILLS TYPE [BACKED 90.11] 319.130		П		1:336					_
GLOS POLYMOTTHS HIGALN BACHOOSTICIBLY VINIS TYR 1 (NAL 150LATE) 16-11 18-130				93.326	1				<u>.</u>
CALO PALTROTTEN		Т	=						
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OLD POLYMOTER COLD		3	T	92,126					
GAG POLYMOTER GAMAND BACHOGGETICENCY VILLE TYPE GAMESALVE 191111 191111			T			_			
GAG POLYPROTER GALAN BOATHOGISTICIBECY VILLS TYPE I (01/1804/TE) 781-318		1	T		-	L			
OLG POLYMOTERN AUGUST DESCRIPTION 1912-131 1912-131			1				L		
CAG PCLYPROTERN FIGHAL BEACHAST STREET (GRAAT SOLATE) 1911			1	97:328		1			
CAG POLYPROTERN HOLAND RATINGELINGLY VIRES TYPE I (STAIN UGANOAN) [1-13]		E)	1	93:128					_
CAG POLYTROTEIN		FENCY VIRILE TYPE I ISTRAIN UGANDAN 87-1.	-11				-		L
CAGE POLYMOTER		THE LANGE TANKED ISOLATED 1892-	910		1	1			_
GAG POLYPROTEIN		1111 101 110 1111 110 A 1111 1		163-337					L
GAO POLYPROTER ALTROYNULE ALATED GAO POLYPROTER ALTROYNULE ALATED GAO POLYPROTER ALTROYNULE ALATED GAO POLYPROTER ALTROYNULE ALATED GAO POLYPROTER ALTROYNULE ALATED GAO POLYPROTER ALTROYNULE ALATED GAO POLYPROTER ALTROYNULE ALATED GAO POLYPROTER ALGO PO		CIENCY VIXOS LIVE I (ESCENTIVI 1993)	2			1			1
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RETROYNUE RELATED GAG POLYMOTER MOUIS BYTACHITEMAL A-PATICLE 16-133 131-132	MALCON PROTOCOL	Т	Ī						1
MALVOR COLT PROTEIN AGUISE BITLACTISTENAL A-PATICLE 172-194 114-194 AGUISE MALANDOLOG POLYPROTEIN 1902-194 114-194 114-194 AGUISE MALANDOLOG POLYPROTEIN 1902-194 114-194			T	11.133	-				
NATIONAL STRAIN OF CONTROL SHEEP FULAGOVANY ADEADAM/TOSIS VIRUS			Ī,		-				
OAD POLYMOTERN MOUSE MAJOLANY TAKOR VIRUS (STAIN BIR) 19-17-1 15-17-10	ED CAC POLICE		T	91.35					1
OAG POLYMOTER MOUSE MADDIANY TUNGS VALUS (STACK) (Ī	100	-				<u> </u>
GAG POLYPROTEIN SIMILAR MATONIFIZER VIRUS 17-1-10			I						1
QAO POLYROTEN ADDIS \$ARCOMA VRUS (STRAIN PAGDE C) 171-171 171-171									1
GAO PGLYMOTEN SACCHARONTES (TREATES) 101-119 171-419 171			١	117 000		-			-
A MAJOR COAT PROTEIN SEGAM FOAMY VIRUS (TYTE !) 171-17 17			1	T			L		
040 PCLYROTER SIMILAL FOLANT VIRUS (TYTE) (STRÁN LK.) 191-407 191-312 040 PCLYROTER SIMILAL FOLANT VIRUS (TYTE) (STRÁN LK.) 161-316 040 PCLYROTER SIMILAL FOLANT VIRUS (TACALTS SOLATE) 161-316 040 PCLYROTER SIMILAL BACKADOCE FICENCY VIRUS (GALTE CASALT CONE CASALT RELIEVAN SOLATE BACKADOCE FICENCY VIRUS (STACTE) 191-316 040 PCLYROTER SIMILAL BACKADOCE FICENCY VIRUS (STACTE) 191-316 040 PCLYROTER SIMILAL BACKADOCE FICENCY VIRUS (STACTE) 191-316 040 PCLYROTER SIMILAL BACKADOCE FICENCY VIRUS (STACTE) 191-316 040 PCLYROTER SIMILAL BACKATOCE CONTOCE FICENCY VIRUS (STACTE) 191-316 040 PCLYROTER SIMILAL BACKADOCE FICENCY VIRUS (STACTE) 191-316 040 PCLYROTER SIMILAL BACKADOCE FICENCY VIRUS (STACTE) 191-316 040 PCLYROTER SIMILAL BACKADOCE FICENCY VIRUS (STACTE) 191-316 040 PCLYROTER SIMILAL BACKADOCE FICENCY VIRUS (STACTE) 191-316 040 PCLYROTER SIMILAL BACKADOCE FICENCY VIRUS (STACTE) 191-316 040 PCLYROTER SIMILAL BACKADOCE FICENCY VIRUS (STACTE) 191-316 040 PCLYROTER SIMILAL BACKADOCE FICENCY VIRUS (STACTE) 191-316 040 PCLYROTER SIMILAL BACKADOCE FICENCY VIRUS (STACTE) 191-316 040 PCLYROTER SIMILAL BACKADOCE FICENCY VIRUS (STACTE) 191-316 040 PCLYROTER SIMILAL BACKADOCE FICENCY VIRUS (STACTE) 191-316 041-316 PCLYROTER SIMILAL BACKADOCE FICENCY RELIEVAS (PRECURSOR BOYNE CORONA VIRUS (STACTE POLITICAL STELASS PRECURSOR 041-316 PCLYROTER SIMILAL BACKADOCE FICENCY RELIEVAS PROGRAM POLITICAL STELASS PRECURSOR 041-316 PCLYROTER SIMILAL BACKADOCE FICENCY RELIEVAS PROGRAM POLITICAL STELASS PRECURSOR 041-316 PCLYROTER SIMILAL BACKADOCE FICENCY RELIEVAS PROGRAM POLITICAL BACKADOCE FICENCY RELIEVAS PROGRAM POLITICAL STELASS PRECURSOR 041-316 PCLYROTER SIMILAL BACKADOCE FICENCY RELIEVAS PROGRAM POLITICAL BACKADOCE FILENCER PARTICIPATION POLITICAL BACKADOCE FILENCER PARTICIPATION POLITICAL BACKADOCE FILENCER PARTICIPATION			1	Ī		-	-		
OAG POLYMOTER SHIPM SHIP			٦			-			· ·
0.40 POLYPROTERN SHAMP BACHOOFFICENCY VIRUS [AGAI] SOLATE 10-50			1						<u>-</u>
0.00 PGC YPROTEIN 1900AND PGC YEACH 1910 191-101			26-346		1	+	-		
QAG PGLYROTEN SURAN BENEVICE 1913.18		-	3.21.7	473-503		-			! -
OAG POLYPROTEN SPACE CONTROL (SIVICPE) 191-315		$\overline{}$	92-336			 			Ļ
QAG PGLYPROTEN CHROCARGE INCIDENT (180-194 113-194			11.335	1				-	!
OAG POLITROTEIN SIRAIAN DARANGOLIAN 194-31 194-31			2.50		_	1	1		
ORG POLYMOTERM THE MAN SAT COMANY WILLS IT STRAIN 17) 173-706 186-810 186-810			100		-				:
PROBABLE FELICASE			27.50	164-120		1			 -
PAGGABLE PELICASE	100	15	61.502						+
PROBABLE FELECASE			19.30	Г	_	-			ļ
PROBABLE PELICASE VALICELIA-SOSTEN VALIS ISTANDEN DUMANY			15:51	711-621				1	1
PROMOGOLUTION-LETELASE PLECIASOR BOYING COLOMAYRUS (STRAIN F19) HEMAGOLUTION-LETELASE PLECIASOR BOYING COROMAYRUS (STRAIN LE-18) HEMAGOLUTION-LETELASE PLECIASOR BOYING COROMAYRUS (STRAIN QUEBEC) HEMAGOLUTION-LETELASE PLECIASOR BOYING COROMAYRUS (STRAIN QUEBEC) FEMAGOLUTION-LETELASE PLECIASOR HUMAN COROMAYRUS (STRAIN OCL) FEMAGOLUTION-LETELASE PLECIASOR RICHARDS (STRAIN ANCHOLVE)		(V)	54.247						1
HEMOGULIPON-ESTEMAS PLECUSOR BOYDE CORONAVRIUS (STAMPLY-119) HEMOGULIPON-ESTEMASS PLECUSOR BOYDE CORONAVRIUS (STAMP QUEBEC) HEMOGULIPON-ESTEMASS PLECUSOR BOYDE CORONAVRIUS (STAMP QUEBEC) HEMOGULIPON-ESTEMASS PLECUSOR BOYDE CORONAVRIUS (STAMP OCES) CHEMOGULIPON-ESTEMASS PLECUSOR BOYDE CORONAVRIUS (STAMP OCES) CHEMOGULIPON-ESTEMASS PLECUSOR BOYDE CORONAVRIUS (STAMP ACCOUNTS)	2								1
Y HEMACOLITIRALE INVESTIGATE PRECINSOR BOYING CORONAVRIUS (STRAIN MEBUS) 4 HEMACOLITIRALE STEAMS PRECINSOR BOYING CORONAVRIUS (STRAIN QUEBEC). 1 HEMACOLITIRALE STEAMS PRECINSOR RICHARD CORONAVRIUS (STRAIN CALL) 1 HEMACOLITIRALE PRECINSOR RICHARD (STRAIN VALCHOVAS).					-			-	-
HEMACOLUTION ESTEMASE PRECURSOR BOWNE CORONAVIRUS (STIAIN QUEBEC). HEMACOLUTION ESTEMASE PRECURSOR HUMAN CORONAVIRUS (STIAIN OCCU). HEMACOLUTION ESTEMASE PRECURSOR HUMAN CORONAVIRUS (STIAIN AAACHVAM)			300						1
HEMADOGLUTHING ESTERNIS PRECURSOR HUMAN CORONAVIRUS (STIAIN OCA)) HEMADOGLUTHING LETTRASE PRECURSOR RIFLUENZA A VIRUS (STIAIN A/AICHUZNE)									1
C HEMACOLUTION ESTACE PERCENTION (STRAIN VAICHONS)					-				\downarrow
				1					-
HENAGGLUTDEN PILLUSON PRECUISON		(40)		1	-		 -		4
INDIVIDUAL PLECUISOR		S (STRAIN A/BUDGENIGAR/HOKKAIDOVI/77) 31							

		111 Menter for heritalisation		17	П		П		
PCCEME	ALLMOTTS		415	ARCA LANGE	48641-	1000	4	Ī	
THERANT	NEW ACCEPTION PRECIDENT	ENZA A VIRUS (STRAIN ACHICKEWALABAMAI/7)	376.454						; ;
Ment Andre	AND A COST OFFICE PERSONS			7					:
PICENT MENO	TOTAL SOCIETY OF STREET	Ē		716-121					!
THE PARTY OF THE P	VIEW ACCUITION PRECITISOR	×13.6				 -			
יובאיר ואכאיר	CONTRACTOR OF THE PROPERTY OF THE PARTY OF T	INTLUENZA A VIRUS (STRAIN ACHICKENSCOTLAND/19)	277.460	20.70	 		†		
PIENT MEN	INSTAGOS ITTOM PRECURSOR		*	****					
TANK TANK	NEW ACCULTONN PRECURSOR		7						
PATENTA IADAS	NEWADOLUTINE PRECURSOR	INTLUENZA A VIRUS (STRAIN ADUCK/ALBERTA/6076)		003-34 i	+			Ī	
PACKA TABAS	MENANCE LITTING PRECURSOR	INFLUENZA A VIRUS (STRAIN ADUCK/ALBERTA/TU/6)	2						
THE PARTY	MANAGO I TOWN PRECIDENDS	DEFLUENZA A VIRUS (STRAIN ADUCIVALBEATA/15/16)	179-478	204-368	+				
PIGENT AUA	MENACOLI LITTORI PRECUESOR	INFLUENZA A VINUS (STRAIN ADUCK/CZECHOSLOVAKIA/36)	7.7.		+	-	†	T	
THE WAY	AND AND AND AND AND AND AND AND AND AND	INSTUENZA A VIXUS (STRAIN ANDICK/ENGLAND/1/36)	21.55	172-472					
PREMA IADE	ACTION OF THE PARTY IN SOME	INFLUENZA A VIRUS (STRADY A/DUCK/HOKKAIDO/5/77)	164-440				†		
PIESTA IADRI	HENNOCH I PRINT DE COMPONE	INFLUENZA A VIRUS (STRAIN ADUCKAIOKKAIDONNO)	164-440						
Mark Mark	THE PARTY OF THE P	INTLUENZA A VIRUS (STRAIN ADUCK/HOKKAIDO/J/No)	364-440			-			
1	Land A COLUMN PRECITE SOR	RIFLUENZA A VIRUS (STRAIN ARUCKMOKKAIDOT/182)	164.440						
WHEMA MOTO	THE ACT OF THE PARTY AND THE SOUTH S	INFLUENZA A VIRUS (STRAIN ADUCIÓNOK KAIDOZIAZ)	364-440				†		
THE NAME OF THE PARTY OF THE PA	LELA COL TETRAN PERCITE SOR	Drituenza a virus (strady aguckaiokkaidorgas)	364-460		1		1		
PREMA IAURE	THE PARTY OF THE P	INTLUENZA A VIRUS (STRAIN ADUCKHOKKAIDO/1045)	364.40		1	+	1		
PREMA IAURI	CHANGO PRODUCTION	INTLUENZA A VIRUS (STRAIN ANDUCKARELAND/113/83)	179-471	186-381	-		1		
PROM AND	TOTAL PROPERTY OF THE PROPERTY	INFLUENCE A YTHUS (STRAIN ANDUCKAGENTHUS/S46/76	21.55		-		1		
PHENA IADRA	ROMACCION TRECONOR	INFLITENZA A VIRUS (STRAIN A/DUCKAEMPHIS/921/74)	380-456						
PIEMA IADIA	HEMACGLUTININ PACCASON	DATLIENZA A VIRUS (STRAIN ADUCKNEW YORK/12/14)	21.55			-			
PIENA IADRY	HEMACGULTURIN PRECURSOR	MELLIENZA A VIRUS (STRAIN ADUCKNEW ZEALANDOIMS)	338-454						
PHEMA IADIZ	HEMAGGUITMIN PRECURSOR	INTLIENZA A VIRUS (STRAIN ADUCKUKRAINE/1/80)	21-35						
HENA IADU	PENACEUTING PRECIONAL	MELLIENZA A VIRUS (STRAIN ADUCKURRAINEJ181)	380-456						
PHEMA IADG	MENACOLULINA PRECUNSOR	INSTITUTION A VIRUS (STRAIN AEMOLANDIZIO)	380-456						
HENG MEN	MEMACALUI INUN PRESCURSON	INTELLENZA A YRUS ISTRAIN AFOWL PLAGUE VIRUSMOSTOCK 111411	לודיונס						
MENA MAN	HEMACION OF THE PARTY OF THE PA	INFLUENZA A VIRUS (STRAIN MOREY TEALVAUSTRALIA2/19)	378-454			1			
PHENA LAGRE	MEMACALULINIA PERCENSION	INFLUENZA A VIRUS (STRAIN A/CULL/MARYLAND/19/17)	374.473						
PHENCA LACED	PERMACULATION PRECIOENTS	INTELESTA A VIRUS (STRAIN AGULLASTRAKHANDI)784)	377-476						
MENCY INCOM	PENALCAL DI IMIN PRECUMBEN	DELUENZA A VIRUS (STRATH A/EQUING/ALGIERS/72)	379-455						
PENA MAR	LICENACOS ITTIMA PRECITICOS	DOLUENZA A VIRUS (STRAIN AEQUINE/CAMBRIDGE/IM))	113-146	٦					
THE WAY	LIGHT OF THIND PRECINGOR	INGLUENZA A VIRUS (STRAIN ACQUINECAMORIDGEIM))	113-146	360-414 503-537		4			
CHAIN AND	HEMACOLUTION PRECURSOR	INTLUENZA A VIRUS (STRAIN AEQUINE/C DETROIT/1/84)	360-414	103-507		-			
MENA MOS	HEMACOLUTININ PRECUNSOR	INTLUENZA A VIRUS (STRAIN ACQUINE/DETROIT/IMA)	360-414	705-027	+				
PIEMA IMBO	HEMADOLUTININ PRECURSOR	INTLUENZA A VIRUS (STRAIN ARQUINEFUNIAIREGUEAUTO)			-	-			L
PHEMA JANGG	HEMADGLUTTHTN PRECURSOR	INTLUENZA A VIRUS (STRAIN AEQUINEMENT LUCK 1/204)	557						
PHEMA LANK?	HEMAGGLUTININ PRECURSOR	INTLUDICA A VICUS (STRAIN ARQUINGRES) CARATTONINA	113.146	160-414 503-537					
PHEMA WALE	NEMA OCEUTIVIDI PRECURSOR	INTURKA A VIKUS (STRAIN MEQUINGALEMINOLOGICAL)	13:18	T					
PIEMA MEO	HEMADOLUTDAN PRECURSOR	TATLUENZA A VOICE (STRAIN ARCOINEACHAIGH) (STRAIN ARCOINEACHAIGH) (STRAIN ARCOINEACHAIGH) (STRAIN ARCOINEACHAIGH)		1					
PIEMA IMPO	HEMAGGLUTIMIN PRECURSOR	INTEREST & VIEW 1971 AND AND UNITED BY MARKETON	179.455						1
PIEMA MOON	NEWACCLUTOW PRECURSOR	INCLUENCE A VIRUS (STRAIN ACOUNTANEW MARKETHITT)	113.146	366-414 503-537	1				
PICKA INDO	HEMAGGLUTIMIN PILECUISUR .	INTELLEGIZA A VIRUS (STRAIN A/EDUNE/PRAGUE/1/36)	113-146	360-484 503-537					
PHENA INDIA	HEMAGGLUTININ PRECURSOR	INFLUENZA A VTRUS (STAATN A EQUINE A OXIANIANO)	178-455						
PHEMA IMPRO	PENACKLUTIMIN PALLUASON	INGLIENZA A YIRUS (STRAIN AEGUINE/SANTIAGO/1/85)	179-455						-
PIESKA IAHSA	MEMACACUININ PACOMOON	INFLUENZA A VIRUS (STRAIN A/EQUINE/SAO PAULO/1/1/6)	113-146	360-434 503-53					
PHENA LAHER	HEMACALOLININ PRECOMOS	INTLUENZA A VIRUS (STRAIN AEQUINE/SWITZERLAND/137/12)	113:146	366.484 503.537					
WIEDA IAHSW	HOMACOUNTY PROPERTY SOLVEN	DIFLUENCA A VIRUS (STRAIN AEQUINETENNESSEE/1/16)				+			
ACAN MATE	MENANCE ITTION PRECIABOR	INFLUENZA A YIRUS (STRAIN ARQUINE/TOKYO/TI)	130.435		.				-
MON MARIE	TOWNS TO SELECT MONEY	INTLUENZA A VIRUS (STRAIN AEQUINEAURUGUAY/1/A))	379-455		-				
PREDATA LANGE	HEMACOLUININ TREVOREST				-				

		All Viruses (se betterleghefft)	AREAL	Γ !	AREA ARE	AREA A	4 1938	1	Q Q	1
PCGEME	ALLXON			502-547		1	†			
THE RANGE	PROTEIN			306-341						
PIEDIA IAIAP	MENACOLUTININ PRECUASOR		Τ	506-348						
PHENA LAKE	HENCADOLUTINA PASCUASOR	-	Γ				 			
HENCE TALEN	HEMACOLUTIVITY PLECUMSON	KINAN		-	-		-			Ì
PIENA IAMA	HEMAGGLUTBRIN PRECURSOR	- 1	757 91	-			 			
PHEMA INMAS	HEMACOLUTININ PALLONSON	_	180.4%							
HEMA IAMAO	HEMADOLUTININ PRELOMSON	т	47, 40				1			
HEDA IAMEI	KENAGGLUTBITK PRECURSOR									Ì
HEMA IAMES	HEMAGGLUTININ PRECUESAS			1	-	-				
PHELIA IAMES	HEMAGOLUTININ PRECUISOR	ş								1
PHENA IAMIN	NEW AGGLUTININ PRECURSOR		360-630							į
PUEMA TANTE	HEMAGGLUTOWN PRECURSOR	NESSEMM)	718-477	6.6.93		Ī				:
MANA IAM	HEMAGGLUTIONEN PRECURSOR		376-478	Š	1	† 				. !
	HEMACOLUTININ PRECURSOR	ENEW IERSI	378-454							
	LELA COLLITION PRECURSOR		338-454			ļ				
HENCE INCOM	SELLA OCT ITTININ PRECURSOR		119434	30A-552		1	Ī			<u>:</u>
HEMA INSE	TOTAL DESCRIPTION	DOLUENZA A VIRUS (STRAIN ASSIERAM CONTRACTOR A STRAIN	13:146	377.469						
PIEMA IASHO	PENADGLUTININ PRICORDI	DALUENZA A VIRUS (STRAFN ASTARLINGVICTORIAS)	110.41	18:38						:
PIEMA IASTA	PEMADOLUTPIN PRELUMON	INFLUENZA A VIRUS (STRAIN ACTURKEYARELANDI) 1971)							ļ	:
HEMA LATE!	NEWADOLUTOWN PRECURSOR	ACTUENZA A VIRUS (STRAIN ATURKEYAIINNESOTAATIMO			-	İ				نـ
NUTAL IATION	HEMADOLUTIMIN PLECURSOIL	THE STATE OF THE STRAIN ANDREE YOUTANOT 112/46)	207-7.00	2						-
O III VIVE	HEMADOLLTOWN PRECURSOR	INCLUENCE STREET AND AND REPONTARION (1946)	378-454	41.340	1				_	_
	MENAPOR UTDATA PRECURSOR	DOLUMAA VIACO (STANTA ANTINE VARE CONT.)	10-64	314.474	1					:
NOW WIN	ACTUAL OCU LIFERING PARECURSOR	DALLENZA A VIRUS (BITACIA ALLONAMIA)	111-111	417.539		ļ				:
PER INTE	Transport to the state of the s	INTLUENZA A VIRUS (STRAIN ALIGANE LINEINCOLONIALI	5							
PIEMA IATKW	MENANCE CONTRACTOR	INTLUENZA A VIRUS (STRAIN ATERAVAUS INCLINATION	717							
HEMA INTIA	MENADOLUTININ PRECURSOR	DELUENZA A VIRUS (STRAIN AUDORNIO772)	200	100.343	-					
HEMA IAUDO	HEMAGGLUTININ PRECUASOR	DITLUENZA A VIRUS (STRAIN AUSSRAOT)								1
HENA LAUSS	ADALOGIUTININ PRECUISOR	INFI 1/FNZA A VIRUS (STRAIN AVICTORUA) (1)								
PASSA IAVIT	HEMACK UTDAN PLECUISOR	TAKE LENZA A VIRUS (STRAIN AWILSON-SHITTUD))								-
MONA LAWG.	HENALOGIUTINAN PRECURSOR	PART THE VALUE (STRAIN ASWINE/COLDRADO/1/7)	380-4%	1				_		ا
NATURA 1AZCO	HEMADOLUTININ PILECURSOR	THE LEAST A WRITE (STRAIN ASWINEHOND KONGALITI)	364-440	1	+				_	_
	HELLA CICE LITTONIA PRECURSOR	INTEREST TO THE PARTY OF THE PROPERTY OF THE P	164-440		1					_
	LIFEWACCE UTININ PRECURSOR	INPLUENCE A VINUE (STATE AND A AUTHENNIANALLY (STATE)	379.478	17.90						<u> </u>
\ \ \	LELY ACCULTANT PRECURSOR	DOLLERZA A VIROS (STRAMS ASSUMENTED PRESEVITIVE)	179.470	506.547						!
MENA IAZIN	LINES AND THE PRECIESOR	PATUENZA A VIEUS (STRAIN ASWINDS IN 1974	380-456	L						-
DA MA	AND A STRAIN PRECIATION	DOLUENZA A VIRUS (SIRAIN ASMINICAM	188-473							!
MONA MZUK	TOTAL TANKS OF THE STATE OF THE	INTLUBRIZA B VIRUS (STRAIN BITTELLING III)	178.463							 Ļ
HENLY INCOME	HEMACOLULIAN PACCOCCI	DALUENZA S VIRUS (STRAIN MONNAS)								1
PHENA DOBBO	HEMADOLUTININ PRECUESOR	INTLUENZA 8 VIRUS (STRAIN INFINOLAND/12/82)		-	 					
HENC DOEN	MENIAGGLUTDON PRECUISOR	INTITIENZA B VIRUS (STRAIN BAIONG KONGENI)	181-401							
HENCY DIBIO	HEMAGGLUTININ PRECURSOR	DATITIONS A VIEWS (STRAIN BAEE/40)	787-473							_
MENA POLIS	HEMAGGLUTDAN PLECURSON	PACT I TENZ & WELLS (STRAIN BALARYLAND/S9)	337-462		1					
CONTROL ALVERTA	HEMACOLUTINEN PRECURSOR	SELLENDA B VIETE (STRAIN BACEADHISAGA)	381-468							
STATE OF THE PERSON	ADJANCE UTININ PRECURSOR	DATOLINE AND COME ON BOLE GON STO	386-471						-	Ľ
	NEW AGGLUTINGS PRECUBSOR	INPLOEMENT STATES OF THE AM BUSINGAPORE/22/79)	129-916					-	-	L
S	HOLLAGGE UTIONS PRECURSOR,	DOLUZIA A VINOS (STEAM BATICS LIDAD)	379-464						-	
	MEMACOR LITTON PRECURSOR.	DATUENZA B VIAUS (21100): TOTALI DATUENZA	38-186				 	\downarrow	+	ļ
PHENA PHENS	HEALTH OF THE PRECIESOR	INTLUENZA B VIRUS (STRAIN BYNL LUGANOSTS)	18.43						-	+
MENA PRIVI	ACT TO SECURE STATE	ł	187-1831						1	<u> </u>
PIEDAS DIBVR	HEMACALO INTERNATIONAL PROPERTY RECORD	RELUENZA C VIRUS (STRAIN CCALIFORNIA)	651.53	\ -				_	1	+
PHEDA INCCA	HEMANGEO LINES PROCESSES	INTLUENZA C VIRUS (STRAIN CENGLANDRY 193)	95	-						1
HENA DICEN	HEMAOGLUTININ PACCURSON	INFLUENCA C VIXUS (STRAIN COREAT LAKES/1167/14)		-			٠			-
PHENA DICOL	HEMAGGLUTING FILECURSUA	INTLUENZA C VIRUS (STIVAIN CHYOGOLIA))		1						1
PARTIES DECITY	MENADOLUTINON	PATH 1 THATA C VIRUS (STRAIN CJOHANNESBURG/1/66)	436-372	1						
	HEMAGGE UTTIVEN PRECURSOR	LATER AND CHANGE	470-558							

	SHOP AND	All Viraces (ne bacteriophages)	П	Ιī	П			7134		14,187
1000	PEOTECH IN		I	A SECTION AND ASSESSMENT OF THE PERSON AND ADDRESS OF THE PERSON AND A	T	Ţ	ī	Τ		1
100	SENANCE LITTING PRECIASOR	DOTLUENZA C VIXUS (STRAIN CAUSSISSIPPINO)	470-55	1	\dagger	t	1			
AVOID ALONG	MPMACCE LITTING		470-558		†	\dagger	1			
1000	VENANCE INTROM PRECIESOR		471.539	1		1				
THE PARTY OF THE P	MENACON UTININ PRECURSOR		471-559		1	1		Ī		
MENA PATE	ANTARI ER VIRUS (STRAIM HALLE)	62	471-559	<u> </u>		+				
PIENA DICTA	HEMAGGLUTDIN PRECURSOR		431-350		1	1				
PHEMA DACYA	HEMAGGLUTININ PLECURSOR	ATAION!)	471-534	1	1	†	1			
PHENT MEASE	HEMADOL LITBIN-HEURANDHIDASE	เรอเก	8		\dagger		İ			
PHENTA MOTABLE	HEMADOL LITERIA-NEUTAMINIDASE		26-90		1		1			
MENA MEAS	HEMACCE LITTEN NEUTAMINEDASE		46-87		1		1			
PLEMA MEACV	MEMACI LITINGH MELITAMINIDASE	MEASLES VIRUS (STRAIN YAMAGATA-1)	46-87		1	1	1			
BUTTAL VARIABLE	SEMANCE INDOMESTICATION SE	AKDAPS VIRUS (STRAD) SBL-I	34.99			1	1			
AUTON AUTON	MENAGOR LITTOWN ACTOR AND TO A SECOND ASSE	MUDDES VIXUS (STRAIN AIIYAHARA VACCINE)	34.99		1		1			
MONTH MANDE	HEMADOR LITTORN-NEUTANIDASE	INDERS VINUS (STRADH RW)	34.99	-	1	1				
PARTY MANAGE	HEMADOR LITTORINACINAACTION SE	INDIACYS VIRUS (STRAIN SBL)			1		1			i
THE PARTY	NEW ACCOUNT OF THE AMENDO SE	NEWCASTLE DISEASE VIRUS (STRATH AUSTRALIA-VICTORUA/32) 1-52		477.529		1				
THE PARTY	NEW ACCUITMENT NOTIFICATION SE	NEWCASTLE DISEASE VIRUS (STRAIN BEAUDETTE C45)	9		1	1			-	
	HEMACOS LITININ-NEURAMINIDASE	NEWCASTLE DISEASE VIRUS (STRATH D26/16)								-
MENT MOVE	HEMAGG LITININ-NEURANDMIDASE	NEWCASTLE DISEASE VIRUS (STRAIN MIYADERAJI)	:- :-			1	Ī			
CACA MOVE	HEMAGG: LITTOWN-NEUTANOMDASE	NEWCASTLE DISEASE VIRUS (STRAIN QUEENSLAND/66)	2							
	HEMACO ITTOTALNET BANDODASE	NEWCASTLE DISEASE VIRUS (STAAIN TEXAS G B./41)	67		1					
	VENANCE FORMS MEIRANDOMSE	NEWCASTLE DISEASE VIRUS (STRAIN ULSTEINST)	1-52				1			
VACAL AND TO	LIPLACOLITION AND MANDASE		19-73	-	1					
MULTINA BILITAR	SEMACON INTONNABILITA AND IN A SE	VIRUS (STRAIN WASHINGTOW1951)	66-110		1					
PRESENT PRINT	NEWACCE INDONVELEANDEDASE	HUMAN RABAINFLUENZA 2 VIRUS	347-781		1					
THE STATE	HPMAGG 17DND-NEURAMBYDASB	HUMAN PARAINFLUENZA 1 VIRUS (STRAIN TOSHIDA)	247-281	-		1				
PLENA PUB	HEMACOLUTININATURANOMDASS				1	1				
PIGENA PURA	NEMAGGLUTDRINNEURALUMANTOMIDASE	1	T	394-428	1	1				
PHEMA PITHA	HEMACCLUTOWN-NEURALMIDASE	KUMAN PARAINTLUENZA 3 VIRUS (STRAIN AUS/12485474)	30-610	100	†	1	T			
PHEMA PUSHT	HEMADOLUTINEN-HEURAMHIDASE	HUMAN PALAINPLUENZA 3 VIRUS (STILAIN 18.XXXXXXI)	T		1		1			
PHENA PICHU	HEMAGOLUTHEN-VEURAMMIDASE	HUMAN PALAINT UENZA 3 VIRUS (STRAIN TEXMOSTE)	01.010	167.701	T					
PIEMA PURV	HEMACCLUTHON-NEURAMINDASE		Τ	104-428						
PHEMA MINW	MENTAGOLUTUM NEURANDANS	_	T	304.428						
MENA PURA	KENACCEUTINITHE LICOMINALASE	STRAIN PARAMETURIZA 4A VIRUS (STRAIN TOSHIDA)	10-35	-						
PIEMA PIANA	PERMACKED INTO PRECIDENCE AND PROPERTY OF COLUMN PRICE OF COLU	PACCOON POXVIRUS	166-214 25	256-290						
HOMA MACA	HEN A COLUMNIA THE WASHINGTON	AUNDEAPEST VIRUS (STRAIN KABETE O)	П							
PLENA BOOL	HEMACCI UTINDA NEURAMBUDASE	ANDERPEST VIRUS (STRAIN L.)		191-225		1	1			
PARTA COMM	HEMAGGLUTDM-NEUNUMINIDASE	SENDAI VIRUS (STRAIN Z / HOST MUTANTS)	37.110			1				1
MENA CENTR	NEMACCL UTING WELDLANDNIDASE	SENDAI VIRUS (STRATN FUSITINTI)	2:12	1	1	1				İ
MENA SENDA	HEMAOGLUTDER-WEURANGNEDASE	SENDAJ VIRUS (STRAIN HAURIS)	37:10		1	1				
MICKA SEND	HEMACGLUTIONSHIPLINANIMIDASE	SENDAI VIRUS (STRAIN HV))	37.110	1	1	İ				
PAGNA KDOZ	HEDLAGGLUTTNEH-NEURAMINTDASS	SENDAI VIRUS (STRAIN Z)			1	 	-			-
PHOMA SV41	HENCAGG UTININ-HEURANINIDASE	SDAAN VOUS 41	1		1	†				
PHODALA SVS	HEMADOCLUTININ-NEUTANINIDASE	SDIDAN VIDUS S (STRAIN W.))	17.12	1	1	1	1			
PYEMA SVSUN	HENZAGGLUTININ-YEUKAMINIDASE	SDAAN VOUS S (ISOLATE HUMANLM)	****	-	1	1				
PIGEMA VARV	H	VAJUOLA VIRUS	117:311	+		1				
PHE YO ADEGI	PERIPENTONAL HEXON-ASSOCIATED PROTEIN	HUMAN ADENOVIRUS TYPE 1	\$6.0	1	1	1				
PHEXT ADEOS	PERIPERTONAL HEXON ASSOCIATED PROTEIN	HUNCAN ADENOVIRUS TYPE 5	2	$\frac{1}{1}$	1	1				
PHEXY ADEOS	HEXON-ASSOCIATED PROTEIN	HUMAN ADENOVIRUS TYPE 2		+		1				
HEXP ADEON	HEXON-ASSOCIATED PROTEIN	HOAAN ADENOVITUS TYPE 5			Ť	1				
PEXT ADEO?	HEXON. ASSOCIATED PROTEIN	HUMAN ADENOVIRUS IYPE I, AND HUMAN ADENOVINAS THE	1,1,1	1	1					

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		PAN)	3-44	338-410	-				<u> </u>
		(AA)	100	378-419					
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		MAIN STRASBUOKU)			-				
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		DXS)	2			ŀ			
			7	117.00			_		
	100	AT DAY OVEDAL DVIRUS (STRAIN AD169)	27-96	T		-	L	L	
	2		331-365		1			-	L
		GELOTTI)	131-365						L
			124-162				-	-	L
			466-500		1		 		L
Π	TWOILE		341-375						L
\prod	T STORE		20.93			1			L
T	AND TRANSPORT PROTEIN		60-112	290-340 647-691	169		+		ļ
	T PROTEIN	MUMINE CYTOMEDALOVINOS (3 INVINA SPECIAL SPECI	186-333	303-337					1
	ACESSING AND TRANSPORT PROTEIN	SEUDORABIES VOUS (STRAIN INDIANATIONS	76.22						
T			190-224					-	\downarrow
1	201 A191	BOVINE KERPESVIRUS TYPE I (STRAIN NAV)	1022.1056						1
٦	VATOR PR		30.00	-	_				1
PICH HSVAO TRANS-ALTIMO	EN CA		1	1	-				4
٦	-		100						1
PIEED HONNA THANSCHULLION	Γ			+		L			4
	TRANSCHIPTIONAL PEDULATION TEN HOMOLOG			100	-				
	MOLOG	VALICELLA-ZOSTER VIRUS (STRAIN DURIAS)		+					1
PEAN V2VD TRANSCIUTIO		EQUING HEIPESVIRUS TYPE 4 (STRAIN 1942)		1	-	-			4
		EOUTHE HEAPESYINUS TYPE I (STRAIN ABAP)		+					4
PEGS HIVED DOGDLATE-E		GENDESVIRUS SAMORU (STRAIN !!)							-
	DOCEDIATE EASE, TRUIBIN	HIDGA CYTCHEGALOVIRUS (STRAIN AD169)		+			-		
PIEGS HOAVA HYPOTHETICA		HIMAN CYTOMEGALOVIRUS (STIMIN AD169)		1	1			Ĺ	
Г	TORE CHAPT	THE THE BARCOMA VIRUS (STRAIN HARDY-ZUCKERWAN 2)	ě	1		-			
Γ	TOTAL DECIT	ARET CON MUNDE LEUKENDA VIRUS							
		AVTO AGE OF DE LETTE BATA VIRUS	13.23	261.304	+				L
Γ	AKT KINASE TRANSFORMING PROTEIN	ANTERNA ANTONIA VITALE (STRAIN GARDNER ANNETER)	ž	104-171	+	+	-		
Γ	TYROSDIE-PROTEIN KONASE TILANSFURIENO PRO	AND PROFILE THE SAFCOMA VIRUS (STRAIN GALDNER, RASHEED)	22	Τ					_
	TYROSDIE-PROTEDN KONASE TRANSPORGUNO PROT	CHING THOU THE TAX COMA VILLIS (STRAIN MCDONOUGH)	22.5	200	1		-		Ц
L	PAS TYROSDE KDIASE TRANSFOLLING FROIEIN	A GAN EAR-COMA VIRUS (STRAIN PRCII)	\$	1					

		An Vicase (se bacterios): 15	T	i	Ī	ADTAG	ARFAG	ARIA	
PCCENE		YRUS]	200	1	1	Ţ	l	-
CHERANG	PROTEIN PROFES TO ANGEORISM PROT	FUTINAME SARCOMA VIRUS		١				-	:
PKIPS FUISV		AMERICA MODRE! ENTOMOPOXYIRUS	17.61						i İ
PKITH AMENY	THYMODIRE KINASE	CABBIOCYCEL CTRAIN KF.							:
PKITH CAPY	THYMODEL KINASE	CONTRACTOR CALLS COLLAND BOS.E.	238-362 43	431-472		1			
PKTH EBV	THYMODOL KONASE	PARTY OF THE PARTY	90-124			-			
PKITH HSVII	THYMORE KINASE	CALLES AN ALL DA VIDER CTARE I ATTRADA CL. [0]	\$6-136			-			
PKITH MSVIC	THYMDRE KINASE	TEN 23 ALICE AND RESTORED TO STRAIN WEEK	90-134						!!!!
PICITH MSVIB	THYMORIE KRIASE	SEASON OF THE CASE OF TAKEN AND STREET	90-124						
PRITH MSVIK	THYMDOM KINASE	THE POST OF THE PARTY OF THE PARTY STATES	20.134						
PRITH HSVIS	THYMIDINE KINASE	Lease on the Evidence (TVPE 27 CTRAIN 333)	61:15						
PKITH HSV13	THYMODUS KINASE	REPUTED SINCIPLE AND ACTUAL AC	616463						
PKITH HSVBM	THYMIDING KINASE	BOVING MALES VINGS TITE 2 (2015)	T	71.219					:
PKTTH HSVE4	THYMDONE KINASE	EQUING SERVESVIRUS TYPE 4 (STRAIN 1942)	Ī	78.130					:
PKITH MSVEB	THYMIDING KINASE	EQUINE IGENESVIRUS LTTE 1 (STRAIN AUT.)	١.						1
PKITH H3V	THYMIDINE KINASE	FELINE HERPESVIAUS (FELID HILATESVIAUS I)	4.0						•
PKITH HSVAR	THYMIDING KINASE	MARKOSET HERPESVIRUS					 -		
PKITTH HSVXA	THYMIDME KINASE	HEAPESVIRUS SAINIRI (STRAIN 11)	,,,,			 -	 -		1
SVE STIME		PSEUDORABIES VIRUS (STRAIN NIA-1)	101 9		-			-	
PKWIL AVINO	MIL SERING/THREONINE-PROTEIN KINASE TRANSF	AVIAN RETROVIRUS ABIZ	1						i
PKE15 HSVI)		ICTALUMD HERPESYIRUS I	Τ	301.116	-				
PKES HEVIL	PROBABLE SERING/TIMEONINE PROTEIN KINASE	KERPES SIMPLEX VIRUS (TYPE 1/STRAIN 17)	Ţ,	19:00					
PY B 34 WEVEL		ICTALUMD HERPESVIRUS I	Ţ			-	_		
AVE AT LACUTA	BAS STRING THURONING PROTEIN KINASE TRANSF	MURINE SARCONA VIRUS 3611							
	10 KD PROTEIN KINASE HOMOLOG	VACCINGA VIRUS (STRAIN COPENTIAGEN)							
7777	10 KID PROTEIN KINASE HOMOLDG	VACCINTA VIRUS (STRAIN WR)							: : !
NAN LANGE	16 KD PROTEIN KINASE HOMOLOG	AAUGEA VIRUS				-		!	• •
PERRY VACCE	POSSIBLE PROTEIN KINASE B12	VACCINIA VIRUS (STRAIN COPEMIAGEN)						_	
PKERS VACCV	POSSIBLE PROTEIN KINASE BIZ	VACCERIA VIRUS (STRAÍN WR)	100.00						,
NACCE VACCE	POSSIBLE PROTEIN KINASE F10	VACCINIA VIRUS (STRAIN COPENHAGEN)	136		-		_		
PERSON VACOO	POSSIBLE PROTEIN KINASE F10	VACCINIA VIRUS (STRAIN L-IVT)	100 001		-	 	 -		
PELUT VARV		VANIOLA VIRUS			-				
PICROS AVISU			1						
PLATE AVOU	TYROSINE-PROTEIN KINASE TRANSFORKING PROT		133-169	-		L			
PKTHY VACCV		VACCIMA VIAUS (STANIM WALL (STANIM COLUMNS)	176.333						
PKYES AVISY	NASE TRANSFO	WING PROT AVIAN AMELONA VIAUS (STANIA TO)	441-475						
71.100 ADE02	LATE 100 KD PROTEIN	LUNAL A DENOVIETE TYPE 5	30.364			j	 -		!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!
PL 100_ADE05	LATE 100 KD PROTEIN	INDIAN ADENOVIRUS TYPE 40	П	101.413					
PLICO ADECO	LATE 100 KD PROTEIN	HUMAN ADENOVIRUS TYPE 41	П			+			
PL 100 ADE41	LATE IOURD PROJECT	HUMAN ADENOVIRUS TYPE 2	П	301-349					
PLSS ADEA	LATER SECTION	HIDAAN ADENOVIRUS TYPE S	٦	301.34	1		1		
M32 Allens	MACOUNTY TENTON	EPSTEIN-BARA VIRUS (STRAIN 895-1)		244-138	1				
A 2002	VANA CAPPING ENZYNG	SHOPE FIBROMA VIRUS (STRAIN KASZA)	2	623-636					
100 m	LANA CAPPAGE DIZYNE	VACCINIA VIRUS (STRAIN COPENHAGEN)		623-657					
	LAND A CAPPING ENZ YICE	VACCINIA VIRUS (STRAIN WR)		150-120		+			
PHOEL VALLY	Agrica Capenio EXZYME	(VARIOLA VIRUS		621-657		1			
PHOEL VALV	ACCOUNT DAY WATER	VACCIMIA VIRUS (STRAIN COPENHAGEN)	1	205-286			-		
WCS VACC	AND CASE OF STATE OF	VACCINIA VIRUS (STRAIN WR.)	T	30.516		1			
PMCES VACCY	MAKAN CAPANO BAZYAGE	VARIOLA VIRUS	Į	1					
AVGS AVG	ACCA CAMPIO DOWN	AFRICAN SWINE FEVER VIRUS (STRAIN BATIV)	_	179-313 738-772	F				
PMC ASPE	MONTH PROTEIN	ODONTOGLOSSUM RINGSPOT VIRUS	23-90		+		1	$\Big $	
2004	MONEY PROPERTY	PEPPER MILD MOTTLE VIRUS (STRAIN SPAIN)	35		1		-		
PAGOVE PPAVS	MOVEMBAL PROTECT	TOBACCO MILD CREEN MOSAIC VIRUS (TAVY STRAPM U.)	29-66	_	$\left\{ \right.$				
PACOVE THOMS	MOVEMENT FASTERS								

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TOBALCO MOTALC VIRUS (STRAIN TOWNOR)	33.44				+	Ì		i
	13:40							
	17-60							1
	111-156							
	116.164							
IAI	139-266	115-419						
	130-363	176-420				1		
ACCTLANSFORMEN PROTEIN	130-367	176-420						
	133-431							
	134-361	170-414						
	193-437							
	183-437	_						
TEN	97.	_						
	117.211							
	3	133-136						
	62-100	163-200	141.303	343-383				
NUCLEOCAPSID PROTEDY	176.239							İ
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	135.22							
NUCLEOCAPSID PROTEIN BUNTAN WALLA VIRUS		413.461						
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AFEAST ES VINUS (STRAIN IP.) CA)	186-336	180.4				1		

TULEANE BEST PROCESS OF THE STATE OF THE STA	HACLEGGASID PROTEIN MACLEGGASID PROTEIN	(css)MO	65.106 114.235	11-12-12-12-12-12-12-12-12-12-12-12-12-1	AREA J	ARTA	S S S S S S S S S S S S S S S S S S S	de la constant	4	
	CLECAND MOTEN CLECAND MOTEN	(cse/iAO)	$\top \top \top$	171-369						
	CLECCAPIO PROTEN CLECCAPIO PROTEN	(ESA)/NOI	$\Pi\Pi$	171-503						
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	LECCATED MOTERN LECCATED MOTERN LECCATED MOTERN LECCATED MOTERN LECCATED MOTERN LECCATED MOTERN LECCATED MOTERN LECCATED MOTERN LECCATED MOTERN LECCATED MOTERN			20.36	144.401	440.49				
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	TEOCAND MOTEN TEOCAND MOTEN TEOCAND NOTEN TEOCAND NOTEN TEOCAND MOTEN	PICHTHOL ARENAVIAUS	65-113							
	LEOCASIO MOTEN LEOCASIO MOTEN LEOCASIO MOTEN LEOCASIO MOTEN		71.116	175-159					_	
	TEOCAPSID MOTEN TEOCAPSID PROTEIN TEOCAPSID PROTEIN	PURIALA VIRUS (STRAIN HALLINAS RI)	1.35	40.75	337.392			i	-	
П	TEOCAVSID PROTEIN	PUDMALA VIRUS (STRAIN SOTKANO)			317-115		-	-		
П	LEOCALSID PROTEIN	PNEUMIONIA VIRUS OF MICE	93-141	741-303	144-114				-	•
1		1	133-147				j]		
۲	MICH ECCAPETH PROTEIN	ST AIUTANTS)	111.111	145.404					; 	
1	A PL COLABOR PROTEIN		ur.en	343.404					-	
T	MICH BOCAPUD PROTEDA		117.171	145-408						:
T	Mary encloses and the second s	113	1.33	40.74	100-000					
THE SECOND	A PER PARTIES.		315.267	373-406	418-466					
T	TOTAL TOTAL BANKERS	IV NET VIEWS	337-366							
	TECCASIONE		Γ	210-264						
1	NUCLEUCAVSID PROTEIN									·
1	LECKARD PROJECT	TO WILLY VIBILE (SOAZE) LAN ISON ATE COMMINGE	20.170						ĺ	
7	NUCLEOCAPSID PROTEIN		78.120							
٦	MUCLEOCATSID PROJEM		70,120	Ì						
_	MUCLEOCALSID PROTEIN	T	31:102	İ			 			
T	MACLE CLANSING PACIFICATION	MEAN MENORAHAGIC SEPTICENTA VINUS (STRAIN 07-71)	349-325							
Ť	TOTAL CONTROL BATTER	٥	147-110	149.325						
T	AUCIECA PER PROTEIN	Ž	43.108							
T	AND ROCAPED PROTED		67.115							
DIEN TRANSPORT	MACH ROCAPSID PROTEIN	Ĺ	13-113							
Ī	NEGATIVE FACTOR	TE BEN)	7-41							
T	NEGATIVE FACTOR		141						j	-
	NEGATIVE FACTOR	_	3:5	_						
Ī	AEGATIVE FACTOR	S S	29-150					1	1	
Γ	NEGATIVE FACTOR		101.149							:
Ī	HEGATIVE FACTOR	2						1	ĺ	
Ī	NEGATIVE FACTOR	SCHILAH DIGITHODEFICIENCY VIAUS (F316/SARH ISOLATE)	1	1				İ	j	
PINEAL LABOA NEUT	REURAL CONTRACTOR .	רעטעער				1	†		j	
Ī	WEURANDHORSE	MOLIANS)	+	†	T	1	+	1	Ì	į
Г	NEURANDIMASE	INFLUENZA A VIRUS (STRAM ACHILE/IM)		1			1	+	†	
	WEUDLANDASE	INFLUENZA A VIRUS (STILAIN ACHICKEN/PENNSYLVANIA/13/5/ 34		†	1	1		1	l	
PHEAM LACKS NEW	NEURANDASE	AKIMA125	74.30	1		1		\dagger	1	:
	NEURAMINIDASE	RETUENZA A VIRUS (STRAPH ADUCENGERALANYAP)				1	+	1	İ	
П	HELIKANDASE	2	Ī				\dagger		\dagger	
	<u>YEURANDYIDASE</u>	DOLLERZA A VILUS (STRAIN AEQUINECOLUEZA				†	-	T	Ť	
	NEURANDASE	T	100	70	T		+	1	+	Ī
	KEURAAMYDASE			1			1			Ì

PCGENE		All Virgini Indian Control Con	TOTAL	7917	ARAL	1000				
		VIRUS	20-01							
THE TANK	VALUE AVAINABLE	BELLALIYMT	11-05							
POLAN LALEN			16.61							
POLAN IANTE	WEIT AND ODASE		10-44							
MAN IARUS	VEID AVOIDASE		1							
TOTAL IN SIL	WEI THE AMERICA SE	ŝ	10-07							
1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	NEI IR AMENIDA SE	Γ	10-01							
WINE IN IN	ME IN AMDRIDASE	BATLUENZA A VIRUS (SURAIN ACKNIA) SAIAREJIAA)	16.61							
HOLAN LAUSS	VIET IN A LIDRIDA SE		24.	348-113						
MACH LAWRON	ALIONALDA CE		3	349-383						!
PACK DATE	NEGOCIAL PROPERTY OF THE PROPE		1	148.383						
PHILAM INBITE	NEUROMINIUMASE			141.312						:
PARAM DIBLE	KELIRANGRASE	AS) (STRAIN BA		115.00						į
PHILM DIBLY	NEURALEMIDASE	-	5							j
MAM POSMO	NEURANIMOASE		37.							
PARAL DIBLO	NEURALIMIDASE		3							
AND ALL PARCE	MELIZAMINIDASE		9-30	145.10						
1000	MEITHANDASE		9.39	16-11						
MINUS PARTY	MELITAMORDASE	51	61.5	=						
STORY INCOME			790-828							i !
PARAM INBVI	PACENTAL ESTRUCTURAL PROTEIN PRECURSOR		65-129	204-238						
PAST SIDE	THE PROPERTY OF A PROPERTY		12.	L						
PASS DISVA	MONTH OF THE PROPERTY		12							
PHSS TSWVB	NOS-STRUCTURAL PROTECT	TOMATO SPOTTED WILT VIRUS (STRAIN L.)	97.	10.10						
FRSS_TSW/L	MON. STRUCTURAL PROTEIN	AMSACTA MOOREI ENTONIOPOXVIRUS		97517	314.555					1
PHTFI ALGEN	MAC EDSIDE IMPROSITATION	CHORUSTONEURA DIENNIS ENTONOPOXVIRUS		348.200	249.59	_				
PHITPI CREPY	NOCHOSIDE TRUMOSTRATAGE	VACCINIA VIRUS (STIVAIN COPENHAGEN)	8	500	340.590					
PATE VACCC	MJCLEOSIDE IMPROJETATE	VACCINTA VIRUS (STRATM WIL)	,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,	131.503						į
PHTP1 VACCV	MUCLEOSOB INFROSTRATAGE	VARIOLA VIRUS		569.33						į
PINTEL VARV	MCC EQUID INTRICATION AT PROTEIN	HERPES SIMPLEX VIRUS (TYPE & STRAIN UNAMINATION	917.61							
PP100 HISWEU		VACCINGA VIRUS (STRAIM COPEMIAGEM)	9							!
PARI VACCC	POLY(A) POLYNIE ASE CATALYTIC SUBLINE	VACCINIA VIRUS (STRAIN WR)	9							İ
PPAPI VACCY	POLV(A) POLYMENASE CALALLY TO CHICKET	VARIOLA VIRUS				L				j
PALPI VARV	POLY(A) POLYTERANE CALALTIC CONTRACT	CAPADPOXVIRUS (STRAIN KS-!)								
PAPI CAPYK	POLY(A) POLYMERASE RECOMMENDED	FOWL POX VIRUS								1
PPAP2 FOWPV	POLY(A) POLYLERASE REGILATOR SOCIETION	VACCINIA VIRUS (STRAIN COPEMIAGEM)	1							:
PPAP VACCC	POLY(A) POLYMENASE RECOLATION SURINIT	VACCINIA VIRUS (STRAIN WR)								
PAPI VACCV		VARIOLA VIRUS		20.00		_				1
PPAPT VARV		ALTOGRAPHA CALIFORNICA MUCLEAR POLYIEDROSIS VIKUS								
PPELL NOVAC	11.1 KO PROTEIN IN PE STEGRON	CHECKIA PSELIDOTSUGATA MICETICAPSIO POLYICOMOSIS VIRUSIII-98								
PPERS JOVOP	II S KD PROTEIN IN P26 STECTION	A IT OCHAPHA CALIFORNICA NUCLEAR POLYHEDROSIS VIRUS								-
PEIS NEVAC	HAJOR DOJEDIA TE EASE, Y PROTEIN	CHECKIA PSEUDOTSUGATA MULTICAPSID POLYIEDEOSIS VIRUSING 240	200		100		_			j
SPESS NOVOP	MAJOR DAREDIATE EARLY PROTEIN	ATTICAL APIER CALIFORNICA POCLEAR POLYHEDROSIS VIRUS	3					_		
PPEAS NOVAC	띩	CARCYLA PESTIDOTSUGATA MULTICAPSID POCYTIEDROSIS VIRUS		-				_		
ON AN ANA	47 3 KD PROTEIN IN PE-P26 INTERCENIC MEDION	LA DA A DEMOVIBUS 1978 7	=				<u> </u>			
MAN ADEGY	MATURATION PROTEIN	TOWNS TARESTONE TARES	=							
AND ANEOL	PROTEIN W PLECURSOR	DUMON ADELICATION AND A	17.71				23,000	3104.3153	2168-3404	L
The American	PROTEIN W PRECURSOR	HUNDALAN ADENOVINOS INTERIOR (CERNIAN ISOLATE)	174.361	£		100	86	+	307.356	7166.240
	CONTACT POLYMOTED !	BALLET TELLOW MODIFICATION (1APANESE STILATA)	129-363	671.705	70.77			т		
אסריו פעושים	CENTRAL POLYPROTEIN I	BALLEY YELLOW MOSAL VINCENT VI	130-161	165-216	130-373	11745			1004.1041	1
WOL! BATH	SHELL BOX VALUEDA	HUNDARIAN GIAPEVING CHANNE MOSTIC	100	486-519	636-677	123	M			
	BALL POLICE TO THE PARTY OF THE	GRAFEVER FANCEAF VIRUS	200	119-911						
מנו מור	WIND BOX NO CONTROL	TOMATO BLACK KING VIACUS (STIANING)	100 E				1			1
191	MAN 1 000 100 100 100 100 100 100 100 100	TOMATO KINGSPOT VIRUS (1904) IS A A TEL	240.201	869.733	119.773	117-118				
POL TOW	KKAI POLITINGE	THE SECOND RIGHT WANTER THE SECOND RIGHT								

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MCGNE	Attacoms	All Viruses (no becteriophages)	П	П	П	П	Π	П	П	
FILE MANT	PROTEIN	1	I	10.00	7	1	1	1	1000	
POC BAYOU	DENOMINE POLYPROTEIN 2	IRUS (JAPANESE STRAIN II-1)	٦	1	117-128			1		T
PROL 2 GFLV	ENA2 POLYPROTEIN		ş	342-602						Ī
PPOL 2 TRAVS	ENA3 POLYPROTEIN		- T							
POLT TRIVE	ANAS POLYPROTEIN	PDERLY)	36.70	334.363						Ī
PPOLG BOVEV	GENOME POLYMOTER		٦	•	1313-1416	103-100	370-1017			971.
POLO BYDYN	GENCHE POLYPROTEIN	3	T	T		1077-1070	1707-1707	174. 101.	-	3136.3130
PPOLG BYDYS	GENOME POLYPROTEON	JS (STRAIN SD-1)	245.289	648-471	077-603	1033-1074	Т		Т	
PPOLG BYNAY	GENOME POLYPROTEIN		%-130							
PPOLO COXA2	CENOME POLYPROTEIN	COXSACKIEVIRUS AZI (STRAIN COE)	9-43	362-596	664-698	8	408-1340	1607-1648	MO3-1974	01:01:04
PPOLO COXAS	GENOME POLYPROTEIN	COXSACKIEVIRUS AP (STRAIN GRIGGS)	15-49	1040-1084	1895-1940					
	CENCACE POLYPROTEIN	COXSACKIEVIRUS BI	67-51	1021-1067	1876-1921					
TEXT OF THE	CRIMING POLYPROTEIN	COXSACKIEVIAUS DI	61-51	1024-1070	1879-1924					
Protection and an arrangement of the protection and arrangement of the protection arrangement of the protection and arrangement of the protection arrangement of the protectio	CENTRAL POLITICAL	CONSACRIEVEUS BA	15.49	642-681	1022-1068	1877-1922				
roto coxes	STATES OF STATES	CONCECNICATION	5.5	1034-1070	1879-1924					
NO.	CERCINE FOLITROICIN	CONTRACTOR VIEW VIEW	120-154							
FOLO CYVV	CERCASE FOLTERO	Course their time and the course	14.100							
PPOLO DENIS	GENOME POLYPROTEIN	DENGUE VIRUS ITPE I (SIRAIN 230-1)	3							
PPOLO DENIA	GENOME POLYPROTEIN	DENGUE VIRUS TYPE I (STRAIN AIG 12.50)	14-108							
PPOLO DENIC	GENOME POLYPROTEIN	DENGUE VIRUS TYPE I (STRAIN CYIOSONI)	901-27				200	****	7776 2176	1016 1016
PPOLG DENIS	GENOME POLYPROTEIN	DENGUE VIRUS TYPE 1 (STRAIN SINGAPORE 5275/90)	74.108	132-873	960-996	64 11-25 11	1360-1420	1014-1046	*677-1167	0107-0247
PPOLO DENIW	GENOME FOL YPROTEIN	DENGUE VIAUS TYPE I (STRAIN WESTERN PACIFIC)	74-106	133.874	\$61-908	1143-1180				
1000	CENOME FOR YPROTEON	DENGUE VIRUS TYPE 2 (ISOLATE MALAYSIA MI)	448-492							
200	CENTRAL POR CONTENT	DENGUE VIRUS TYPE 1 (ISOLATE MALAYSIA M2)	448-495							
Protect Description	CENTRAL CONTROL	DENGUE VIRUS TYPE 2 (STRAIN (661))	74-108	728-777	S66-196	0111-9+11	0621-7921	1416-1452	613-1649	2517.2531
	CONCRETE CONTRACTOR	DENCTIF VIBIG TYPE 2 (STEATH (441)-PDK 5))	74-104	724-777	\$66-196	0111-9911	1346-1210	1418-1452	1615-1649	2485-2551
Protect Derical	CONTROL FOR THE SERVICE OF THE SERVI	DENOTIFE VINUS TYPE 2 (STRAIN D2-04)	111-111							
Process Devices	upromit routing	Indiana in create type a certain Tit. 14)	497.546							
Protto DEDON	GENOMO: POLITION	DEPOCE TENDS I THE STORY (ANALYS)	74.108	774.777	561.99	1144-1160	1244-1380	1416-1452	1615-1649	1517-2551
Pod o DENZ	GENOME FOLTPRUIEIN	UCANOGE VINCE LITTLE & COMMUNICATION OF THE PARTY OF THE	311.347	217 501					1	
PPOLO DENZIN	GENONG POLYPROTEIN	DENGUE VICUS ITTE 2 (STRAIN NEW GOINEA C)	Ţ	***	119.076	1001	11461180	1244-1280	1419.1452	1615-1649
PPOLO DENTE	GENOME FOLYTROTEIN	DENGUE VIRUS TYPE 2 (STRAIN PRIBWS!)		203 693	315-107	W 777	044.1000	1205-1219		
PPOLO DEDUT	GENOME FOLYPROTED	DENGUE VIXUS TYPE 2 (STRAIN TONIA 1974)	141-01-0	226-373						
PPCE G DENTU	GENOME FOLYPROTEDY	DENGUE VIAUS TYPE 2 (STRAIN PUG-215)	614-563						9401 0700	1000
PPOLO DENS	DENOMS POLYPROTEIN	DENGUE VINUS TYPE 3	830-872	939-993	1313-1419		767-0007	1100	2147-0447	1000
POLO DEN	GENOMS POLYPROTEIN	DENGUE VIAUS TYPE 4	957.993	1380-1414	2514-2555	7	CLATTING	2011-3015		
PPOLG ECHIO	GENOME POLYPROTEIN	ECHOVIRUS 11 (STIAIN GREGORY)	113-239	111.6401						
PPOLO EMEY	GENOME POLYPROTEIN	ENCEPHALOMY OCARDITIS VIRUS	1034-1113	121.51	1322-1370	1063-1706	784-187			Ī
PROLO EMCVB	GENOAGI POLYPROTEIN	ENCEPHALOMYOCARDITIS VIRUS (STRAIN EMC-8 NONDIABETO 145-179	145-179	1076-1117	1474-1920	1324-1572	E			ŀ
PPOLO EMCVD	GENOVE POLYPROTEIN	ENCEPHALOMYOCALDITIS VIRUS (STRAIN EMC-D DIABETOGEN 145-179	145-179	1076-1117	1474-1520	1524-1572	1667-1708			
PPOLO ENACE	GENOME POLYPROTEIN	MENGO ENCEPHALOMYOCALDITIS VIRUS (STRAIN 37A)	£ 13							
PPOLG ENACO	GENOME POLYPROTEIN	MENGO ENCEPHALOMYOCARDITIS VIRUS	71:12							
PPOLO PADVI	GENOME POLYPROTEIN	FOOT-AND-MOUTH DISEASE VIRUS (STRAIN A16-61)	£	24:33	578-613	103-133	100	20027-0012		
PPOLG PADVA	GENOME POLYPROTEDY	FOOT-AND-MOUTH DISEASE VIRUS (STRAIN ALZ)	230-234	193-321	11-11	107-1284	1761-146	1617-1019		
PPOLO TABVO	GENOME POLYPROTEIN	FOOT-AND-MOUTH DISEASE VIRUS (STRAINS OIK AND OIBFS)		101-1011	1261-644	2.00.5				
PPOLO FINDVS	GENOME POLYPROTEIN	FOOT.AND-MOUTH DISEASE VIRUS (STRAIN CI-SANTA PAU (C-S		867-178						
PIOCO FADVI	GENOME POLYPROTEIN	FOOT-AND-MOUTH DISEASE VIRUS (STRAIN C!)	62-122	/16-682	119-776					
770.0 KCVI	GENOME POLYPROTEIN	HEPATITIS C VIRUS (ISOLATE I)	<u>7</u>							
AVOU D TORK	CENCHE POLYPROTEIN	HOG CHOLERA VIRUS (STRAIN ALFORT)	440-493	626-660	622-569	1033-1070	196-1235	1307-1343	1779-1820	2116-2170
			2466-2500	2525-2559	1667-2708	3057-3098	155.153	3406-3440		
PROVIDE HEAVE	GENOME FOLYPROTEIN	HOG CHOLERA VIRUS (STRAIN BRESCIA)	40493	626-660	695-739	1033-1076	1171.133	1979-1820	2136-2170	2311.2436
			3466-3500	2525-2559	1667-1708	3057-3098	3133-3195	3406-3440	3521-3563	
THE CASE OF THE PARTY OF THE PA	GENOMS POLYPROTEIN	HEPATITIS C VIRUS (ISOLATE DK)	357-391	2321-2365						
	CONCACT DOLVEROTEN	MEPATITIS C VINUS (ISOLATE ECIO)	63-99							
TOLO M. YA	UCACHE COLUMNICA									

POCIONE PPOLO HCVM	PROTEIN	Mark								
POLO HCYM			J	1	4	1000	Γ			
POLO HCWIT	CONTRACTOR OF SECURITY	MEPATITIS C VIRUS (ISOLATE M)	366-398							
POLO HCVA	CONTRACTOR OF THE PARTY OF THE		364-398							
	OE COME FOL FACE		236-270							
POLO HCVAS	DENDACE FOR TITIONE		246-282							
POLO REVIO	GENORGE POLITICAL	LEPATTIC CARUS (ISOLATE RCV-KF)	157-390							
PIOLO HCVII	GENOME FOLYPROTEIN	LINES ATTITUTE OF VISION (15 OLATE HC-13)	187-184							
POLO HCVIS	GENCHOS FOLTMOTERN	LINESA TITLE C VIRTIS (ISOLATE RC-15)	364-398							
MOLG HCVM	GENORG POLYTROTEIN	MESATTHS CYRUS (SOLATE MC-16)	364-401	1716-1750	2042-2116					
POLO HCV17	DENOME FOLTPROTEEN	WENT THE CANDING ATENCIA	367-791			7				
PFOLO HCVIS	OEMONG FOLVFROTEIN	THE A LITTLE OF VINCING ATT HE LES	361-398	1716-1750	9116-6802	2468-2502	2538.2572			
PFOLO_HCVIA	GENOME POLYPROTEIN	THE PARTY OF WASHINGTON ATT TAPANT OF	Г	2331-2365						
PPOLO_HCV/T	CENCIAG POLYPROTEIN	TECANOLIS C VINCOLIS CONTROL DE LA CONTROL D	357.391	1111.2165						
PPOLO HEYTW	ODIONG POLYPROTEIN	PEPAILITIS C VIANDE (LEONANIE AND TATALANA	Ī	3330.2365	1444-2503					
PPOLO SPAYS	GENOLG POLYPROTERY	HEPAIIIIS C VIAUS (ISOLATE IN TO)	243	101-133	201-117	\$70-904	1621-1055	1117-1151		
PPOLO IMANA	GENOME POLYTROTEIN	HEPAILIS A VIRUS (SUMMING)	2	10.15 10.15	201-237	170-904	1021-1055	1117-1151		
PPOLO_IPAVI	GENOME POLYPROTEDI	HEPAILIES A VINUS (STANIS)	7	101-135	201-237	170-904	5501-1201	1117-1111		
PPOLO_IPAVC	OENONG POLYPROTEIN	HEVAILLE A VINCE (STEATH PERSON)	Ş	\$(1-101	103-237					
PPOLO IPANO	GENOME POLYPROTEIN	TAPATILIS A VINCE (STATING COLD)	11.03	103-216						
PPOLO HPAVH	GENOME POLYPROTEIN	HEPATITIS A VIROS (STANIS CANA)	5	101-135	203-337	170-904	1021-1055	1103-1151		
PPOLO HPAVIL	GENONG POLYPROTEIN	HEPATITIS A VIKUS (STRAIN TAILES)	7	101-135	703-237	120-904	1021-1055	1103-1151		
PPOLO HPAYA	GENOME POLYPROTEIN	HEVATITIS A VINUS (21 NOT LA)	17.	\$61-135	203-237	170-904	1021-1055	1103-1138		
PPOLO HPAYS	GENOME FOLYPROTEIN	MEPATRIS A VINUS (3) INC. Pubel)	ĵ	105-139	207-241	149.904	1025-1099	1115-1155	8611-1511	
PPOLO HOAVT	CENOME POLYPROTEIN	SPECAL IEPATITIS A VIAUS (STRAIN AURILI)	17	101:13	201-137					
PPOLO HOVIA	GENOME FOLYTROTEIN	STATISTICAL PORTION AND STRAIN COLORS	1070-1054	1393.1427	1479-1515	1877-1920				
PPOLO HOVIA	GENOME POLYPROTEIN	HUMAN BUINGVIRUS 14 (HRV-14)	149.384							
PPOLG IGAVIB	GENOME POLYPROTEIN	HUMAN TOTING THE CANALAN	127.01	163-904	133-1168					
PPOLO ION	GENOMS POLYPROTEDY	MOMAN IDUNOVINUS IN (AATVID)	156-407	136-1169	1552-1593					
PPOLO HRYST	GENONG POLYPROTEIN	MUNICIPALITY OF THE PROPERTY O	1366-1607							
PPOLO, HUEVY	GENONE POLYPROTEIN	HOMOS LOS CONTROLS OF CONTROLS OF THE PARTY	159.397	116-918	1003-1001	1403-1443	1896-1934	1		
PPOLG BDV0	GENOME POLYPROTEIN	HUNAM EMIEROVINGS FOLST NOW THE STREET OF	134.168	28.20	475-524			_		
PPOLO JASVI	STRUCTURAL POLYPROTEIN	AVIAN DO ECTIOUS BURSAL DISEASE VIAUS (STRAIN OF)			138.63A	1960-1014	1409-1450	2663-2497	1739-2777	2762-2823
PPCK G JAEVS	GENOME FOLYPROTEIN	IAPANESE ENCEPHALITIS VIRUS (STIAM SA-14)	74-122	1207,4430						
			200		769 636	944.014	1409.1450	2463.2497	2739-2777	2782-2875
PROF G TARY?	GENOME POLYPROTEIN	JAPANESE ENCEPHALITIS VIRUS (STRAIN SA(VI)	77:17							
					10.02	920-1614	1409.1430	2463-2497	1719.2777	2762-2823
PPOLG JAEVN	GENOME POLYPROTEIN	IAPANESE ENCEPHALITIS VINUS (STRAIN JAGAKSTIZ)	031.2	1117.1421						
		ANALYS NATIONAL TITLE STREET SETS A DLINAK A YAMA)	7	2	467-504	17 TO	1337-1376			
PPOLG KUNDA	CENCAGE POLYPROTEDN	WANTED CHARLESTON VINCENTY	74-101	207-251	\$17150	3464-3498	2528-2579	2740-2778	3325-3359	1319-3433
PPOLO LANVT	GENOME POLYPROTEIN	AUNIO VINOS (SI NOTA PROPERO)	51.162	- F	965.98	101-167	9961-2161	2536-2591	1967-3001	1003-3037
PPOLO LANYY	DENOME POLYPROTEIN	LANCAL VINCOLOGICALITY)	3102-3145							
	2014	LANGAT VIRUS (STRAIN YELANTSEV)	64-103	431-465						
Proto LIV	GENOME POLITICAL CONTRACTOR	ורסתשואפ עדר אואיתא ערט	64-123	100	÷					
PPOLO LIVSB	GENOME POLITICAL	LOUPING ILL VIRUS (STRAIN SB 526)	1131-118							
NO PO	CONCRET COLLEGE	MOSQUITO CELL FUSING ACENT (CFA FLAVIVILUS)	10-114	25. 25. 25.	2049-2087	2630-2689	107-1082	3290-334		
POLO MYRV	CENTRAL POLICE IN	MURRAY VALLEY ENCEPHALITIS VIRUS	67-115	20.5		979-1013	1			
200	CONTRACT POR YPROTEIN	ORNITHODALUM MOSAIC VIRUS	481-515	2	1072-1108					100.1.2011
200	CONTROL OF CONTROL	PEPPER MOTTLE VIXUS (CALIFORNIA ISOLATE)	35-100	101.20	744	10-10	23.462		2001	071-/017
100	OCHOPE COLLEGE		1488-1529	=	1948-1982	277-277	27.75	A(87-5087	cor-roor	
31 24 0 25	CENCECS POLYPROTED	POLIOVIAUS TYPE I (STRAIN MAHONEY)	3	101		200	101	1410-1411	1808.1843	1904-1949
200	GENORGI POL VPROTEDI	POLIOVINUS TYPE I (STRAIN SABIN)	3	2	1907-1102	100		1601.1640	1804.1845	1902.1947
1	CENTRE CONTROL	POLIOVIRUS TYPE 2 (STRAIN LANSING)	679	847-833	1001-100	1413-1447	1307-130	1000	2	

PCCENE	(A11240TIS	All Viruses (no bacteriophoges)								
PILE NAME	PROTEIN		ABEAL	1478	14384	<u> </u>	1	AREA	AREA 3	AREA
POLG_POLIZ	GENOME POLYPROTEIN	POLIOVIRUS TYPE 2 (STRAIN W-2)	943	167-831	1045-1100	1413-1447	1502-1547	1608-1649	1806-1840	1902-1947
אסנס אסנזו	GENOME POLYPROTEIN	u	9-43	016-961	1044-1091	1413-1446	194-154	1607-1643	1205-1839	1901-1946
PPOLO PPVD	GENOME POLYPROTEIN	EONJ) AND PALEON (2A(1)B)	(1-6	006-961	1044-1099	1413-1446	1498-1546	1607-1648	1805-1839	9761-1061
PICILO PPVEA	GENOME POLYPROTEIN	PLIAK POX POTYVIRUS (STRAIN D)	164.208	(05-177	128-769	113-167	921.955	1741-1782		
PPOLO_PPVNA	CENOME POLYPROTEIN	PLUM POX POTYVIRUS (STIAM) EL AMAR)	116-157	114-111	1146-1197					
PPOLO PPVRA	GENOLGE POLYPROTEIN	PLUM POX POTYVILUS (ISOLATE NAT)	164-208	403-437	440-502	127-768	114-173	920-954	1740-1781	
PIOLG PISVH	GENOMG POLYPROTEIN		164-208	167-604	205-009	727-748	999-718	156-0Z6	1340-1381	
POLO PRSVP	GENERAGE POLYPROTEIN		64-102	134-461						
PPOLID_PPLSYW	GENOME POLYPROTEIN	MUTANT HA 5-1)	650-520							
PPOLO PSBMV	GENOME POLYPROTEIN	PAPAYA RINGSPOT VIRUS (STRAIN W)	325-359							
PPOLO PVYC	GENOME POLYPROTEIN	PEA SEED-BORNE MOSAIC, TOTAL (STRAIN DPDI)	253-315	38.319	528-519	913-816	1101-716	1080-117	15x8-1627	1808-1660
			1971-2015	2775-2413	2712-2746	2870-2907				
PPOLO PYYNU	GENOVE POLYPROTEIN	POTATO VILUS Y (STRAIN C)	131.186	701-735	20.03					
POWA D POWA	SECOND POLYPROTEIN	POTATO VIRUS Y ISTRAIN HUNGARIAN)	144-131	201.735	102.863	96.108	3401-1441	1492-1526	1728.1773	1777-1810
			2272-2306							
0204	GENOME POLYPROTEIN	POTATO VRUS Y (STRAIN N	Т	213-245	701-735	102-163	1401-144	1472-1926	1728-1773	1777.1118
			lg							
PPOLG PUVSE	CONOME POLYPROTEIN	POTATO VIRUS Y (STRADY O)	\$1-\$ 1	52:17	701-735	102-156				
POLO PVIVIE	GENOME POLYPROTEIN	PASSIGNFAUT WOODDESS VIRUS (STRAIN SEVERE)	203-237							
POLG PYTVI	GENOAG POLYPROTEDA	Ĕ	203-237							
PROLD STEWN	OENONG POLYPROTEDN	Γ	194-228	111:112	1379-1413	1858-1899	182-561	2703-2737		
HACAS OXON	OENONG POLYTROTEIN	ST. LOUIS ENCEPHALITIS VINUS (STRAIN MSI-7)	106-143	67).707	119.713	975-1009	1604-1438			
POLO SVDVU	GENOMAS POLYPROTEIN	76)	84	1024-1070	1179-1813	1690-1924				
PPOLID THEVS	GENOME POLYPROTEDY	(ii)	15-49	1024-1070	1890-1924					
WOLD THEW	GENOMG POLYPROTEIN	TICK-BOXNE ENCEPHALITIS VIRUS (STILAIN SOFIIN)	01-19	221:122	131-465	1150-1192	2621-1621	9961-6261	9122-2912	2515-21990
			2945-2999	1011-1092	1100-1143					
PPOLO_TEV	GENOME POLYPROTEIN	TICK-BORNE ENCEPHALITIS VIRUS (WESTERN SUBTYPE)	63-140	231-272	431-463	1138-1192	1431-1492	1932-1966	2536-2591	1967-3001
			1003-1017	1053-3094	3103-3148					
POLG TAEVE	THEREA'S MUNDA ENCEPHALONMELTHS VIRUS (S	S VINUS (S) TOBACCO ETCH VIRUS	13-134	166-222	\$40-584	720-783	\$28-828	1148-1192	0911-9111	1494-1535
			1668-1702	1747-1711	1792-1826	2395-2434	1787-1821			
PPOLO_THEND	CENCHAE FOLYTROTED	ΖĪ	1304-1340	1483-1916	\$£91-1097					
PPOLO TACKO	DENOMS POLYPROTEDA	THEIR EN'S MUNICHE ENCENHALCHATELTIS VINUS (STRAIN DA)	104-1336	141-1516	1599-1643					
PPOLO TUMY	GENONG POLYPROTEDI	EPHALOXYELITIS VIAUS (STIAIN GOVIE)	7	163-151	\$61-163					
אינים הייי	GENOME POLYPROTED			76.762	494-538	762-639	1443-1477			
POLO WAY	GENOME POLYPROTEIN	TOBACCO VEIN MOTTLING VIRUS	T	401.40	704-199	761-613	25.433	249 .1013	1011-1072	1643-1677
AUA D AUG	Marco and visit of the Carrier	WATERNET ON MOSAIC VIRUS II	(F.10)	302.236	40/ P-10/7	9747-0197				
2000	ADVANCE OF CHECKED			36.361	100.170	1001	6777	2441.3204	3636.3636	
	Various rotations		2	1385-1426					Т	
EALER O ROLL	GENOME POLYPROTEDY	YELLOW FEVER VINUS (STRAIN 170)	Т	\$35-563	721-745	1385-1444	2231-2276	2477-2565	2950-2994	3097-3143
PPOLO YEPVI	GENOME POLYPROTED ⁴	YELLOW FRVER YIRUS (STRADI PASTEUR 170-104)	111-453	325-563	131.368	1335-1444	2231-2276	2477-2545	2956.2994	3097-3143
MOCH NOCIM	GENOME POLYPROTEDI		35-116	418-432	525-363	716-748				
PROLY EBWT	GENOME POLYPROTEDI	POCIOVINUS TYPE I (STILAIN MAHONEY)	171	1047-1103	1415-1449	1301-1549	1610-1631	1104-1142	1904-1949	
POUNTONC	NONSTRUCTURAL POLYTROTEIN	VENEZUELAN EQUINE ENCEPHALITIS YIRUS (STRAIN TRINIDAD) 145-313	Γ	198-912	1943-1979					
POLY FCYES	NON-STRUCTURAL POLYPROTEDI	FELDIS CALICIVILUS (STRADY CFUAR FIV)	310-544							
URVEN KLOPY	HON-STRUCTURAL POLYPROTEIN			369-410	926-1020	1023-1061				
PPOLY HEWAE	NON-STRUCTURAL POLYPROTEDM			1135-1177						
PPOLIN HEWAY	NON-STRUCTURAL POLYPROTEIN		П							
PPOCH, KEVPA	NOW: STRUCTURAL POLYPROTEDN		T	1135-1114						
PPOLM_MIDDV	HON-STRUCTURAL POLYPROTEIN	ITKAIN PAKISTAN)	٦	11111						
DANA CHORA	NONSTRUCTURAL POLYPROTEIN	MEDDELBURG VIRUS	113-677		•				_	

POLY ROY POLY RAY POLY RAYY POLY RAYT	Manager Manage	VIRUS	100-600		3444.3452	ĺ				
POLN RAYN POLN RAYN POLN RAYT				942-1916						
POLY RAY	SOURCE STATE AL POLYMOTERI			105	657-00	11657-1716				
POLN RAYT	TOWNS WITH A PURI VIEW COTTON	KUS								
POLN RUBYT	NOISE INCOME TO THE OWNER.		424-54	1041-074						
POLY RUBY	NONSTRUCTURAL POLITICAL PROPERTY.		207-631	111111111111111111111111111111111111111		7001 1701				
	MONSTRUCTURAL FOR CONDITION	(N)	200	31:32						
POLY STV	NONSTRUCTURAL POLITICAL	٦	20.00	1158-2392						
NOW SPECO	NOWSTRUCTURE CONTINUES.	16 OCKELBO / STRAIN EDSBYN 82-5)	1,6-616	1491-1523	*					
אסמנו איזטע	NOGITACIONAL POLITRO EN		1491-1525	25.	2442-2470					
TOLK ETMY	MONETELECTURAL POLITICAL		116-648	1127-1161						
POLS EEEV	RNA REPLICASE POLYFROTEIN	E A CTERN BOUNT ENCYPHALITIS VIRUS	372-406	914-951						
PPOLS EERVI	STRUCTURAL POLYPROTEDA	SASTEM ENTERNATIONS VALUE (STRAIN VASILTEN BRQ 373-407	173-407	115-952						
PPOLS EEWI	STRUCTURAL POLYPROTEDI	CASTERN EXPONE ENTER THE VIRUS (STRADY TC-41)	1216-1250							
PIOLS EXWT	STRUCTURAL POLYPROTEIN	VENEZOLEAN COURT ENCEMALITIS VIRIS (STRAD) TURIDAD 1116-1250	1316-1250							
PPOLS IBDVS	STRUCTURAL POLYPROTED ⁴	VENEZUELAN EQUINE ENCERNOS PROPERTOS (CTE A DA (2/70)	134-168	231-266	470-523					
PPOLS DIDVA	STAUCTURAL POLYPROTERM	1	134.164	231-286	470-523					
PPOLS INDVC	STRUCTURAL POLYPROTEIN	AVIAN INTECTIOUS BOASAL DISEASE VINCE (STEATH CILL)	134.168	231-216	470-523		Ц			
BACE S BONE	STRUCTURAL POLYTROTER	AVIAN IN ECTIODS BOASAL DISEASE VIDIO (CTRAINE)	134-168	231-286	304-340					1
PROCES DEDVY	HOMSTRUCTURAL PROTEIN VP4	AVIAN INFECTIOUS BUILSAL DISEASE VINUS (STEATH SPICE)	11.16	112.267	451-304					
SACE BOAR	STRUCTURAL POLYPROTEIN	Τ	134.165	249-283	470-523					
PPOLS DWV	STRUCTURAL POLYTROTED		5	237-057						
NAME OF THE	STRUCTURAL POLYPROTEIN		214.786							
SANGE TOWARD	STALLCTURAL POLYPROTEIN	INTECTIOUS PANCHEATIC NECKOSIS VINOS (31 NOTAL)	1204-1238		_					
5000	STRUCTURAL POLYPROTEIN	ONYONG-WYONG VIRUS (STRAIN GULU)	97.75							
70.00	STRICTURAL POLYPROTEIN	ROSS RIVER VIRUS (STRAIN 213979)	100.001	110.011		 -				
1000	STRUCTURAL POLYPROTEIN	ROSS RIVER VIRUS (STRAIN MB5092)	010.071							
NACT A LIBRAR	STRUCTURAL POLYPROTEIN	ROSS MYEX VIRUS (STRAIN 148)	960,1016				L			
PPC1 S RIBVE	STRUCTURAL POLYPROTEIN	RUBELLA VIRUS (VACUINE STRUM PLY 77)	909-1036							
PPOLS RUBYT	STRUCTURAL POLYPROTEIN	RUBELLA VIRUS (VACCINE SINGERICE)	9601-666							1
OCIVIS \$ 1044	STRUCTURAL POLYPROTEIN	ENVIRONMENTAL COLUMNATION OCKELBO / STRAIN EDSBYN 02-5)	362-396							1
PPOLS SDOV	STRUCTURAL POLYPROTEIN	ENTHAIR VIEWS (STEAMS MASP AND HALP)	362-396							\downarrow
WORLS SPOR	STRUCTURAL POLYPROTEIR	COLUMBIA VINITE CANT D TYPE SB DELIVED FROM STRAIN AR19)	19-90							\downarrow
POLS WEEV	STRUCTURAL POLYPROTEIN	WESTERN FOUNDE ENCEPHALITIS VIRUS	913-947							\downarrow
PPOL BABYM	STRUCTURAL POLYPROTERN	BARDON ENDOCEROUS VIXUS (STRAIN M7)	43.80	676-743	794-133	1001-1042	-		\downarrow	1
PPOL BLVAU	POL POLYPROTEIN	BOOWH I FIREMA VILLS (AUSTRALIAN ISOLATE)	525-673							1
PPOL BLVI	POL POLYMOTEDA	BOYDAE LELIKEMA VIBUS (JAPANESE ISOLATE BLV-1)	625-473					1		1
PPOL CARVC	POL POLYTROTEIN	CAPRINE ARTHURIS ENCEPHALITIS VIRUS (STIVAIN COUK)	179-974			1				ļ
TOL CAMP	FOL FOLTFRUIEN	CAULIFLOWER MOSAIC VINUS (STRAIN DAY)	17-211				000 700	131101111	-	1
TOL COTO	ENTYMATIC POLITIONS	CONDIGIONA YELLOW MOTTLE VINUS	17-131	200	24.48		i.		-	ļ
MOL ELAV	POINTE POLITICAL	EQUING DISECTIOUS ANEMIA VIRUS (CLONB 1369)	ž	1037-1030			\downarrow			
POL ELAYC	SOLDEN VERNIEN	EQUING INTECTIOUS ANEMIA VIRUS (CLONE CL22)	98.	2017	1	1	-	1		-
TOT ENVI	NEW YORK THE	EQUINE INTECTIOUS ANEMIA VIRUS (ISOLATE WYOMING)		1071-103	20.00	-	ļ			ļ
TOTAL SEAVE	NA NO VEOTEN	FELINE ENDOGENOUS VINUS ECR.)	B	ACC-170		+				
TOL PIVE	NOT DOLVEDTED	FILLING DOLUMODETICIENCY VIRUS (ISOLATE PETALUMA)			1			-		L
	NOW BOY VAROTEDA	PET INE DIGUNODEFICIENCY VIIUS (ISOLATE SAFE DIEUX)					-			L
	POL POLYPROTEIN	FELTINE DIAKUMODEFICIENCY VIRUS (ISOLATE TAG)		100	\downarrow	-		ŀ		-
1	ENCONATION OF VAROTEIN	FIGWORT MOSAIC VIRUS (STRAIN DXS)			1	-			L	Ļ
POL FOAN	and the control of	HUMAN SPUNALETHOVIRUS (FOAMY VIRUS)	2		ayr.c.	+	1			L
מינים מינים	AND CONTROL	GEBON APELEUKENDA VIRUS	2	975-740	-	+	1			ļ
N I	TO TOO VERDITED!	HUMAN T-CELL LEUKENDA VIRUS TYPE I (STRAIN ATK)	970-71		1		\downarrow	-	-	Ļ
TO HE	TOT TOTAL STATE OF	MUNCAN T-CELL LEUKENDA VIRUS TYPE I (CALBREAN ISOLATE) 670-711	E 670-711		1	-	1	-		ļ
2	TOUR STREET, S	HUMAN BOADNODEFICTENCY VIRUS TYPE I (ARVZ/5/7 ISOLATE JOI-13)	E 501-537	3		+	-	-		1
POC. HVIBI	M. M. M. M.	HADAAN DAAGDODEFICENCY VINUS TYPE I (BHID ISOLATE)	513-549	619-676		-				1

PCCEME	ALLWOIS	nes in carifornian [11]				I I			
THENAME	PROTEIN	П	AREAL	AREA: AREA!	AREA	AREAS	AREA	ABEA 2	AREAJ
POL HVIBE	POL POLYPROTEIN	I INDALINODEFICIENCY VIRUS TYPE I (BHS ISOLATE)	Г	Γ	Γ				
PPOL_HVIEL	POL POLYFLOTEIN	INDIAN DOADNODEFICIENCY VIRUS TYPE I (BAU ISOLATE)	913-549	918-436	_	_			
PPCK_HVIND	POL POLYPROTEIN	HUNGAN BOARMODEFICIENCY VIRUS TYPE I (ELI ISOLATE)	500-536	626-663					
PPOL HVID	POL POLYPROTEIN	٣	501-337	606-664	_				
PPOL WYIMA	POL POLYPROTEDA		505-541	899-019					
POL WYDON	POL POLYPROTEIN		476-536	199-109					
POL HVINS	POL POLYPROTEIN		504-540	609-667					
POL HVIND	POL POLYPROTEIN	9	501-537	199-129					
POL HVIOY	POL POLYPROTEIN		500-536	636-663					
POL HVIPV	POL POLYPROTEIN		501-537	199-909	H				
POL HYINH	POL POLYPROTEON			693-476					
MOL MVIUM	POL POLYPROTEIN	MUMAN INGRINODEFICIENCY VIRUS TYPE I (NEMAT ISOLATE)		605-463					
POL HVIZI	POL POLYPROTEIN	HUMAAN DAMIDHODEFICIENCY VIRUS TYPE I (STILAIN UGANDAN 100-536		(99-109					
POL HV2BS	POL POLYPROTEIN	Y	\$00-536	626-663		L			
POL HYZCA	POL POLYPROTEIN		(1-6)	LB9-CS9 285-1411	1817-851		L		
POL HV2DI	POL POLYPROTEIN)		999-269 295-109		L			
POL HY2D1	POL POLYPROTEIN	П	П		П			-	
POL HV201	POL POLYPROTEIN		376-410	484-524 529-577	633-687				
POL HYZNZ	POL POLYPROTEIN	3	195-999						
POL KVIRO	POL POLYPROTEIN	3			633-667				
MOL HYSS	POL POLYPROTEIN		160-656	165-363 634-648					
PPOL HV2ST	POL POLYPROTEIN	LISN,	01-90	295-629 295-629					
NO. DHA	POL POLYPROTEIN	E 2 (ISOLATE ST)	484-318	332-577 653-647					
POL MAV	PUTATIVE POL POLYPROTEIN		467-503						
POL MLVAX	POL POLYPROTEIN	rosis virus	190-221						
PICE MEVAY	POL POLTFROTEIN		325.392						
TOL MENTS	POL POLYPROTEIN		677.744						
TAC MENT	POLYRUIEM		612.749		1				
10 MAY 1	INC. THE CHANGE OF	TALEND PIORUNG LEURENIA VIRUS (1902ATE 1929)							
200	Incl. Incl. was offered				1				
PICK AND VICE	NOT NOT YOUR ONLY		277.163	1	+				
PPOL MONO	POL POLYPROTEIN	STRAIN KANLAN			+				
POL OLAVIS	POL POLYPROTED ¹	T	T.	578-613		\downarrow			
POL RSVP	POL POLYPROTEIN	OVINE LENTIVIRUS (STRAIN SA-OMYV)	Γ	155.910					
POL RTBV	POL POLYPROTEIN	EC)	119-91						
POL RTBVP	POLYPROTED		7-46		176-236	325-362	433-434	1005-1039	1405-1439
POL SPVI	РОСУРКОТЕМ	RUS (ISOLATE PHILIPPINES)	144	59-94 101-135	176-236	325-362	433-434	1005-1019	405-1439
POL SPYJL	POL POLYPROTEIN		П						
POL SIVA!	POL POLYPROTEIN			П					
FOL SIVA	POL POLYTIONEIN		آڃ	637-678 133-371	934-979				
POL SIVAG	POL POLYTROTEIN	C C	T	٦					
TOUR STATE	NO. POLITACIEM	SUMAN INDIVIDUAL CENTRAL VIRUS (AGAS ISOLATE)	915-22-	642-683 743-783					
ZIALS BUG	POL POLYBOTEIN	STRUCK DATE MODELLICITATION CHARLES TO A 100 LATER	T	00/-1M0 616-014	M2-98.	10201		1	
POL SIVED	POL POLYPROTEIN		T	967-161				1	
PPOC. SIVINI	POL POLYPROTEIN		T	446-413 629-471	761-627	413.046		1	
POL SIMME	POL POLYPROTEIN	ATE)	485-519	T				T	
PPOL SIVSA	POL POLYPROTEDI		Γ	634-613	-	ŀ		T	
PPOL SIVISP	POL POLYPROTED	6	448-462	617-651				Ť	
PPOL_SOCIAY	POL POLYPROTEIN		Г	620-654	-			İ	
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	A LI MOTHS	All Virgies (no bactertophages)		AREA 2 AR	AREAS	AREAS	AREAS	AREAS	AREA	4
PCCENE	201108		Ī	Γ	Γ					
TOWN THE	INC. BOLVEROTED!		T		Ī					
ATC. ATC.	The four wearings		T	******	T					
POL VILV	TO TO THE PARTY OF		٦	274-478						
POL VEVI	AL POLITACIONE		489-524	174-929						
PPIS HOWA	PULLIFICATION STATES AND AND AND AND AND AND AND AND AND AND	STRAIN CYTOMEGALOVIRUS (STRAIN AD169)	116-150	122-131						
PRTS BOTTYB		(9)	22.20							
PR73 LOCTVC	PROTEON PRO		20.72							
PPR75 NO-TIVO	PROTEON PRIT		11-95	143-201						
PRIL JOSTVO	PROTED/PR73	NAMES AND AND THEOR VIRUS (STUAD) GR.)	145-304	270-311						
PRIR LOCTYO	PROTEDY PATS	ALEN INTELLATIONAL PRINCE STRAIN GR.)	141-200	104-307						
PYND CPYBM	PROTED PATS	POURSE MANAGEMENT TO THE SERVICE FOR THE DROSES WAYS	13-45							\downarrow
PPYIND NOVAC	POLYHEDRUN PRECURSOR	BUTTER THE TOTAL TOTAL TOTAL TOTAL POLICE DROSES VIRUS	13-47							
PYND NEVAS	POLYHEDRIN	AUTOCKATRA CALIFORNICA POCCACA CALIFORNICA	7							
PYIO NIVEL	POLYHEDRIN	AGROTIS SEUB TOULEAN TOUT INCOME CAST	13.56							
SEVEN COVY	POLYYEDRIN	BONDYX MOU NOLLEAR TON TREAMOND THOSE	7							
PYND NAVLD	POLYMEDAIN	BUZUIA SUPPLESSAUA MOLLEAR POLITIERA POLITIERA								
PAND GIAN	POLYAGIDADY	LYMANI MA UISPAK AND INCOMES ON VARIABLES VIRUS	87							
PYTO NOVOP	POLYNEDRUN	MANGSTRA BRASSILAS NOCESAS POR INCOME.								\downarrow
SOV ST GOT	POLYNEDRIN	ORGYIA PSEUDOISUGAIA MULIMA SID IOLIILEGIOSI	7							
14V 50 Var	POLYHEDRIN	OROTA PSEUDOISOUA IA BINALE CASED POLITICALIS		-						
PYYOU OFYER	POLYNEDRUM	PANOLIS PLANORA MULITURE INCREMENTATION VISITS (STRAIN	3							
ISADY OHARA	POL YREDAIN	SPONOPTERA EXICUIA MULLEAA AND INCOMO	14.48			L				
ISAON OUA	POLYHEDRIN	SPODOPTERA PRUGIPERDA NUCLEAR POL INSCRISSION VINCE	32							
NATE ASSAULT	POLYNEDRDA	SPODOPTERA LITTORALIS NUCLEAN FUE INCOME.	142.136							
PREV BIVZZ	TRANSFORMANG PROTEIN 21	KIRSTEN MUMINE SARCOMA VIRUS								
PREV ELAV9	REV PROTEIN	BOVING GOODPORT NEWS TAKES (1902)	9							1
PREV ELAVO	MAY PROTEDY	EQUINE DIFECTIOUS ANEMA VIALIS (CLONE CL22)	8 5							1
PASV ELAVY	REV PROTEIN	EMINE MECTIONS AND AND VINUS (ISOLATE WYOMING)	611-119							1
PREV HV112	REV PROTEIN	KOMAN BALINODEFICIENCY VIRUS TYPE I (CLONE 12)								
PREV HVIAS	ALV PROTEIN	INTERNATIONAL PROPERTY VIRUS TYPE I (ARV2/3F1 ISOLATE	32-69							1
PREV HVIBI	REV PROTECT	ARAZAN MAN MANDARICIENCY VIRUS TYPE I (BILIO ISOLATE)	35-69							1
PREV HVIBS	REV PROTEIN	GANAN BANAN BANANCESICIENCY VIRUS TYPE (1844 ISOLATE)	65.52							\downarrow
PREV HVIBN	REV PROTED	LANGE BANKARATE FILE PACY VILLS TYPE (BLAIN ISOLATE)	22.59							
PREV HVIBA	ARV PROTEIN	LABOUR DAMPINGER CIENCY VIRUS TYPE I (BRU ISOLATE)	25.65							1
PREV HVIEL	REV PROTED!	IMPANISAL INCOMPETERNCY VIXUS TYPE I (ELI ISOLATE)	22.44							\downarrow
PREV HVIND	AEV PROTEIN	MANAN MARRIED TO YOUR TYPE I (HXD2 ISOLATE)	33-69							1
PREV HVID	REV PLOTEIN	MONTH IN THE PROPERTY VIEWS TYPE I (TH) ISOLATE)	1962							\downarrow
PREV HVID	REV PROTEIN	MANAN MAR MODEFICIENCY VIRUS TYPE I (IRCSF ISOLATE)	31-66							\downarrow
PREV HVINA	NEV PROTEIN	MALAN DAMPHODES KIENCY VIRUS TYPE I DIAL ISOLATE)	71							1
PREV HVINO	REV PROTEIN	HADAAN INDRINODEFICIENCY VIRUS TYPE I PRI ISOLATE)	31-46		İ					\downarrow
PREV HVIOY	NEV PROTEIN	HUBAN BANDHODEFICIENCY VIRUS TYPE I (OY) ISOLATE)								1
PREV HVIPV	REV PROTEIN	HUNLAN DENUNODEFICIENCY VIRUS TYPE I (PV12 ISOLATE) AN					1			ļ
PREV HVISS	NEV PROTEIN	HUMAN BERUNDEFICIENCY VIRUS TYPE ! (SF1) ISOLATE)					1	\downarrow		ļ
A SA	ary profess	HUMAN INDIUNODEFICIENCY YAUS TYPE I (SC ISOLATE)	2							L
AND STATE	SEC PROTEIN	SINDAN INDIGNODESICIENCY VIRUS (ACMISS ISOLATE)					ļ			L
אור אור אור אור אור אור אור אור אור אור	Ostone Can	SOUTH DOUGHOUS (FILE (AGAI) ISOLATE)	1							L
PREV SIVA	SEC SOCIETY	SIDITAN DOMINODEFICIENCY VIRUS (ISOLATE AGM / CLONE GR		†			-			
NA SIVA	ALL VACUE OF	SDADAN DONUNODEFICIENCY VIRUS (TYG-1 ISOLATE)	ŝ	1			•	ļ		
MEV SVC	TO LOUIS ON THE PARTY OF THE PA	CHOLO ANG EE DANIONODE FICTONCY VIRUS		1						L
A TAN	National Age	VISNA LENTIVIRUS (STRAIN 1514)	2	T						L
AST AST	MAY TAULEN		17	I					-	

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PCCHE	ALLMOTIS ALLMOTIS	All Virtues (no bocterioghages)				ABTAA	* 74.4	48544	10549	48548
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PAGE BONE	LIANE LAS		14.10				Ī			
74. C. C. C. C. C. C. C. C. C. C. C. C. C.	37 357 137		124-365							
Print VACCV	CTASE LAR	AGEN	367-462							
PRIRI VARV	UCTASE LAR		347-402							
PALRI VZVD	AIRCHUCL EOSIDE-DIPHOSPHATE REDUCTASE LAR VARIOLA VIRUS		367.462							
PAIRL EDV	AUBONUCLEOSIDE DIPHOSPHATIS NEDUCTASIS LAR VAUCELLA	DUNIAS)	123.257							
PAIRL HSVB)	JCTASE SNA		19-137							
H	TASE SALA	BOVING HEAVESVIRUS TYPE I (STILAIN 34)	<u>6</u> -5							
ı	TASE SMA	ATM AB4P)	106-140							
	RIBONICLEOSIDE-DIPHOSPHATE REDUCTASE SMA HERPES YIR		135-159							
l	TASE SMA	SHOPE FIBROXIA VIRUS (STRAIN KASZA)	20-135							
אי טאי	TASE SAIA	MAGEN	201-16							
ı	TASE SALA		94-133							
ļ	TASE SALA		56.132							
PILL HSV2H	TASE SALA		2(1.12							
PILM VACCV			171-213							
PIDE VARV	TED TRANSCRIPTION S	VACCINIA VIRUS (STRAIN WR), AND (STRAIN COPENHAGEN	16-150	465-540	187-781					
PIPOI VACCC	SCRIPTION S		41-75	21-911	465-540	157.791				
PINOI VACCV	KD POLYPE	ENIAGEN	162-62	612-616		116-166	1006-1057			
PRPCI VARV	7 KD POLYPE	VACCIDIA VIRUS (STRAIN WA)	162-002			184-556	1034-1038			
PROJ COWK	7 KD POLYFE		162-595	959-219	184-791	954-911	1006-1057			
PLUO2 COVPX	DNA-DIRECTED RNA POLYNCRASE 133 KD POLYPE CAPRIPOXY	CAPRIPOXYIRUS (STRAIN KS-1)	19-60		019-685					
PILIOZ VACCV	EXD POLYPE		П		\$33-874					
PRIOZ VARV	I KD POLYPE	VACCORIA VIRUS (STRAIN WR), AND (STRAIN COPENHAGEN)	502-112		133-134					
PRIVOL VACCC	DNA-DDECTED RNA POLYMERASE 112 KD POLYPE VANOLA VIRUS		211-245	359-400	133-674					
PRIVAL VACCV	KD POLYPEP	ENMAGEN)	62-116							
PRIPOR VALIV	KD POLYPEP	S (STRAIN WR)	62-116							
SINOS AYCCC	DNA-DURECTED RNA POLYNGRASSE 35 KD POLYPEP VARIOLA VIRUS		9:1:0				1			
MACCV		ENHAGEN)	2	Ī			1			
PLPOS VARV	KO POLYYEV	(SIRAIN WR)				1				
PLYON WACEV	CHANGE CITED THAT FOLL METANS IN NO. 17 FFF VACCOUNT VIAUS	CASTA AND AND ASTRA IN CORPORATORIO	36.56			Ī	T			
אינייייייייייייייייייייייייייייייייייי	KD FOLVER	Т	65.55							
PROJ VARV	DNA-DIRECTED RNA POLYNGRASS 19 KD POLYPEP VACCINIA	(STRAIN WR), AND (STRAIN COPENHAGEN)	4.6							
PLYON LELY	DNA-DIRECTED RNA POLYNGRASE 19 KD POLYFUP VARIOLA VIRUS		43.93							
PROL_EAV			1533-1567	1721-1758	П	2109-2157				
PILLE LANN	٦		_	1477-1518	1633-1673					
PLUV! LABELI	1	ĝ	Т	T						
PRINT LABON	1		T	T						
PIUPI IAGUA	1	T	T	110-412		1	1			
PLUP I LAGO	1	T	Ţ	111.4/2						
PRUPI INVITE	ANA-DETECTED BNA POLYMERASE SUBUNIT PI INTLUENZA	INTLUENZA A VIXUS (STRAIN AZQUINELLONIXON) (1607))		206-412						
PILLP LYKE	1	T	T							Ī
PLUT LAKOR	Ť	INTUENCA A VINUE (STRAIN ANTENNAVIE)	200	11000						ſ
PRINT INTE	Ť	14467)	Τ	11174						T
PROFILES	1	5	T	110.000	Ì	Ī				
PROPERTY.	BAA-DDECTED RAA POLYMEAASS SUBURIL FI		Τ		T	Ť	ŀ			T
MAN I MAN	T	W740781	Τ	115.00		Ī			T	
TOWN INCOME.	ANA-DIRECTED ANA PULT MENASS SUBJECT 1 INCLUDIOS		T	275.313						Ī
PREST IAMIE	Т	DOLUENZA A VIRUS (STLAIN AATHONS)	Γ		Ī					
MAN I MAN	1		1							

NCC CALL					AREAL	AKIA!	7			
	P=0.17.18		107.30	Γ	Γ					
TEVER	NA DESCRIPTIONA POLYNORASS SUBURUT PI		Τ	178.313						
ACC: IASON	ENGA-DUCCIES MAN TOCHAN AS CIRCUM PI									
PERFORMAN	TAX-DIRECTED MAY FOR TAXEBARET CHIRACATE	OTABIJAR	731-747							
TAVE LAVE	RNA-DIRECTED ANA POLITICAL SE CIPIDAT PL	1	Ţ							
PLUT IAWIL	KRA-DDECTED AND TOLINGS AND STREET BY	23)	T							
PEUP LAWIS	INA-DOECTED INVA POLITICAANS SUSSINI 1	٦	٦	117.62						
ממאן ושווי	RICA DOLLCTED ANA POLITICIONAL SUSCIENT SI	ŝ	107-242							L
PRIET IAZON	ANA DOMECTED MAA POLYPRAANS SUSTAINT 91	1	27.5	275.31.2						
MEDI WZTI	NA-DOLCTED DA POLTADANA SUSTAINE	m)	171-343	110.42			-			
IN DONC	NA-DIRECTED DA PALTMERASE SURVIII II		208-249				+			L
DAMA DAMAD	ANA-DIRECTED ANA POLYMENASE SUBURILLY	WILD-TYPE]	206-249							
PLUS DALE	NALDGRECTED RWA POLYAGRASE SUBLING PI	Г	602-802							
PERSONAL DECISION	MAN-DOLECTED RIVA POLYNOBLASE SUBUNIT ?!		350-384	919-119	307.752					
MARKET IAANON	INA-DESCRED RNA POLYMERASE SUBURIT PI		100	177-210						
CAN'T MUST	ANA-DIRECTED RNA POLYMERASE SUBUNIT PI	Ī	77	137.218		L				
Į	ANA DIRECTED LINA POLYMERASE SUBUNIT PA	INFLUENZA A VIRUS (STRAIN ADUCK/HORRAIDON W)	7	815.571			L			
Ţ	THE PARTY OF THE PARTY OF THE PARTY	DOLUENZA A VIRUS (STRAIN AFONT PLAGUE VIRUSAUS IUCH	2							
1	ANA-DARCHED BOX BOX WATERASE STRINGT PT	INTILIENZA A VIRUS (STRAIN AGUALAMARYLANDMONT)	*1011						L	L
1	KHA-UNEC LES MAN 105: TO A CO CO CO CO CO CO CO CO CO CO CO CO CO	INTLUENZA A VIRUS (STRAIN AEQUINEA ONDON'I (1671)	1							L
- 1	INA-DUELTED RAY POLITICANE SOCIETY PA	THE LENZA A VIRUS (STRAIN A/EQUING/TENNESSEE/3/16)	2	77-216		\downarrow				
ار	RNA-DIRECTED RNA POLITICASE SUSUMITY	TAGE PERSON A VIRUS (STRAIN ANOREA 1966)	======================================	177-218						
PLUT INIE!	NAM-DIRECTED RAY FOR THE KAN SUBURILLY	THE THEY A VINITE (STRADY ALENTHORADY 19457)	110-144	177-318		\downarrow	1			
1	ANA-DIRECTED THA POLYMENASE SUBURILLY	THE STATE A CHIEF STRAIN AN ENGINEERING (\$1)	110-144	177-118			1			L
ᇫ	RNA-DOECTED RNA POLYMERASE SUBURIT F2	THE PERSON OF THE ANALY AND AND AND AND AND AND AND AND AND AND	110-144	177-218				-		-
PLUT TOTAL	RNA-DIRECTED RNA POLYNGRASE SUBUNIT PT	_	110-144	177.218				1		\downarrow
PELT WB	RMA-DIDECTED RWA POLYNGRASE SUBURIT PT	ALBERTA/119/79)	110-144	177-211						\downarrow
PROPERTY LANCES	RNA DOLECTED RNA POLYNGRASE SUBUNIT PZ		11014	177-318				1	1	\downarrow
TUT WILD	ANA-DOLECTED BUG POLYNOBASE SUBLIMIT PA	RANGW KERS	110-144	177-218						
אנעז נעניי	INA DOLECTED INA POLYMONASE SUBURITY		10-144	177-218						l
HUT WITH	NAA-DOLECTED NAA POLYNGAASE SUBUNII 72	01 A/13 3/10)	1014	177-218			-	1		
PLAZZ TAVT	RNA-COLCTED RNA POLTMOMANS SUBJECT 1		10.2	177.218			1	\downarrow	-	L
PELLY IAWIL	MAA-OIRECTED MAA POL TMEANSE SUBSCITE	(10)	10.1	177.218			1			
PERFO IAZHO	ANA-DIRECTED BINA POLTMENASE SUBJECT PO		2	177-318			+	1		L
PRUPT INZHO	ANA-DESCRIPTION AND TOTAL AND STREET BY		10.15	177.211					-	
PLEPS IAZII	NAA-DOLECTED NAA POLYMAAASS SUSUMI 172		2	177-318		1	-			L
PILLE WETT	DAA DOLCTED DAA FOL I MEAASS STORY	THE LENGA A VIRUS (STRAIN ASWING/TENNESSEE/26/77)	2	111:41		1	1		-	L
PILLET DIBAC	RNA DOLECTED RNA POLTNEAAN SUBJECT BY	ш	¥:-:34	349.380		1	+	-		
PRUPT DOBAD	ANA-DIRECTED RIVA POLYNERANA SUBURIT 92	DETLEMEN BYTHUS (STRAD) BANN ARBORING (WED-TYPE)	¥	26.45		1	$\frac{1}{1}$	1	-	-
PRATT DOMEST	INA DOECTED DAY POLINEAMIN SOCIETY		¥ =	16-31						
PRILYS IAANON	NA DOLECTED RAY POLYMERASE SUBJECT 11	THE LENZA A VOLUS (STEAM MANY ARBOTHMO)	3	163-402			35. 501	1	-	
PREFIT LABOR	RNA DELECTED RNA POLTMEASS SUBJECT BY	DATIFICA A VIRUS (STLAIN AND COCERIGARATOR KATDONINI)	<u> </u>	163-402				1	1	
PERFY IACID	INA DIRECTED RAA POLIMERASE SCENICI	DOT JENZA A VIRUS (STRADY ACHILE/1/83)	3	363-462		20.00	+	-	-	ļ
PRUTT TAUTH	ANA DUECTED INA POLITACIA SUBSINITION	THE LIENZA A VIDUS (STRAIN AFOWL PLAGUE VIRUSROSTOCK	3	363-401		200		-	-	_
PRUT LATEN	ANA-OBECTED INA POLIMICANA SUBSITION DI	Т		163-401			-	-	-	L
FILES IAGUS	ENA-DOECTED INA POLINGAME SUBDICE PA	Τ	_	363-402	1	201-100		1		-
PRUD LAGUA	ANA-DOLECTED MAA POLIT MEANAGE SCHOOL	T	 -	762.402		2		1		1
LRP) IAHK6	RAA ORECTED AND POLITICAL SOCIETY PA	1	3	207-695		201		1		
FRRF1 IAIRO	RNA-DIRECTED RNA POL T MERKASE SCHOOL	T	7	363-402	1	2		-	-	ļ
PRILLY INFOR	NAA-DURECTED INA POL-TREAMER SOCIETY	T	<u>=</u>	76,760		200	-		-	
PREP LACES	ANA-DIRECTED RAN POL INCOME A CR STREAM P	T	7	363-602			-	-	L	
PRUTT LAKOR	DA DOLC I ED MAA POLYACIASE SUBURET PO	T	<u>=</u>			30.73	-	-		L
PREST VALET	CALCAGE IED NAME OF STREET PO	Γ	3	100		1	-	-	L	L
PRUM INLES	THA CHIEL IED INV IN THE PARTY	1	5	141.40			-			

FULL WANT	PROTEIN RNA-DIRECTED RNA POLYMERASE SUBUNIT PI	MATURISA A VRUS (STRAIN ALENINGRADI) 44777)	LASEA 1	AREAI	AREAJ	ANTA	48543	AREAS	ABEA 2	AREAI
AND WAN	RNA-DIRECTED RNA POLYNGRASS SUBUNIT PI	INTLUENZA A VIRUS (STRAIN ALENDIRADI) 44757)	10.71							
	TO LINGS IS BUT BATCA FOR THE WALL	TOTAL STATE A STATE OF THE STAT		363-402	473-514	381-105				
	MANAGER BY BY FALTMERADE SUUCITION	INTERCEPTARY VIRUS (STEAM AMALEMANEM TOMOSTALIS)	363-402	473-514	307-158					
ı	RMA-DIRECTED RNA POLYMERASE SUBUNIT PI	_	154	363-403	413-514	107.755				
	ANA-DOJECTED RNA POLYNGRASE SUBUNIT PI			163-402	113-814	207.755				
	ANA-DIRECTED RNA POLYNGRASE SUBUNIT PI	-	1-12	363-401	473-514	201.755				
١,	ANA-DOLECTED ANA POLYMOLASSE BUSUNIT PJ	_	7	363-402	473-514	767.755				
PRILITY IASDN	RNA-DOLECTED RNA POLYNGIASE RUBUNIT PI	-		163-402	473-514	707-755				
Ļ	RNA-DOLECTED RNA POLYNGRASS SUBUNGT PT	-		207-191	473-514	707-755				
	RNA-DIRECTED RNA POLYNGRASE SUBURIT P3	-		363-402	473-514	201-755				
PRUTT IAWR.	RNA-DIRECTED RNA POLYMERASE SUBUNIT PS	INFLUENZA A VIRUS (STILADA AVVICTONIANZAS)		Z00-196	433-514	707-755				
PREED LAZES	RNA-DIRECTED RNA POLYMERASE SUBUNIT PI	DEPLUENZA A VIRUS (STRAIN AVVILSON-SMITW)		363-402	473-514	201-755				
PRESS LAZTE	ANA-DIRECTED RNA POLYMERASE SUBUNIT PI	INFLUENZA A VIRUS (STRAIN A/SWINE/IOWA/15/10)		363-402	413-514	257.755				
MY DOMC	RNA-DOLECTED RNA POLYMORASS SUBUNIT PI	DOLLENZA A VIRUS (STRAIN A/SWINE/TENNESSEB/14/17	14.	363-403	473-514	257-707				
TREAD CREAD	ANA-DIRECTED ANA POLYMERASB SUBUNIT PI	INTLUENZA B YIKUS (STRAIN BVANN ARBOIN/144 (COLD-ADAPTE 455-51)	451-533							
PILLED DECISE	NNA-DIRECTED RNA POLYMERASSI SUBUNTT PI	INTLUENZA B VIRUS (STRAIN BVAIN ARBORVING [WILD-TYPE])	(18-833							
PREMI DACII	ENA-DIRECTED ENA POLYMERACE SUBURIT PE	DELLENZA C VILLIS (STRADY CREPLINGIAS)	215-269	275-309						
PRICE THOOP	KNA-DIRECTED RNA POLYNGRASH SUBUNGT P3		Γ	375-316						
MA CWG2	MAA-DIRECTED RNA POLYMORASE SUBUNIT PS	THOCOTO VIAUS	343-401							
AUTA CYMUR	RNA-DIRECTED RNA POLYMEJASS	VIRUS (STRAIN 229E)	354.392	165-571	1742-1776	1971.2008	3664-3724	3912-3946		
PRUCE BEV	RNA-DIDECTED RNA POLYNERASE	JPM)	617-631	1364-1398	2769-2803	3566-3620	3821-3855	4075-4121	43194353	
PILLOS CYNAS	KNA-DOLECTED RNA POLYNGRASS		Γ	157-619	943-1009					
PULLE CYNCH	MA-DIRECTED INA POLYMERASE	MURINE CORONAVIRUS MHY (STRAIN AS9)	1129-1170	1103-1337	1453-1494	1693-1726	2629-2670			
ALLE CAVE	RNA-DIRECTED RNA POLYMERASE	MURLINE CORONAVIRUS MINY (STRAIN HOA)	1129-1170	1103-1337	1433-1494	1690-1724	2627-2668			
AND BAK	RNA-DOLECTED RNA POLYNGRASS	AVIAN INTECTIOUS BRONCHITIS VIRUS (STRAIN BEAUDETTE)	494-550	656.695	1460-1494	1509-1548	2244-2287			
PRUPL BTV10	RNA-DIRECTED RNA POLYNGRASE	1523)								
PRUPIL BUNCHW	INA-DIRECTED INA POLYNERASE	SEROTYPE 10/ISOLATE USA)	2	705-748	125-903	1021-1076	114-1201			
mer covo	IDIA POLYMERASE		2-36	2	308-363	171-412	1704-1741	1802-1861	1819.1935	
PRUPL KANTV	ANA POLYMERASE BETA SUBUNT	IN ONDERSTEPOORT)	1	٦						
PRUPL, HRSVA	INA POLYNŒLASE	HANTAAN VIRUS (STRAIN 76-118)	7	T	12-21	557-591	655-696	(11.1C	905-949	1276-1310
			<u> </u>	142-1776	1993-3027					
PIUUL MABVA	INA POLYMERASE BETA SUBUMT	ARUS (STRAIN AL	┪	127-161	131-1179	1115-1220	1465-1517			
RUL MABYP	MANDRECTED ANA POLYNGRASE	KE)	597-631	D46-1092	1490-1552	1804-1838	2029-3063	3194-2366		
PRUPL NEASE	INA-DIRECTED INA POLYMERASE		٦	D46-1092	490-1552					
TUTE MUNOW	ANA POLYNGRASE BETA SUBUNIT	MEASLES VIXUS (STRAIN EDMONSTON)	Т	200	169-903	1064-1109	1203-1317	2121-215		
PRUPL NOVE	INA POLYMERASE DETA SUBUNIT	MUMPS VIRUS (STRAIN MIYAHARA VACCINE)	┪	220-254	267-304	576-627	752.607	1231-1216	1447-1481	1487-1531
		1		1191-2223						
PRAL PINT	INA POLYMENASE BETA SUBUMT	2	T	I	1969-2013	2043-2077	2103-2162			
PRUM, PITH	JUNA POLYMERASE DETA SUBUNIT	HOMAN PARAINFLUENZA 2 VIRUS (STRAIN TOSHIBA)	П	575-618	750-785	1226-1284	1316-1357	1417-1479	1564-1630	1617-1721
			<u> </u>	٦						
PERT, PURG	ENA POLYMERASE BETA SUBUNIT	UN NIN 47815)		Т	7	747.781	1044-1129	•	↲	1924-2036
FRUT, RABYP	MAN-DIRECTED BWA POLYNGRASE	PUTHALA YIRUS (STRAIN HALLNAS BI)	╗	_	287-777	183-581	633-696	111.10	922-976	119-1153
			چ	<u>.</u>	1991-2012					
PRESE_RABYS	INVA POLYMERASE BETA SUBUNIT				696-730	1174-1222	1523-1580		2068-2123	
RATE RDV	ANA POLYNESASE BETA SUBURIT	AIN SAD BIP)	33-114	167-231		749.783	1174-1222	1522-1580	1584-2123	
JUNE RVIVE	NAN-DIRECTED RWA POLYNORASE		19-61	\$14-\$75	144-171	910.915	1017-1071			
MUN. SENDS	RNA-DERECTED RNA POLYNERASE	NUT VALLEY FEVER VIRUS (STRAIN 2H-348 NI 2)	391-439	M1471	132-407	1081-1115	1653-1647	1819-1170		-
HUPL SENDE	ILVA POLYNERASE BETA SUBUNIT	SENDAI VIRUS (STRAIN 2 / HOST MUTANTS)	109-343	340-600	612-456	147-781	1064-1119	1239-1280	1499-1536	2000-2034
			2146-2216							
MUN. SENDS	RNA POLYNŒJASE BETA SUBUNIT	SENDAJ VIRUS (STRAIN ENDERS)	129-163	927-990	432-476	109-196	114-939	1059-1100	1319-1356	1120-1134
			ļ	Γ	Γ			Т	Т	

		All Vicence (no becteriophages)	Ī	Ι	. 7467	7 7 10 7	A DEA S	A 855		
PCGENE]	Т	7010	Г	l.	l.	9	2000-2014
TIL HAME	PROTEIN	I VIRUS (STRAIN 2)	Т	240-600	007.00				г	
MAN, SEOTH	NA POLTAGIASE BELA SUBURII		2146-2216	٦				72.6	1601, 1001	1003.2023
		100 mm (410 k ft) 20,18)	91-139		557-591	655-696	21:-163		t	
PREME SYSWR	RNA-DOLECTED RNA POLYNETASE		\$47-627	747-781	1225-1280	1319-1353	1592-1626	1676-1713	2074-2036	
PREPL SYNV	RNA POLYMERASE BETA SUBUNIT	22	Γ	825.659	977-1014	1089-1137	1978-2032	2059-2107	┪	
2402	ENA POLYNGRASE BETA SUBURIT		Г	100.411	538.573	žĢ.	1119-1153	1195-1236	921-1261	1511-1572
	THE PARTY BUY SOLVATEASE	TOWATO SPOTTED WILT VIRUS (BRAZILIAN ISOLATE CPUHINGA)		Т		21.04	1206.2247	2315-2364	2376-3419	2109-2843
PREM. UUR	WA-DUEL ED WAS 100 III		25-173					3016.3040	2061.2098	
		IN REPORTED VICES	127-183	22.23	200	101-001				
PRINT, VSVIN	NYA POLYMETAST	SECOND AS STONATITIS VILLE (SELOTYPE NEW JEASEY / STIA 119-358	119-350	674-715	726-763	1522-1567	1837-1838			
PREM. VSVXO	RYA POLYNERASE BETA SUBUNIT	SCHOOL STORY OF SECURITY SECURITY SECURITY STORY (STORY) STORY (SCHOOL SECURITY SEC	319-351	674-713	730-743	1802-1836				
PREPL VSVS	RINA POLYNGRASE BETA SUBUNIT	VESICULAR STORATILIS VIACIS (SERCITORIS)	674.719	130.763	1019-1074	1743-1799	1066-1107			
73 67 50000	NAME POST YOUTH ASSET A SUBUNCT	IN SAN JUAN		70.	914.66	1235-1260				
	ANA THE PER BUY POLYMERSE		707-17	200						
Mary Barre	ACANDOMINE TO SERVICE BUY BOX WAS BASE		ž							
PRUO BYDVI	PUTATIVE KICK-DURCHED MAKEURE	BABI BY VELL OW DWARF VIRUS (ISOLATE MAV-PSI)	234-205							
PREUM BYTOVE	PUTATIVE RIA-DOLCTED ENA POLTMENASE		234-285							
PRUPO BYDYR	PUTATIVE RNA-DISCIED RNA POLTNERATE	WALLE TELEGRAPH WATER OF A TE P. PAY	234-285							
PRESO CAUNY	MUTATIVE RNA-DIRECTED RNA POLYMERASE	BALLEY TELLOW OWALD VINOS (1300-012)	2							
PREPO CGMYS	PROBABLE RNA-DIRECTED INVA POLYMERASE	CANATION MOTTLE VIRUS	5	127-21	95	726-767	1645-1479			
200	MITATIVE BYA-DIRECTED BNA POLYNERASE	1								
	PITTATIVE RNA-DIRECTED RNA POLYNCRASE	AVIAN INTECTIOUS BURSAL DISEASE VIRUS (STRAIN 32/10)		10,7%	100.757	1.58		L		
2000	STATE OF THE CITED BNA POLYNE LASE	AVIAN INFECTIOUS BURSAL DISEASE VIRUS (STRAIN AUSTRALILIES)		100-009		160				L
TENO DISC	PULATIVE INTO-DIMENTED BOX BOX VACE ACT	INTECTIOUS PANCHEATIC NECROSIS VIRUS (SEROTYPE JASPER) 147-151	=	207		136-005				
PLUTO DINYS	PUTATIVE RIVA-DIRECTED RIVA POLITICANS	PARECTIONS PANCHEATIC NECROSIS VIAUS (SEROTYPE SP)	147-181	364-407	<u>×</u>	20.00				
PRUPO LYCVA	PUTATIVE MA-DIRECTED MA FOLTMENASE	44C-10C NORTHWAT STRAINS (STRAIN ARMSTRON)301-346	301-346	903-509	926-960	1509-1543	2000-2134			
PILLIO LYCVW	NA POLYMERASE	LTMPROCETTIC CACAGOMETIC VIRUS (STRAP)	301-345							
PILLIO MONTY	RNA POLYNŒILASE	LINGUICATION CONTRACTOR	10,213	167.799						
PEUD PEANT	PROBABLE RNA-DIRECTED RNA POLYMERASE	MAZE CHLOROILE MOLLIES VINOS	31.350							
PREPOR REVI	NA-DOECTED BYA POLYNGBASE	PEA ENATION MOSALC VIXUS	114.11	421-457		-				
AN A COLUMN	MITATIVE MA-DESCTED RNA POLYMENASE	POTATO LEARGIL VIRUS (STIAIN I)		197	L					
	MITATIVE BNA-DIRECTED RNA POLYNGRASE	POTATO LEAFROLL VINUS (STRAIN WAGENINGEN)			197.63	163.696				
	MITATIVE BNA. DIRECTED RNA POLYMERASE	PEPPER WILD MOTTLE VIRUS (STRAIN SPAIN								
A PORT	THE A THE WAS DURECTED BYA POLYNERASE	RED CLOVER NECROTIC MOSAIC VIRUS	B. 98			-				
PRIOR RECORD	THE PARTY OF STANDINGS	REDVIKUS (TYPE 3 / STRAIN DEALING)				-	-	-	-	L
WEND MEDA	MANDOCCIED FOR TOWN AND ASS	REOVENUS (TYPE 2 / STRADA DAJONES)	200	1		-				
PRING REDVE	DAY-DURELLED MAY TOUR ASS	REGOVEUS (TYPE I / STRAIN LANG)	36.361	-				ANDARA	56.00	771-105
MOUNT NOTES	MANAGERIES AND AND AND AND AND AND AND AND AND AND	BOVING ROTAVIAUS (STRAIN RF)	ş	201		2			100.134	771.405
PRILITO ROTTEU	INA-DOCETED ANA POLIMENASS SUBJECT OF	BOVING BOTAVIDUS (STRAIN UK)	3	135-167	ş Ž	\$ \$	2			
PRUPO ROTTC	RNA-DIRECTED RNA POLTMEANAS AUBURILL VI	BONDARY BOTAVERIS (GROUP C/STRAD) COWDEN)	344	255-299	25.37	03E-50	2115	B		1
PILIO ROTTO	RNA-DOJECTED RNA POLYNGIASE SUBUNIT VP	LONG TOTA VIET (STEAM COTTINED)	62.96	133-167	336.377	5	2000	660-724		\downarrow
PRUPO ROTS!	RNA-DESCRED BNA POUNCELASE SUBUNIT VP	FORCING ROLL VINE RETEATO CALLY	8.3	133-163	335-369	179-631	639-686	56.72	171-605	1
PREPO SBACY	INVA-DIRECTED INA POLYMERASE SUBUNIT VP.	SINDAN II KULAVIKUS (SIRAIN SA S	K28.465		L					
A N.S. Conne	PROBABLE RNA-DIRECTED RNA POLYMERASE	SOUTHERN BEAN MOSAIC VIRUS		1			_			
	NA DIRECTED RNA POLYNGRASE	SACCHAROMYCES CEREVISIAE VIRUS L-A			355	18.51	191-925	1030-1081	1285-1319	1961-2015
A STATE OF THE PARTY OF THE PAR	T	TACALBE VINUS	P. S.	200					Т	
TREO TAGA	1	TOBACCO MILD GREEN MOSAIC VIRUS (TMV STRAIN UZ)	401-446	55.73 27.73	100	-		1	1	
את סטאי	PUTATIVE KNA-BUELIED KNA POLITICALINA	TOBACCO MOSAIC VIRUS (VOLGANE)	75.	401-433	\$ 3	-		1		\downarrow
PRING TAYKA	PUTATIVE RNA DIRECTED KNA POLIMENOS	THE ACT OF THE VIEWS (STEATH KOREAN)	7:33	401-453	\$ \$	-				
PRUPO TANTO	MUTATIVE RNA-DIRECTED ILNA FOLD	TOBACCO MARINE AND POLATOR 1	15.1	401-453	160-194			4		
9	I	TOBACCO MOSAIC VIRUS (SIRAIN IVMANANI								

PCCENE	ALLMOTIS	All Viruses (ne becterlephages)			1	7	٦	7	1	
TILE NAME	PROTEIN		1	ABEA1 ABEA2	1	AREA 4	ABEA S	ARTA	4824.	4854
PRATE BRSVA	RNA-DIRECTED RNA POLYNGRASE	TOBACCO NECROSIS VIRUS (STRAIN D)	103-144			1				
PLANT COVO	ANA POLYNGBASE ALPHA SUBUNIT	BOVINE RESPIRATORY SYNCYTIAL VIRUS (STRAIN AS 1901)	99-158	160-216		1				
PRAPP HOLSV	RNA POLYMERASE AL PHA SUBUNTT	CANDVE DISTEMBER VIRUS (STRAIN ONDERSTEPOORT)	212-273							
PREP, HOLSVI	ANA POLYNGRASE ALPHA SUBUNIT	HIDAAN RESPIRATORY SYNCYTIAL VIRUS	96-158	160-216		1	1			
PRAPE HRSVA	ANA POLYNERASE ALPHA SUBUNIT	HUMAN RESPIRATORY SYNCYTIAL VIRUS (SUBGROUP B / STRAI) 99-158	99-158	160-216						
PLUTP HOLYL	INA POLYMERASE ALPHA SUBUNTT	HUMAN RESPUEATORY SYNCYTIAL VIRUS (STRAIN AZ)	99-158	160-216	_					
PRUP MEASE	NAM POLYMERASE ALPHA SUBURIT	HUMAN RESPIRATORY SYNCYTIAL VIRUS (SUDGROUP A / STRAU99-158	99-158	160-216						
PRUP MEASI	NA POLYMERASE ALPHA SUBUNIT	MEASTES VIRUS (STRAIN EDMONSTON)	315-374	860-493						
PLUSP MEASY	NAM POLYMETASE ALPHA SUBUNT	MEASTES VINUS (STRAIN IP-3-CA)	115-374	560-495						
PRATE MODEL	RNA POLYMERASE ALPHA SUBUNIT	MEASTES VIRUS (STRAIN YAMAGATA-I)	115-374	560-039						
PREP MAGE	INA POLYMERASE ALPHA SUBUNIT		149-183	\$42-518						
PRAPP MIDADM	INA POLYMERASS ALPHA SUBUNIT	MUNUS VIRUS (STRAIN ENDERS)	214-376		_					
PRUP NOVA	RNA POLYMERASE ALPHA RUBUNIT	MUNDS VIRUS (STRAIN MOYAHARA VACCINE)	214-276							
PLEAT NOVE	ANA POLYMERASE ALPHA SUBUNIT	NEWCASTLE DISEASE VIRUS (STRAIN AUSTRALIA-VICTORIA712) 100-134	100-134							
PRUP PLING	NA POLYMERASE ALPHA SUBUNIT	NEWCASTLE DISEASE VIRUS (STRAIN BEAUDETTE CAS)	100-138							
PRATE MINE	RNA POLYMERASE ALPHA SUBUNIT	HUMAN PARADYFLUENZA I YIKUS (STRAIN CJS)	10-114	313-164 375-437	437					
PLANT PILITO	INA POLYMENASS ALPHA SUBUNIT	HOWAN PARADITUDIZA I VIRUS (STILAIN COS)	10-114	313-366 375-437	637					
PLAYP PINES	RNA POLYMERASS ALPHA SUBUNT	73)	\$0-114	113-366 375-618	03					
PLUY PUSH	TANA POLYNOEMASS ALPHA SUBUNOT	6	66-114	P9C-EIC 112-1EZ		119-417				
THE PER	THA POLYMENASS ALPHA SUBURIT		218-281							
PLEAT POS	INA POLYMERASB ALPHA SUBURIT	HUNGAN PARADIFLUENZA 2 VIRUS (STRAIN TOSHIBA)	216-281							
PREST POST	INA POLYNGRASE ALPHA SUBURIT		31-130	414-470						
PLLYP PIGHA	MAN POLYMETASE ALPHA SUBUNT	HUMAN PARADRELLENZA 3 VOLUS (STRAIN KIH 47885)	410-499							
PRIRES PINES	INA POLYMERASE ALPHA SUBURET	(Y)	4.31	122-215						
PREP PERYV	TOTA POLYNGRASE ALPHA SCBUNGT	HUMAN PARADITLIENZA 48 VIRUS (STRAIN 64-333)	222-215		1					
PREP RABVA	NAA POLYMEDASS ALPHA SUBUNIT	PIRY VIRUS	137-174		1	1				
PREF EABVC	RNA POLYMERASE ALPHA SUBUNT		93-127		+					
PRUP RABVE	ENA POLYMERASS ALPRA SUBUNT		93-127		1	1				
PRESP. RABVE	RNA POLYMBRASE ALPHA SUBUNTT	I), AND (STRAD) PM)	72-127	1	†	1	1			
PRESP. RABYS	RNA POLYNERASB ALPHA SUBUNT		1	+	+	+	Ī			
7KU7 \$5005	KNA POLYMERASE ALPHA SUBURIT	MABES VICES (SINCE AND BIV	111 166	277 744	T		T	Ī		
PLUT SENDS	ANA POLYMERASE ALPHA SUBUNIT		Τ		\dagger	\dagger	1			
TOTAL STATE	ENA POLYMERASE ALPHA STRIDGE	(SVG)	Г	175-447	T	t	T			
TOOLS TOOL	NAA POLYMERASE ALPHA SUBUMT			375-447		Ľ				
PREFE EVS	ANA POLYMERASB ALPHA SUBURIT		313-364	375-447						
PIUUP SYRV	RNA POLYMERASE ALPHA SUBURIT		П		1	1	1			
PLUS VSVIO	RNA POLYMERASE ALPHA SUBUNIT		2	233-231	1	+	1			
PRATP VSVDA	RNA POLYNGRASE ALPHA BUBURIT	VESICULAR STOMATITIS VIRUS (SEROTYPE INDIANA / STRAIN O	3		1	+	1			
PAULY VSVDA	RKA POLYMERASE ALPHA SUBURIT	VESICULAR STURATIONS (SEAULTED INDIANA) STRAIN	7		1	1				
PRRP VSVIO	RNA POLYMURASU ALMIA SUUUNIT	VESICULAR STOMATITIS VIRUS (SEROTYPE NEW JERSEY / STRA)				+				
PILLUP VSVSJ	RNA POLYMERASE ALPHA SUBLIMIT	SEY/STILL	2		1	1	1			
PSPHD, AMEDY	RNA POLYMENASE ALPHA SUBUNIT	48AN 10AM)	Т		†	+	1	I		
PSPD VACCV	NOODIN	XVRUS		341-345	1	+	1	T		
PSP12_VARV	SEALING PROTEINASE INNIDITOR	(STRAIN WR)	9		+		1			
PSPID_VACCC	SCALNE PROTEINASE INITIBITOR 2		Т	770 700	1	+	1	ĺ		
PSP13 VACCV	SEADER PROTEDNASE DOMBITOR 3	ENHAGEN)	Т	907-677	1		1			
PSPU VARV	SEADE PROTEDIASE DAGSHOR 3	VACCINIA VIDUS (STRAIN WR)	111-167	225-256	1	1				

1911 1912 1914 1915		STON 11	All Viruses (no battertophuges)	T	Ţ		7 7 2 2 7	AREAS	AREAG	AREA?	AREAS
PARTICIPATE PRINTERS PRINTERS	1			I	Τ		Γ	Γ		ı	
THE STATE OF STATE	100			Ī							
THE TREE PROPRESS OFFICE COLUMN A LANGE LOUGH MATCH NO LOUGH M	TANK WALE	Of OG FIRST	VACCINIA VIRUS (STRAIN COPENHAGEN)								
THE BIRD LEGGE OF THE PARTY VICTORY YOUR STEAK VILLE VIL	יייים סיייי		PANANTERING RIMSARIA CIC. ORELLA VIRUS I	11-13							
TAMAS-ACTIVATOR PROTEINS UNION VARIES STATEMENTS, (FEADLY CORPORATED) 151 154-	MAAL VACEV		AND VALUOLA VI		173-207						Ī
TAMOS ANTICOLOGICAL STATES AND	MAGS FOWTY			1-61							
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Index Antiche Debug Control	MAGS VARV			15.							
LAGGE 1 APTICIDED	TALA BIDY		CINCLING DISEASE VIRIES		167-751						
LAGGE 1 ANTIGEN	PTALA POVIO	ויאוטני ז אינוניני		Γ	495-537						
LANGE VATIORE	PTALA POWIA	LAAGE T ANTIGEN		Γ	587-621						
LAGGE 1 SPTICES	PTALA POVIC	LARGE T ANTIGEN		T	(10.63)						
LOGG ANTIGOR LYANGO LY	A SOLUTION A SOLUTION	LARGE T ANTIGEN				117.730					
MAGE ANTIGED MOUSE POLYCLANDER (TRLAN 1) 505.314		ABOR T ANTIOEN			- CP CP CP CP CP CP CP CP						
LAGG T APTICES* MOUSTER FOLY-GLAVING STALL: PLAGES 195131 195	2 4 7	Machine Parkers		309-344							
LAGGE 1 ATTICES 190115 1	PIALA POWA		_	507-542							
HANGE ANTIGEN WASTER FOLYOWAND IN THE STATE OF THE ST	PTALA POVIAC	LAKGE I AMILIAN		304.539							
	PTAME POWIA	LAIGE T ANTIGEN	г	339-378							
MODEL IL ANTICES MODEL OF CONTROL STATES MODEL OF CONTROL STATES MODEL IL ANTICES	PTAIN POWAU	MODELE T AVTICEN		211-245	311-422						
Compared Foundation Foundat	PTAUG POWA	MODULE T ANTIGEN		192.226	169.403						
VARIATION AUGUST TANTION AUGUST TO AUGUST TO AUGUST TANTION AUGUS TROUGH TANTION AUGUS TROUGH	PTAME POYME	MODULE T ANTIGEN	MOUSE POLYGRAVILOS (STIASIF AS)	103.234	LOT 67L						
VILLA APPLICATION COLUMN CALLTO-MAINTING	PTASIK POVBO	MODIE T ANTIGEN	בוליאו חוח אשערה נדיילים								
TAMES_ACTIVATION TO NASCUPTONAL REGULATOR FOLVOMANDOS 111-115	A 500	CAALL T ANTIOEN		2							
TAUSE ACTIVATION TAUSCUPTIONAL RECULAT AUTOCIALMY CALF ROUNCE, NO. 176.05 (1)-145 (1		SAAA1 T ANTIGEN	_	7							
TAMES_CITYATING TAMEQUITONAL REGULAT SOMETY MODINGCEAN FOLYNEDOSIS VOUS 511-554 151-151	PIAIR REAL		AUTOCAAPHA CALIFORNICA MUCLEAR POLYNEDROSIS VIRUS	408-442	2	489-323					
TAME-ACTIVATING TRANSCUPTIONAL EGGLAT GROTIA PREDDITIONAL (GAMES ACTIVATING TRANSCUPTIONAL EGGLAT) GROTIA PREDDITIONAL (GAMES ACTIVATING TRANSCUPTIONAL EGGLAT GROTIA PREDDITIONAL (GAMES ACTIVATING TRANSCUPTIONAL EGGLAT VISIA DEPTITIONAL (GAMES ACTIVATING TRANSCUPTIONAL EGGLAT VISIA DEPTITIONAL (GAMES ACTIVATING TRANSCUPTIONAL EGGLAT VISIA DEPTITIONAL (GAMES ACTIVATING TRANSCUPTIONAL EGGLAT VISIA DEPTITIONAL (GAMES ACTIVATING TRANSCUPTIONAL EGGLAT VISIA DEPTITIONAL (GAMES ACTIVATING TRANSCUPTIONAL EGGLAT VISIA DEPTITIONAL (GAMES ACTIVATING TRANSCUPTIONAL EGGLAT VISIA DEPTITIONAL (GAMES ACTIVATING TRANSCUPTIONAL EGGLAT VISIA DEPTITIONAL (GAMES ACTIVATING TRANSCUPTIONAL EGGLAT VISIA DEPTITIO	PTATA NOTA			413-447	\$1712	494-528					
TAMESACTIVATING TAMESACTIVATION TRANSCRIPTORY STANKS DEATMODE/SCIENCY VALUE (SCIATE) 17-100 17-101 17	PIATA NEVOP			391-455	311-334						
TATE PROTECT TATE	PTAT SIVAL	TRANS-ACTIVATING THANKAL HURAL REGULAT		73-109							
TANSE-ACTIVATED TANSCEPTONAL RECOLAY VIRTA LEMTYBOUG (STAAM 1514) 131-24 171-171-171-171-171-171-171-171-171-171	TAT SIVAL	TAT PROTEIN	THE ACAD PARTIES OF THE STATE ACM / CLONE GR	137-185							
TAMES ACTIVATED TAMES DEPOSAL RECOLAT VISAL LETTIVANE (STAAN 134 / CLONE LVI-1K\$) 60-74	TAT VILV			28.74							
TAMES ACTIVATION TRANSCUPTIONAL BEGULAY VINUS TYPE INTRANS IN THE CONTROL OF STATES AND TRANSCUPTIONAL BEGULAY VINUS TYPE INTRANS IN THE CONTROL OF STATES AND TRANSCUPTIONAL BEGULAY VINUS TYPE INTRANS IN THE CONTROL OF STATES AND TRANSCUPTIONAL BEGULAY VINUS TYPE INTRANS IN THE CONTROL OF STATES AND TRANSCUPTIONAL BEGULAY VINUS TAMES IN THE CONTROL OF STATES AND TRANSCUPTIONAL BEGULAY VINUS TAMES IN THE CONTROL OF STATES AND TRANSCUPTIONAL BEGULAY VINUS TAMES IN THE CONTROL OF STATES AND TRANSCUPTIONAL BEGULAY VINUS TAMES IN THE CONTROL OF STATES AND TRANSCUPTIONAL BEGULAY VINUS TAMES IN THE CONTROL OF STATES AND TRANSCUPTIONAL BEGULAY AND STATES AND TRANSCUPTIONAL BEGULAY AND STATES AND TRANSCUPTIONAL BEGULAY AND STATES AND TRANSCUPTIONAL BEGULAY AND STATES AND TRANSCUPTIONAL BEGULAY AND STATES AND TRANSCUPTIONAL BEGULAY AND STATES AND TRANSCUPTIONAL BEGULAY AND STATES AND TRANSCUPTIONAL BEGULAY AND STATES AND TRANSCUPTIONAL BEGULAY AND STATES AND TRANSCUPTIONAL BEGULAY AND STATES AN	PTAT VILVI	TRANS ACTIVATING TRANSCULTIONAL PEDULA		40.74							
TACH ACTIVATED TAXADA TAXADA TRACATS OF FILE AND STACKS VENUS (TYTE I / STRAN 17) 27-51	MAT VILVE	TANKS ACTIVATING TIANSOURTIONAL REGULAL	VISTA LEAST AND ALTO AND 1514 / CT ONE I VILLED	2.00							
T-CELL BECEPTOR BETA CAUAN PRECATION PALINE EMPLEMA VIRUS (TYTE I / STRAIN I?) 27-61 12-61 1	PTCS PLV	TRANS-ACTIVATING TRANSCRIPTIONAL REGULAT		276-321							
TECUMENT PROSPERS NONSENSES NONSENSES NONSENSES NONSENSES	PTECP HSVII	TOBIT RECEPTOR BETA CHAIN PRECURSOR		17.61							
NONSENSE NONSENSE	PTEGP HSVEA	TECUMENT PHOSPHOPROTECN USP	HELPES SDOLLEX VINUS (1778 1731ANIN 17)								
NONSENSE NONSENSENSE NONSENSENSENSE NONSENSENSENSENSENSENSENSENSENSENSENSENSEN	PTEGP HSVEB	NONSENSE									
MONEDNIE MONEDNIE ESTERNAM VIRUS (STAIN BOS-1) 164-401 611-455 918-773 1101-1134	PTECS HAVER	NONSENSE									
MONSENSE 110-1131	PTECS HAVE	MONSBYSE									
LANGE TECHARDYT PROTEIN LANGE TECHARDYT PROTEIN MUDAUN CYTOMEGALD UNDUS (STAAN AD169) 1017-1296	And i Bay	NONSENSE					1101-1111	1200-1242	1479.1516	1700-1753	1809-1867
PLOBABLE LACG TECUMENT PROTEIN HTDAAN CYTOMEGALOVIRUS (STAAN AD169) 34-71 115-349 54-531 TOP-731	4/9/CM 18034	I ARGE TECHNOON PROTEIN	EPSTEIN-BARR VIRUS (STRAIN B95-8)	700	7791 9491	1101					
PROBABLE LANGE TECHAGNY PROTEIN HUDALN CYTOMEGALDVINUS (STAAN AD169) 131-136 131-237 131-136 1	200						11.00	PÉL.	016.077	1004-1038	1163-1200
LAKGE TECUACHY PROTEIN HELPES SINCLEX VIRUS (TYPE 1/STRAIN 17) 113-765 110-1151	מוצאוו אנאזו		HUMAN CYTOMEGALDVIRUS (STRAIN AD 169)	74-71	117-217						
LAKGE TECHAENT PROTEIN HEBJES SINCLEX VIRUS (TYPE 1/ STRAIN 17) 131-715 101-117 101-11				1437-147			1	4000	1115.1370	1130-1411	1609-1669
LAGGE TECUMENT PROTEIN FEATURES SUPPLEX VRUS (TYPE 4/STRAIN GS) 10-11 114-21	CANAD INCOME	I ARGE TECHNENT PROTEIN	HEIDES SINGLEX VIRUS (TYPE 1 / STRAIN 17)	731.765	7	201-7201	3630-3704				
LANGE TECHNENT PROTEIN PROJESS SIMPLEX VILLS (TYPE 6/ STRAIN 63) 10-157 124-101 124-10	20217				1	W 533	113,767	001.100	1001-1131	1192-1233	137-1400
LANGE TECHAEMY PROTEIN EQUINE HERPESVRIUS TYPE I (STIAIN AB4?) 150-155 161-165 170-175 161-165 170-175 161-165 170-175 161-165 170-175 161-165 170-175 161-165 170-175 161-165 170-175 161-165 170-175 161-165 170-175 161-165 170-175 161-165 170-175 161-165 170-175		LANGE TECHNIENT PROTEIN	HERPES SIMPLEX VIXUS (TYPE 6/STRAIN GS)		1		100	110411	1151.1344	138-1458	1487-1549
INDERTITE INDE		· ABOUT TECHNOLISM	EQUINE HEXPESYTHUS TYPE I (STRAIN AB4P)	360-397	2	134-848	2	100			
PRODABLE LANGE TEGUADRY PROTEIN PEDVESYALUS SADITAL (STRAM II) \$10-555 \$40-596 \$615-450 \$12-110	TECH HISMA	LANGE I ECONOMICAL PROJECT		1619-1637	18 18 18 18 18 18 18 18 18 18 18 18 18 1	120		147.183			
MODARE LANCE INCOMENT PROTEIN 101-1502			MERPECVIEUS SAIME (STRAPH 11)	\$20-554	560-598	615-633	673.710	E	144-191	941-916	261-192
LANCE TEGINGPHT PROTEIN VALICELA_ZOSTER VRUS (STAAM DUAAS) 651-496 713-736 104-441 933-573 DNA TELAMAL PROTEIN RODAN TELAMAL PROTE	TEGU VZVD			1414-1502							007. 007.
LAKCE TECHNENT PROTEIN			VARIOTE I A. POSTER VIRUS (STRAIN DUNAS)	617-496	713-747	104-841	273-672	1117-1158	4 5 6 3	528-1582	0291-7761
DNA TEMMAL PROTEIN HIDAMA ADBNOVBUS TYPE 3 DNA TEMMAL PLOTEIN KADANA ADBNOVBUS TYPE 5 DNA TEMMAL PROTEIN KANALA ADBNOVRUS TYPE 7	PTEUM ADEAS	LANCE TECHNOMY PROTEIN		1633-1705	1719-1756	1945-1961	1727-2761				
DAY TERMINA POTEN HABNOVIUS TYPE I DAY TERMINA POTEN HAMAN ADENOVIUS TYPE ? DAY TERMINA MOTEN		CHOCK THE COLUMN	HOMAN ADENOVIRUS TYPE 3	490-572							
DAY TEMMAL PROTEIN HUMAN ADENOVRUS TYPE 7	TELM ADEOS	DNA TEXMINAL PROTEIN	HIDAAN ADENOVIRUS TYPE S	190-191							
DHA TERMINAL PROTEIN	PTELM ADEO!	DRA TEMMINAL PROJECT	INTERNATIONALIS TYPE 7	481-888							
	PTELM ADEI2	DNA TERMONE, PROTEIN	וויושים ישונים יויים								

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THE HAME	PROTEIN		AREAI	7 7787	AREAL	AREA 6	V FVIUV	AREA (AREA?	ABEA
PTIUN AVISI	DHA TERMINAL PROTEIN	KUMAN ADENOVIRUS TYPE 12	43.491	497-538						
PTMM AVISA	TRANSFOLMING PROTEIN IUN		210-214							
PTOPI_SFVKA	TRANSFORMING PROTEIN MAF	ARCOMA VIRUS AS42	347.288	295-340						
PTOPT ASPB?	DNA TOPOISOMEAASE	SHOPE FIBROKA VIRUS (STIJAIN KASZA)	127-163	269-310			7			
PTOP2 ASPAG	DNA TOPOISONERASE II	٦	18-180 18-180	25.5	50-643	25.679		┪		
PTSIS_SMSAV		TRUS (ISOLATE MALAW! LIL 201)	14-130	480-314	2 2 3 3 3	902-936	16.53	1631-1091	1122-1169	
CVZV, VZVD	POGFAELATED TRANSFORMING PROTEIN P21-515		-							
PUBIL NPVOP	THYMOTIATE SYNTHASE	VANCELLA-ZOSTER VIRUS (STRAIN DUNIAS)	13-260							
PULDI MCHYA	UBIQUATON LIKE PROTEIN	ORGYIA PSEUDOTSUGATA KULTICAJSID POLYNŒDROSIS VIRUSA) 40	9							
PULOS HSVII	HYPOTHETICAL PROTEIN UL!		66.703							
PULOS HSVZH	PROTEIN ULS		94-128							
PULCT HSVED	PROTEIN ULJ	HELDES SINGLEX VIKUS (TYPE 27 STRAIN 11GS1)	92:126							
PULDA_HSV11	GENS 60 PROTEIN		70-104					-		
PUL06 EBV	PROTEIN ULA	וואא	102-136							
PULOS HCMYA	VILLON PROTEIN BBILT!	EPSTEIN-BARK VIRUS (STRAIN B95-8)	104-145	113-347	176-410					
PULOS HSVII	HYPOTHETICAL PROTEIN UL6		216-250							
PULOS HSVEB	VIXION PROTEIN ULS)6-94	101-101	584-159	111-111	416-479		·	
PULOS HSVSA	VIZION GENE S6 PROTEIN	EQUINE HEIVESVIAUS TYPE I (STRAIN AD4P)	62-170	117411	446.503					
וענא עצעם	VILLON GENE 43 PROTEIN		90:140	151-164	301-336	364.405				
PULBE HOLOVA	VILLON GENE SA PROTEIN		17.131	150-409	104-738					
PULOS HSVEB	HYPOTHETICAL PROTEIN ULA		6-30							
CAZA 60104	ORIGIN OF REPLICATION BINDING PROTEIN	EQUINE HERPESVIRUS TYPE I (STINUIN ADAP)	134-208							
PLE HONA	ONIGIN OF REPLICATION BRYDING PROTEIN	VARICELLA-ZOSTER VIRUS (STRAIN DUNAS)	122-163							
PLE 13 HONVA	NOWSENSE									
PLEIS HOWA	HYPOTHETICAL PROTEIN ULIS		13.11	105-227						
PULIA HSVEB	HYPOTHETICAL PROTEIN UL 14		105.343							
PULIS PRYND	HYPOTHETICAL CIENT 43 PROTEIN	(AB4P)	8:5	246-283						
PULIA VZVD	UL 14 PROTECH HOMOLOG		0.95					1		
PULIS HSVED	SYPOTHETICAL GENE 46 PROTEDN		-101							
PULIT HSVAU	GENE 44 PROTEIN		266-300							
PULZI HSVEB	PROTEDVIOR	ANDA-1102							1	
PULLU HOLIVA	CIENTE 46 PROTEIN		1	431-474						
PLD 14 HOAVA	HYPOTHETICAL PROTEIN UL23		22.23							
7G.24 E.TVT	INTOTIGETICAL PROTEIN UL24	_							1	1
PULLS HOWA	PROTED ULA HOMOLOG	INFECTIOUS LAKTING INACTELLIS VIAUS (STAKIN INDIANG VIEW	T	141,100						Ī
FULZS RSVII	HTTOTHEIKAL PROJEIN OLIS		T							Ī
FULSI RSVES	VILLOW PROTEIN (B.36		26.41					Ī	Ī	T
BER 16 H TAVE	CALON CENT IS SECTED		Γ	163-231	365.406					Ī
23 72/0	EL I KD VDLON PROTEDN	VIRUS (STRAIN THORNE VOS	Γ	163-306						
POLICY NOW A	VOUCH GENE 34 PROTEIN	VASCELLA-ZOSTER VIXOS (STRADY DORGAS)								
PULJI HSVED	HYPOTHETICAL PROTEIN ULU		24.283							
CAZA ICTOM	GENE 29 PROTEIN		=======================================							
PULJZ HSVEB	GENE 27 PROTEIN	٦	163-197							
GAZA TETRA	MAJOR ENVELOPE GLYCOPROTEZN 300	(STRAIN AB!)								
PULLS HOLVA			٦	296-344						
PULLS VZVO	G-PROTEIN COUPLED RECEPTOR HOMOLOG ULJJ		F-135	309-112						
M4.34 EBV	GENE 25 PROTEIN	DUMAS)	19-61							
PULD4 HCD/VA	BEN'I PLOTEIN		39-200							
PULD4 HSV16	HYPOTHETICAL PROTEIN UL14		13:147							
PULLS HOWA	VIDION PROTEIN ULIA	i	12.2							
PUL17 EBV	HYPOTHETICAL PROTEIN ULIS	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	231-268					1	1	7

POSENE		All the second s			. 7.01		,		
FILENAME	PROTEIN	VIRUS	199						
ME 17 HSV11	פרנו	EPSTEIN-BAUR VIRUS (STRAIN 1995-1)	108-145			$\frac{1}{4}$			
PLA 12 MEVER			1687:59	T					ŀ
NA VS LIEVEA	N. S.	EQUING HELDESVIAUS TYPE I (STRAIN AD4P)	12.137	Ţ		200	101.07		1
		HERPESVIRUS SAIMIN (STRAIN 11)	6-65	682-741				-	 -
		N DUMAS).	719-753	186-427					
A HOMAN	a constant of the	HIDGAN CYTCHCION OVERUS (STEAD) AD169)	10-51						
אבאו אבאם	BITOING INC. TAU IEIN CO.	VARICELLA 2 CETER VIRU" (STRAIN DUMAS)	330-366						
MAA HSVII		MERDER STANKEY VIRUS (TYPE I / STRAD) (3)	134-168	221-263		·			
NUA! HSYEB		man and an annual property of the Annual Ann	111.172			Ŀ			
HEAD HOWA		QUING REPENDENCY 117E (SINGLA CONT)	91			-			
PULAS HSVEA		HERITAN CYTOMEGALOVIRUS (STRAIN AD199)	51.71						
MEAN VZVD	70100	EQUINE HEXPESYIBUS TYPE 4 (STRAIN 1942)	27-68						
Alhan te menta		VANCELLA-ZOSTER VIRUS (STRAIN DUMAS)	312-363						
		HERPES SINCH EX VIRUS (TYPE I / STRAIN KOS)	7(1)-96			,			
PULAS HSVIK		GENERAL EN VIEWS (TVPE 1/STRAIN NO)	96-137				-		
PULEY HOKYA		MALAN CYTOMETAL OVIECE (STRAIN AD169)	114-165	448-415	745-856	-			
PULCY HSVII		APPROPRIES CHARLE (TVBE 1 / CTB APA 15)	433.511						
FULAT HISVIE	VINION PROTEIN ULA?	PERCES SUPPLIES VANCO (117E OF STRONG 17)	431.411			-			L
JULAT HSVBP		CLASS SUCLEX VIACS (117E 1781ANIN 1				-			L
PULAT HSVEA	2	BOVINE HERMESVIRUS TYPE I (STRAIN PA-1)		0,7,00	976 944				
PULLY HSVED	2	EQUING HEAPESVIRUS TYPE 4 (STRAIN 1942)	27.6	T	277				
11E-07 V2VD	7	EQUINE HENDESVIRUS TYPE ! (STRAIN ABAP)	119-251	T	201				
AUNCHON A	D PROTEIN	VANICEL LA-20STER VIRUS (STRAIN DUNIAS)	2	136.208	107-106				
110001	SECTION IS CO.	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	155-189						
1000	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	HERVES SDOLEX VIAUS (TYPE I / STRAIN 17)	118-169						
1000	DENE CONTRIN	EDUTNE HEADESVIRUS TYPE 4 (STRAFN 1942)	131-162						
	ACTION OF THE PROPERTY.	ECURYE HEXPESYTRUS TYPE I (STRAIN ABAP)	130-161			 - -			
2021	CENT SECURITION	VARICELLA ZOSTER VIRUS (STRAIN DUNIAS)	132-163						
FULSA ESP	PROBABLE DAS REPLICATION PROTEIN BSLF!	EPSTEIN-BARR YIRUS (STRAIN 895-8)	148-255						
NAME OF TAXABLE		HELDRES SINGLEX WAUS (TYPE I / STRAIN 17)	146-22)			1			
HEVEA	DNA REPLICATION PROTEIN ULS	EQUING HELPESVIRUS TYPE I (STRAIN ABAP)	2	929.970					
C 25 C 10	PROBABLE DNA REPLICATION GENE SA PROTEIN	HELDESVIRUS SADATU (STRAIN II)	45.483						
NO PARTIE	PROBABLE DNA REPLICATION GENE & PROTEIN	VARICELLA-ZOSTER VIRUS (STILAIN DUAIAS)	101-343						
HE CO HOUSE	PROTEIN UT. 53	HUNDAN CYTOMEGALOVIAUS (STRAIN AD169)	7						
AND ROWA	PROTEDVED SS	HEIDES SOULEX VIRUS (TYPE 2 / STRAIN HOSS)	151-185						
AVAILA ME 115	1. PROTEDIULE	HUNAN CYTOMEGALOVIRUS (STRAIN AD169)	<u>:</u>						
10 M	PROBABLE DWA BEPLICATION PROTEIN UL70	NOWAN CYTCHEGALOVIRUS (STRAIN AD189)	39.99						1
HE OF DEVAL	INTERTICAL PROTECT ULTS	HUNDAN CYTOMEGALOVIRUS (STRAIN AD169)	£.						
MAR BY DEVEA	SAMOTHETICAL PROTEINS	HERPES SOMPLEX VIXUS (TYPE 6 / STILATIN UGANDA-1102)	729-770						
MAC 100 MAC	WYNOTHER CENTE 24 PROTEIN	HELDPES VIRUS SADAROI (STRAIN 11)	366-400	313-616					
1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	UNIOTHERICAL PROTECTION OF AS	HUNAN CYTOMEGALOVIRUS (STRAIN AD169)	157-391						
10 mm	WYSOTHOTTICAL GENEE 30 PROTEIN	HERJESVIKUS SAINGIN (STRAIN !!)	2						\downarrow
1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	KYPOTHEAL PROTEIN BOLFA	EPSTEIN-BARR VIRUS (STRAIN 895-1)	107.144	111-233					
BIN ST MEVEL	HYPOTHETICAL PROTEIN UL92	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	<u>=</u>						
1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	HAMOMORTICAL PROTEIN 98	HEAPES SOCHEX VIXUS (TYPE + / STRAIN UGANDA-1102)	ş <u>ē</u>	174-216	-				
ME OF PETER	HYPOTHETICAL GENE 31 PROTEIN	HELDESVIRUS SAINITU (STRAIN !!)	127		-				
HIN OF MOUNT	PROTEIN 12.43	HUMAN CYTONEGALOVIRUS (STRAIN AD169)	23	799-384					
MIN DE LIEUXII	KYPOTHOTICAL PROTEIN UL95	HEDIAN CYTOMEGALOVIRUS (STRAIN AD169)	2	259-293					
AND STORE	INTERPLETICAL PROTEIN 13R	HERMIS SIMPLEX VIRUS (TYPE 6 / STRAIN HGANDA-1103)	<u>=</u>	22.52					
110.0411	HYPOTHETICAL PROTEST U.S.	HUMAN CYTCALEGALOVIRUS (STRAIN ADIO)	ē:						
THE PERSON	IIVPOTITITICAL PROTITIN 14R	HERPES SIMPLEX VIRUS (TYPI: 6 / STRAIN UGANISA-1102)	=						
HE AS LICTURE	SIYPOTIGETICAL GENE 35 PROTEIN	IEIUESVIRUS SAIMIRI (STRAIN II)	8						
1000	SIVEOTAR TICAL PROTEIN ULIO	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	9	751.772					
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PCCINE	Intraortis	All Virger (se betreriogheger)								
FILE KANE	PROTEIN	YIRUS	ABEAL	AREAI	ABEAJ	AREA	AREA S	48546	AREA!	AREA I
PUNO HSVII	HYPOTHETICAL PROTEIN ULISO	HUDGAN CYTONEGALOVINUS (STRAIN AD169)	14.125							
PUNG HEV23	URACE DNA GLYCOSYLASE	HERPES SINDLEX VIRUS (TYPE I / STRAIN 17)	227-264			-				
PUNG HSV7H	URACIL-DNA GLYCOSYLASE	HEIDES SINDLEX VIAUS (TYTE 2/STRAIN 111)	166-229						•	•
PUNG HSYSA	URACIL-DNA GLYCOSYLASE	HEADES SIMPLEX VIRUS (TYPE 2 / STILAIN HGS)	146-189						1	
PUNG SITVEA	URACE-DNA GLYCOSTLASE	HERPESVENUS SAIMÁRU (STRAIN 11)	135-176							
PUSON HISVED	URACIL-DNA GLYCOSYLASE	SHOPE FIBROMA VIRUS (STRAIN KASZA)	81:113							-
PUSO HSVEK	GENT 40 PROTEIN	EQUINE HELPESVIKUS TYPE I (STRAIN ABIP)	79.120							-
PUSOT HCHAYA	USI PROTEIN	EQUINE HERPESYIAUS TYPE I (STRAIN KENTÜCKY A)	021-91							
PUSIT HON'A	HYPOTRETICAL PROTEDY HOLES		3.36			-				
PUSIG HOUVA	HYPOTHETICAL PROTEDVIDGE!	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)								
PUSIT HOWA	HYPOTHETICAL PROTEIN HYLEA	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	ž							
PUSZI HOLOVA	LOTACIDA NEL PROTEDIO HAVI. P.S.	HUMAN CYTOMEGALOVIRUS (STRAD) AD169)	187-225					_		
PUSZ4 NOWA	HYPOTHETICAL PROTEIN HOLF?	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	Γ	535.378				ľ		
PUS26 HONA	HYPOTHETICAL PROTEIN HOLLS	HUMAN CYTOMEGALOVIRUS (STRAIN AD149)	135-172			-				
PUSZI HONA	HYPOTHETICAL PROTEIN HOLES	HUMAN CYTOLEGALOVIRUS (STRAIN AD169)	535-584							
PUSTO HONYA	G-PROTEIN COUPLED RECEPTOR HONIOLOG US27	HUMAN CYTOMEGALOVIRUS (STRAIN AD189)	6-40			-	-	-		
PV135 ALPAE	HYPOTHETICAL PROTEIN HOUSS	HIMAN CYTOMEGALOVIRUS (STRAIN AD169)	135-169	274-312		-				
PVIO NPVAC	135 KD PROTEIN	ALFALFA MOSAIC VIRUS (STRAIN 425 / ISOLATE LEIDEN	11.52	326-367	191-649					
PVISK TAVPS	HELICASE	AUTOGRAPHA CALIFORNICA NUCLEAR POLYHEDROSIS VIRUS	313-350	1114-1150	1179-1213					
PVIGK TAVSY	16 KD PROTEIN	TOBACCO RATTLE YIRUS (STRAIN PSG)	18:113							
PVIA BBAT	14 KD PROTEIN	TORACCO RATTLE VIRUS (STRAIN SYNI)	111-56			.,				
PVIA BMV	IA PROTEIN	BROAD BEAN MOTTLE VIRUS	31.55	349-405	402.536	710-711	137.884	190-924		
PVIA CO.V	IA PROTEIN	BROWE MOSALC VIRUS	Ī	348.411						
PVIA ONTH	IA PROTEIN	COMPEA CIR. DROTTLE VIRUS	4.55	342.276	348.319	467-100				
PVIA CLOS	IA PROTEIN	CUCINGER MOSAIC VIRUS (STRAIN FNY)	99-11	383-434	\$84-619	916-898				
PVIA CINQ	1A PROTEDI	CUÇÜMBER MOSAIC VIRUS (STRAIN O)	Γ	Г	619-985	616-898				
PVIA PSVI	IA PROTEIN	CUCUMBER MOSAIC YIRUS (STRAIN Q)		393-434		,				
PVIA TAV	IA PROTEIN	PEANUT STUNT VIAUS (STRAIN J)	4-66			7 ~				
PY23K_HSVTH	IA PROTEIN	TOWATO ASPERMY VIRUS		392-433 8	157-923					
PV24K BDV	23.5 KD PROTEIN	TURKEY HERPESYIRUS (STRAIN H2)								
PV2SK MPVAC	24 KD ANTIOEN	BOIDA DISEASE VIRUS	121-69	130-171						
PV2SK PLRVI	25 KD PROTEIN	R POLYHEDROSIS VIRUS	4-50							
PYZEK PLXVW	28 KD PROTEIN	POTATO LEAFROLL VIRUS (STRAIN I)	116-150							
PV790 ASFLS	28 KD PROTEIN	POTÁTO LEAFROLL VIRUS (STRAIM WAGENINGEN)	116-150							
PVZ9K PEBV	LIS 290 PROTEIN	AFRICAN SWINE FEVER VIRUS (STRAIN LISS?)	: :::3							
PVPK TRVSY	29 6 KD PROTEIN	early browning valus	115-192							
PV39K_TRVTC	IN KD PROTEIN	TOBACCO RATTLE VIRUS (STRAIN SYN), AND (STRAIN PSQ)	167.201							
PVIA COAV	19 KD PROTEIN	TOBACCO RATTLE VIRUS (STRAIN TCM)	62.79							
PV1A CHVPN	2A PROTEIN	COMPEA CALOROTIC MOTTLE VAIUS	768-806							
PVIA PSVI	2A PROTEIN	CUCUMBER MOSAIC VIRUS (STRAIN PNY)	16420				1		1	
PYZA_TAV	12A PROTEDM	PEANUT STUNT VICUS (STRAIN I)	117.733				1			
PYJOK TRVTC	2A PROTEIN	TOWATO ASPENAY VIRUS	722-756							
PY360_ASFB7	POLICE PROTEIN	TOBACCO RATTLE VIRUS (STRAIN TCM)	_		-	1	1			
PV362_ASFB7	K740 PROTEDV	AFRICAN SWINE FEVER YIRUS (STRAIN BA71Y)								
PV363 ASFB?	K343 PROTEIN	AFLICAN SWINE FEVER YRUS (STRAIN BATIV)		161-212 2	290-324					
PV3A_BMV	D'143 PROTEIN	AFRICAN SWINE FEVER VIRUS (STRAIN BATIV)	153-199							
PYJA CHATA	3A PROTEIN									
PYJA CACH	JA PROTEIN	ç	215-255							
PV3A_ChV0	JA PROTEIN	CUCINMER MOSAIC VIRUS (STRAIN N)	115-255							
PYJA, Chry	SA PROTEIN		25.53							
PVSIK ACLSV	SA PROTEIN	CUCUMBER MOSAIC VIRUS (STRAIN Y)	215-255					_		

-	ATTACATA		AREA	AREAJ IAREAZ	1	3			
PCCION.			72-104	Γ	 				
TOWN TO	CO C POR DESTITEDA		13:143	194-233 404-451					
PVSIK BWTVP	No ho more and a second a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second a second and a second and a second and a second and a second and a second and a second a second and a second and a second and a			Γ	_				
VIK BWYVO	SI KD PROTEIN			Τ					
PVSCK PLAVI	SI KUP PROTEIN			100	-				
VICE PLAN	M KU TRUICUM	AIN WAGENINGEN)				_			
PVSEK BSAV	S KD PROTEIN								
PV66K BWTVF	38 KD PRUTEIN	IS (ISOLATE FL-I)	76-000	***		 -			
PV70K PLRVI	66 1 KD PROTELM			214.344					
PUTOK PLRVW	69.7 KD PROTEIN		4-14	609-443		\ \			
PVIOK ALIVILE	49.7 KD PROTEIN	(DEN)	107-141				-		
PVADA_VACCC	SO KED PROTEIN		33.66	231-275		1			
PVADE VACEV	PROTEIN A4		33-66	111.275	1				
PVADA VARV	PROTECH A4	(a) Indian	***	210-265					
PVADE VACCC	PROTEIN A4		97.213	314-355					
PVADS VACCV	PROTEIN A4	Colorate		313-354					
PUACH VARY	PROTEIN A6	(3) IANIN WK)	97.213	313-356					
TARREST CALLE	PROTEIN AS		176.236						
	DECTEN AS	VACCINIA VIRUS (STRAIN COPENHAGEN)	136.316	-	_				
PVAUL VALV	STATE OF THE PARTY	VALIDLA VIRUS		-					
FVADY VALLE	NA CONTROL AS	VACCINIA VINUS (STRAIN COPENHAGEN)			-	_			
TVAUP VAKY	SECULE DE LA SECUL	VARIOLA VIRUS		210.213	2				
PVAII VACU	TROISING AT	VACCINIA VIRUS (STRAIN COPENITAGEN)		T					
PVAII VARV	TRUISINANI	VARIOLA VIRUS							
PVAIS VACCE	MOLENA	VACCINIA VIAUS (STRAIN COPENHAGEN)		1	+				
PVA12 VARV	PROJECTIVE	VANIGLA VIRUS	761.13						
PVAII VACE	ALMO ELL MICE LATE PROTEIN	VACCINIA VIRUS (STRAIN COPENHAGEN	101	411.467	-				
TVAIS VALLY	A RO ANGRIVE LATE PROTEIN	VACCINIA VINUS (STRAIN WR)	1	633-467					
20070	SAKD ABORTIVE LATE PROTEIN	VARIOLA VIRUS	19						
VAND VARV	PROTEIN A20	VACCINIA VIXUS (3 I INCLIN CONTRACTOR	5			-		1	\downarrow
SVA12 VACCC	PROTEIN A20	VARIOLA VIRUS	97.			1			1
VANY VARV	PROTEIN A22	VACCINIA VIAUS (31 IANIM COPERVIANCES)	9.60						ļ
NATI VACCO	PROTEIN A32	VANIOLA VIRUS	5:13	113.207 155.219		2			1
7877	PROTEIN A13	VACCINIA VIRUS (STRAIN CUTENHAUGA)	5.10	113-207 255-289	289 344-382				1
787	PROTEIN A33	VARIOLA VIRUS	11.13		-		\downarrow	1	1
7007	PROTEIN A31	VAUGLA VIKUS		_					1
200	PROTEIN A33	VACCINIA VIRUS (STRAIN W.R.), AND (STRAIN COTEMINAL	117.331			Н			
200	PROTEIN AZ	YANOLA VIRUS	1 5						
i i		VARIOLA VIRUS		131.00	-		_		
PVAJA VACCY	TACLEIN AND THE STATE OF THE ST	VACCINIA VINUS (STRAIN WR), AND (STRAIN COPENHAGEN)	è			-			
77436 7427	ACCIECT ANY PRECITION	VARIOLA VIRUS		+					
אאז אינני	PROTEIN ATT	VACCINIA VIRUS (STRAIN COPENHAGEN)			-				
אאון אערר	PEOTEN A17	VACCINIA VIRUS (STRAIN WR)		-					4
200	PROTEIN ALS	VACCING VIRUS (STIVAIN COPENHAUEN)		+					1
	PROTECT AND	VACCINIA VIAUS (STILAIN W.K.)	979	-					
TAN VAL	SEA METOR	VALOLA VIRUS							
אאווא אינדי	100 CE 10	VACCINIA VIRUS (STRAIN COPENHAGEM)		-					
אאלא אערי	PROTEIN A19	VACCINIA VIRUS (STRAIN WR.)				 -	_		
WAGE VALLE	200000000000000000000000000000000000000	VACCINIA VIAUS (STRAIN COPENHAGEN)		+					
PVAUS VACEV	PROTEIN AND	VACCINIA VIAUS (STIAIN WR.)		}	-	-			
PVA& VAKY	TAGISIN A 44	VARIOLA VIRUS		787.787	-		-		
PVA47 VACC	TAULES AN	VACCINIA VIRUS (STRAIN COPENHAGEN)	R			-		-	L

					П	П	П	П		ŀ
PCGENE	ALLAIOTIS	ent (no necessaria)	AREA!	AREA? IA	7 77387	AREA4	FATER	PEAS	TATES	1
TILE MANE		SURUS A VIRUS	62.96	10:EX		Ì	1		T	l
PVAM VACCC		I (STRAIN COPENNAGEN)	9	126-160		1		†	1	1
PVA49 VACCV			00-0	134-160		1	1	1	-	1
PVA49 VARV			3-40	126-160				†		
PVASS VACCC		(STRAIN COPENHAGEN)	91-132		1		1	†	İ	
PVASS VACCV			91-133					T		١
PVASY VACCC		ENHAGEN	134-160			1			T	l
PVASS VACCV	3 8		134-163		1		1			١
WAL! MSWR		N ISOLATE)	210-269				1		T	l
PVAL! AISVN			228-262				1		Ī	ı
PVALI MISVS		KATE)	218-161					1	T	ı
אירו פרכי			117-151							١
PVALL TYDVA		VIRUS (STRAIN AUSTRALIA)	2						Ī	١
PV N.J AUNIWA				2-134				1		ļ
PV ALS BGNIV	ALI PROTEIN		44.78	22:124		Ī				Ì
N'ALI PYRIVA		US (ISOLATE VENEZUELA)		121.71						ı
WALL SLEV	ALL PROJECT					1				1
PVAL) TGMV				1		1				١
PVAT CAMPE	ALL PROTEINS AND TENE	[41]		12-13						
PVAT CANVO	2		٦							
ı				25.127						
\mathbf{I}		1		421.04						
1			Ţ	93-127						
1		BOURG)		021.0						
	Armin the Australian Perinten		34-70	1						
I.	ABUTO TO A WORLD OF THE PROTECT		98-138							
PVB03 VACLY			108-142		***					
200	Z CALLOR	ENHAGEN)		T	Arr-ac					
VARV MEVE	PROTEIN BA	S (STRAIN WR)	27-64	211.72	49.410					L
PYROS VACCO			10, 30	T						
PVROS VACCC	PLAQUE-SIZE / HOST RANGE PROTEIN PRECURSOR		100.71							
PVR05 VACCL		AUEN	364.398	1						L
PVROS VACCV	PLAQUE, SIZE / HOST RANGE PROTEIN PRECURSOR	ER.)	10, 10							
PVB07 VACCV	PLAQUE-SIZE/HOST MANGE PROTEIN PRECURSOR	VACCINIA VIRUS (STRAIN WR.)	1.63							L
PVDGE VACCC	PROTEIN BY PRECURSOR	Τ	26.60							
N'TOB VACCV	PROTEIN BE PRECURSOR	VACCINIA VIANIS (STANIS CONTINUES)	16-60							
PVB18 VACCC	PROTEIN BY PRECURSOR	VACCINIA VIETO (STRAIN COPENHAGEN)	37.375	191-532						
PVD18 VACCV	PROTEIN BIS	VACCIMA VIEWS (STRAIN WR)	335.375	228-140						
PVBIS VARV	PROTEIN BIT	VARIOLA VIRUS	137-378	491-532						l
PVBIS VACCE	PROTEIN BIG	VACCINIA VIRUS (STRAIN COPENHAGEN)	17.121							1
MAIS VACES	SUBSTACE ANTIOCAL STACKS	VACCINIA VIRUS (STRAIN DAIREN I)	===							1
PVBIP VACCV	SUBLINE ANTIGEN CORPUTABOR	VACCINIA VIRUS (STRAIN WR)	3							Ţ
PVB19 VACCC	SUMPLE ANTIOCH STATEMENT	VACCINIA VIRUS (STRAIN COPENIAGEN)	48-15							Ţ
PVB21 VACCV	AND IEST DAY	VACCIMIA VIRUS (STRAIN WR)	<u>6</u>							L
PVBLI BONY	TRO LES TORONTO	BEAN COLDEN MOSAIC VIRUS	150-193							L
אשרו מרכא	DEL CACIONAL DEL C	SQUASH LEAF CURL VIRUS	139-193							L
PVBL: TGNV	BLI FROIEIS	TOWATO COLDEN MOSALC VIRUS	159-193							L
PVBR BCMV	DEL PROTEDA	BEAN COLDEN MOSAIC VIRUS	172.306							L
2012	BAI PROTEIN	SQUASH LEAF CUAL VIRUS								L
AVES VACCE	BAI PROTEIN	TONIATO COLDEM MOSAIC VIRUS		163.100	391-442					L
VOC. 100.10	PROTEIN CI	VACCIMIA VIRUS (STRATM COPENHAGEN)		1						l

	ALLMOTIS PROTEIN CI PROTEIN CI PROTEIN CI PROTEIN CI PROTEIN CI	n Kasza) Emlagen)		341-303	191-041					
	OTEN CO OTEN CO OTEN CO OTEN CO OTEN CO	DNA VIRUS (STRAIN WR) I FIBROALA VIRUS (STRAIN KASZA) NIA VIRUS (STRAIN COPEMHAGEN)	Ш	3						
	OTEN CA OTEN CA OTEN CA		1				1			
	OTEN CA OTEN CA OTEN CA		77 .						-	
	OTEN CA		*							
	OTEN CA		**							
			*							
	PROTEIN CA	VIRUS (STRAIN KASZA)	83-133							
	HYPOTHETICAL PROFEIN CS		31-68							
	PROTEIN CS		1							
	PROTEDICS		2.70							L
	PROTECHES	VAUCUA VIENE	45-86							L
	HYPOTHETICAL PROTEIN CO		63-106							
	LAWOTHETICAL PROTEIN CO		13.116	161-236	289-325	275-412				
		MANAGEN	T	166-226	219-323	575-612				1
	KOTEIN CY		Ţ			 -				1
	PROTEIN CV	ENHAGEN				_				1
	PROTEIN CIO					-				_
	PROTEIN CIO	VARIOLA VIRUS	136-130			 -				_
П	PROTEIN CIO	CLOSE FIREDLY VIRUS (STRAIN KASZA)	Ī		075.001					4
I	IIYPOTHETICAL PROTEIN CIZ	SHOPE FIBROALA VIAUS (STRAIN KASZA)	T							
	PROTEINCID	VACCINIA VIRUS (STRAIN COPENIAGEN)	T				-			_
Γ	PROTEIN C16/822	VACCINIA VIEUS (STRAIN COPENHAGEN)	Ţ	66.67			-			
	PROTEIN CIT/813	THE CENTA VIEW (STEAT) COPENIAGEN)	40.98			1			L	_
	PROTEIN CILIDA	CALCINION (AND CATENIN KASZA)	16-97			1	-			L
T	PROTEIN CIP	SHOPE TENCHAL VICE CONTRACTOR	٦			1	-			L
T	PROTEIN CIMBS	YACCIAIS VINOS (STEAM POS. B)	130-114	670-709						L
1	MAIOR CAPSID PROTEIN	EPSTEIN-BACK VINCS (STEAKS AD169)		27761	260-294	1		1		L
T	MAJOR CAPSID PROTEIN	HOME CT LONG OF CT OF LAST AND 17	116.175	8.38		1	-			L
	MAJOR CAPSID PROTEIN	HEATES SHOWING TO WASTE		330-266	212					L
	MAJOR CAPSID PROTEIN	TOURS WENDERVIELS TYPE I (STRAIN ADAP)	٦	25.35						L
Γ	MAJOR CAPSID PROTEDI	COURT CANADA (STRAIN II)	1		100	-		-		
Γ	ALAJOR CAPSID PROTEIN	THE STATE OF THE STRAIN INDIANA S)	٦	20.00		+	-	-		
	MAJOR CAPSID PROTEIN	CALLOCAL A PROSTER VIRUS (STRAIN DURIAS)	٦	2	1	-	-		_	
[MAJOR CAPSID PROTEIN	VALUE LANGE AND THE POLYHEDROSIS VIRUS	110-248			1	-			L
T	DNA-BOOMG PROTEDY	AUTOMATA CATE AND ED. 1)	145-181			1				L
T	11 6 KD PROTEIN	FOWLING VINCE AND CORPUSAGEN	133-157					-	-	ļ
Γ	PROTEIN DS	VACCINIA VACO (STRAIN)	123-157					-		L
T	PROTEIN DS	VACUALA VINUS (STITEMENT)	123-157				-			L
2000	PROTEIN DS	VAUGLA VIANA	126-160			$\frac{1}{1}$	-			Ļ
Ţ	PROTEIN DP	VACCINIA VINCE (STRAIN WE)	126-160			+		-		L
T	PROTEIN D9	VACURIA VIRILA	134-160				-	L	_	L
	PROTEIN DO	FOUND BOX VORISE (STRAIN PP.1)	65-98			+				H
	PROTECHDIO	GUAGE BIREOMA VIRUS (STRAIN KASZA)	4-32		1	+	-			Ц
Γ	PROTEIN DIG	2000 A VIII.	67-105			-	-			Ц
Ļ	PROTEIN DIO	TATEL TEL DUNE MOCALC VIRUS (STRAIN CM-1841)	1.38		\ +	+	+	-		H
CANAL COLLEGE	DNA BINDING PROTEIN	CAUCH COMES MOSAIC VIBIGS (STRAIN DA)	1:35			+	+			┞
300 ANA	DNA-EDODING PROTEIN	CALLINGS MOSAIC VIEWS (STEAD) BBC)	11-38			+	+	-		┞
2000	DNA-BINDING PROTEIN	CALLE COMES ACCESS OF VIEWS (STRAIN NYS153)	1.35			+	-	-		L
TANA CANA	DNA-BONDING PROTEIN	CAULITICALES NOCATE VILLS (STRAIN STRASBOURG)	1.35		-	-	+	\ 	_	-
מינטי איניני	DNA-BRODING PROTEIN	CAULITICATE VINITE (STAIN COPENHAGEN)	182-736		1	-		-		L
ACCV	PROTEIN E2	VACCIDIA VIRUS (STILAIN WR)	202-336		+	+	1			H
VAN VANV	PROTEIN E3	VACCE IN VIEW	212-336		1	-		_		
AVEOL VACCO	PROTEIN EJ	VACCINIA VIRUS (STRAIN COPENNAGEN)	13-61		1	+	+			Н
2007	PROTEIN ED	VACCINIA VINE (STRAIN WR)	1741		$\left\{ \right.$	1				
* C * C * C * C * C * C * C * C * C * C	E ZELCOS	VACCINGA VIRUS (SINAILY TO)								

FULL NAME PVEDS VACCO PVEDS VACCO PVEDS VACCO			144	Paro Paro					
VESS VACCO			-		-	+			
VEDS VACCO							•		
VEOS VACCO		VAPORNIA VIRUS (STRAIN COPENHAGEN)	28-93						
PVEOS VACCV			38-103					1	
			38-103						
PVEOS VARV			38-103						
PVEOR VACCC		COTE A DA COPENSIA CENS	961-801	332-265					
PVEOR VACEV			Γ	333-266	_				
PVECE VARV		•	105-139	367-401					
PVEIL NPVAC		AT IEGBAICA NIECT FAR POLYTEDROSIS VIRUS	113-163			7.			
PVEI HPVIA	EALLY 18 5 KD PROTEIN	1	171.70						
PVEL HPV31	EI PROTEIN		26-90						١
PVEL SIPVII	EI PROTEIN		5	133-167					
PVEL HPV35	EI PROTEIN		8.45						
PVEI_HPV39	E! PROTEIN		10.07						
PVEI HPV41	EI PROTEIN		5.33 5.43	313-346					
PVE1 HPV42	EI PROTEIN		12.5						
PVEI HPVS	EI PROTEIN		13-67	119-174					
PVEI HOVED	EI PROTEIN		265.200						
PVEI PAPVE	EI PROTEIN		176-210						
PVEN NPVAC	EI PROTEIN	EUROPEAN ELL PATILLOPIA VIROS	71.117						
PVE3 CIUVK	EALLY 25.9 KD PROTEIN	T	1						
PVE2 HOVOS	PROBABLE E2 PROTEIN	COLICATAL KABBIT (SHOVE) PATILLAMATINOS (STATEMATINOS)	653	274.310 342-383	433.471	_			
PVE2 NPVG	PROBABLE E2 PROTEIN	HUMAN PAPILLONIA VIRUS 1 TPE 3		Т	Γ				
PVE3 HPV16	PROBABLE ES PROTEIN	HOMAN PAPELOMANTUS TYPE I	61.100	11.5.546	-				
PVE3 HDVIS	E3 PROTEDY								
PVE3 HDVIA	E2 PROTEIN			150-193		-			
PVE3 HPV2A	E2 PROTEIN	HUMAN PAPILLUAIN VINCS 1172 IN	1	158-193					
PVE2 HPV31	E3 PROTEDY	NUMBER OF A LANGE OF THE SAME	61-105						
PVEL HPV33	E2 PROTEIN	IN PASSES OF LANGE TOPE 33	101-69	166-785					
PVE2 HDV33	EJPROTEIN	NUMBER OF CONTROL TYPE 35	201-52	158-192					
PVE1 HPV19	E3 PROTEIN	TOPICAL CALL CALL WATER TOPE TO	74-110	123-359	_				
PVE2 HPV41	E3 PROTEIN	RUMAN PARLICONA VINCO 1 (12 22	3						
PVE2_HDV47	E1 PROTEIN	SUMAN PARLICUMA VIEWS 1 1 FE ST	25.2	148-113					
PVEZ HOVSI	E3 PROTEIN	HUBOAN PAPELLOMAN WOOD I IVE VI	161-751						
PVE2 MPVS7	E3 PROTEIN	SCHOOL SALES TO CALL VIET R TVPR 53	13-47	179-213					
PVE2_HDVS8	E3 PROTEIN	THE TANK OF THE PARTY OF THE ST	3.36						
PVE1 HOVSB	E2 PAOTEIN	MANAN PART LOMANTHUS TYPE SB	5.57						
PVE1_PAPVD	PROBABLE ET PROTEDI	See a set I CALA VIETIS	107-141						
PVE2 PAPVE	PROBABLE ET PROTEIN	FIRESEAN FLK PAPILLONGAVIRUS	113.150						
PVE2 PCPVI	PROBABLE ET PROTEIN	PYCHAY CHING ANZEE PAPILLONA YIRUS TYPE I	318-361		1	-			
IVES NOVI	EZ PROTEIN	PRESUS PAPELDMAYRUS TYPE I	63-196	307-341			1		
PVEJ9 NOVAC	EL PROJEIN	AUTOGRAMIA CALIFORNICA NUCLEAR POLYNEDROSIS VIRUS	Š						
PVE39 MPVOP	EXELT 19 KO FROIEN	ORGYTA PSEUDOTSUGATA MULTICAPSID POLYNEDROSIS YIRUS 119-156	25.4		-				
SIADE VEA	SALLY 19 AD PROTEIN	HEBACH PAPELDMAYIRUS TYPE 18	3		-	+			
1000 1300	PROBABLE EA PROTECT	HISAAN PAPILLOMAVILUS TYPE 41	3	65.72	+	+			
		HUNCAH PAPILLOMAVIRUS TYPE SII			-				
200	VIRAL ENHANCING FACTOR (VEP) (104 KD GLYCOP	TUCHOPLUSIA NI GRANILIOSIS VIRUS (TNGV)							
PVENT BE V	PANCE ON PROTEIN	BEENE VOLUS (BEV)	127			+			
PVENV DHVII	NOTEIN PRECURSOR	DICOL VILUS (STIAD) PEDIANVILLAS) (DHO)	2	1		+			
PVENV MCV		MOLEUSCUM CONTAGIOSUM YINUS SUBTYPE I (ACVI)	237-218		+	-			
VENY THOOK		MOLLUSCIAN CONTAGIOSUM VIRUS SUBTITIE 2 (MCVII)	27.62	+	+	+			
A CANA	ENVELOPE OLYCOPROTEIN PRECURSOR (SURFACE	THEOCOTO VIRUS (THO)	2						

100 ACCC NATE OF ACC NATE OF ACCC NATE OF ACCC NATE OF ACCC NATE OF ACCC NATE OF ACC NATE OF ACCC NATE OF ACCC NATE OF ACCC NATE OF ACCC NATE OF ACCO NATE OF ACCC NATE OF ACC		TINUS (1)	237.295		_					
				-		Ī				
			341.745	-						
									1	
			+	-						
	2000		10.00							
			2	+						
TTTT	(3) KD PROTEIN) (PJ/K	VARIOUS VIROSNICA NICLEAR POLYNEDROSIS VIRUS ()	1	+	†					
		AUTOCKATA CALL CONFINITORN AND VACCINIA VIRUS 44-10		20.50	1					
П		VACCINIA VIRUS (STIMALY LOTER PROPERTY		124-158	1					L
T	ARD ACAST NOT		31:10		1					
Ī		ENTAGEN	91							
	PROTEINFO		T	0.1.19						
Γ		EMIAGENI	I							
T	A MEMBRANE PROTEIN PRECURSOR		921-18	211.370	1					L.
1	JISOR		11.129	203-321						L
	105	VACCINIA VIRUS (STRAIN WR)	T	221.323						1
VARY VARY	200		Ī							
Γ	1		T							
T	PROTEIN FA	CASE A TALL COPENSA CENT			1			L	-	
	407FP4E11		113-254	265-311	1			-	_	
1		(SIRAIM P.T.)	61-73	268-315						L
	PROTEIN			Γ	199-236	350-381	2			
J	PROTECUPIL	VACCINIA VIRUS (STRAIN COPENIAGEN)	I	Γ		350-311	244-58		4	1
Ī	PROTECUFIS	CONTRACTOR OF THE AND LIVE	1	T	Ī	183-643				
Ī	PEOTEON 712	AACLINIA VINOS VIN	-	077-64				L		
Ī		VALIDLA VIAUS	27.2						-	
٦	TRUE CANADA	VACCINIA VIAUS (STRAIN CUPERIIMUER)	155-194						-	L
	PROTECTOR	VACCINIA VILUS (STRAIN L-IVT)	701.757							ļ
	PROTEIN FIS	VARIOLA VIRUS	1							-
	PROTEDIFIE	FOWL POX VIAUS		316.233						1
PUTPL FOWPY	PROTEDURA	SOW FOX VIRUS								
Versi Bowe	PROTEINTY	FOUND BOX VIBIR	Ž.				L			1
10,000	PROTEON IP?	TOTAL SAN WHITE ICTS AND FP.13	11.11							
	EN EST PROTEIN (FRAGMENT)	CONCORD SECTION OF THE PROPERTY OF THE PROPERT	ž					-		
WINS VALLE	NOTE OF THE PROPERTY.	VACCINIA VIRUS (\$1 AALT)	70.00	٦				-	-	L
PYTUS VACEV	TO STORY OF THE STATE OF THE ST	VACCINIA VIRUS (STEAM WA)	271.306	512-563	191-647	730-76		-		-
PVC01 HSV11	IA KU JUSTANIA COLOR CONCENTRAL	ICTAL UNID HEADESVIRUS I (CHAMPLE CALL	901:336					1		-
PVC01 VACCC	HYPOTHETICAL DEVE 1 THOUSE	VACCINIA VIRUS (STRAIN COPENYAGEN)	346.378						-	1
SYCOL VACCV	PROTEIN GI	VACCINGA VIRUS (STRAIN WR)				L				1
VARV	PROTEIN GI (FRAGNENT)	VARIOUA VIRIJE	Arrior I	1			L			-
200	PROTEDUGI	COUNTY INTERPORT TYPE 1 (STRAIN ABAP) (EHV-1)	10-11				-			
3	SEAST PROTECT	EQUING REPORT (ENV.)	143-177						L	<u> </u>
VC03 HSVEK	Carrent Control 13	EQUINE HEMPESVIRUS LIVE (131 MOLT)	2.3						-	-
VCO) VARV	CENE J PROTEIN TON	VALIGLA VIRUS	201.01	135-289	355-319				-	-
PVC65 VACCC	PROTEING	VALCINIA VIRUS (STRAIN COPENHAGEN)		Ι	355.369	L				1
VEN VARV	PROTEIN GS	VARIOUS VIRUS		T			-			-
100		CHANNEL CATEIS! CHANNEL CATEIS! VIRUS) (CCV)	61-10					L		_
VCD PIST		ICTALDAD RESS CONTROL CATFISH VIRUS) (CCV)	69-103				-		L	
WOW MIN	THE PROTEIN	ICTALIAM REACES (MAIL CONT.)	1114-175	124-158					-	
PYCO! VACCC		VACCINIA VIAUS (STRAIN CUPENTAUCA)	114-13	134-358				-		-
PVC01_VARV	MOTEN G7	VARIOLA VIRUS	164.33				1		+	+
PVCOP VACCC	PROTEING	VACCINIA VIRUS (STRAIN COPENHAGEN)						$\frac{1}{4}$		+
VACA VACA	PROTEIN FI (PROTEIN CS)	VACCENTA VIRUS (STRADE WR)				L	_			1
	PROTEIN PI (PROTEIN OF) (FRAGMENT)	A ACCOUNT					-	H		4
		CATFISH VIRUS (CCV)	커	\int			-	L		
VGIO ROAL	LYCOTHETICAL GENE 10 MENGRANE PROTEIN	ICT ALUMN TOWN SENT THE SENT THAT II	_			1	-	-	-	_
PVG13 SPVIR	ACTION OF PROPERTY	SPIKOPLANA VINCE STATES							-	L
PVOIG MSVSA	CENTER IN THE INTERIOR IN PROTECT	HEADESWALLS SADACID (3 I MALE 11)	52.12	111.211			1		-	L
PVOIT HISYII	HYPOTHETICAL CENTER 12 PROTECTS	ICTALUNID MEMBERVIAUS I (CHANGEL CATATAL MAINS ICCA	1	215-256					1	-
VCIE HSVII	KYPOTHETI CENTER SECTION	ICTALUND PERPESVIRUS I (CILAMPEL CALIFISH	4		-					
PYGIL ALEDY	MYPOTICAL UENE 18 TRUE	AMSACTA MOOREI ENTONIOPOXVIRUS (AMELY)	1							

	CASION ROTTIN CASION ROTTIN CASION ROTTIN INFO INTECAL GENETIN PROTEIN PROTEIN	VIAUSICEY) VIAUSICEY) VIAUSICEY VIAUSICEX VIAU		201-274 74-106 74-106 74-106 74-106 103-196 61-111 76-107 78-107	110-111	1601.053			-	
					241-099	844-1053			-	
			1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	13-100 13-100 10-110 10-110 10-110 10-110 10-110 10-110	260.192	1001.001			-	
			1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	74-100 74-100 74-100 100-190 100-190 100-190 100-190 100-190 100-190 100-190 100-190					-	
1			1.10 (0.10) (0.1	74.106 [16-21] 205-126 [16-13] 16-136 [1-13] 26-107 16-136						Ī
! ; : ;			11.5 (1) (1) (1) (1) (1) (1) (1) (1) (1) (1)	18-116 20-136 26-136 61-111 26-136 935-1078						
1:1111:11111			11.790 14.5) 14.5) 15.10 16.11	116-218 205-124 205-124 206-126 61-121 762-294 935-1073						
: :			2 (-1) (-1) (-1) (-1) (-1) (-1) (-1) (-1)	20-110 20-110 20-110 101-196 111-196 111-196 111-196					Ī	
			23:256 25:200 25	28-134 28-100 16-18 16-11 26-139 36-103						
			1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	166-190 163-194 15-131 163-294 199-1073			Ī			
			2 - 1 - 2 - 2 - 2 - 2 - 2 - 2 - 2 - 2 -	26-190 161-196 15-131 26-296						
			5 - 1 - 1 - 1 - 1 - 1 - 1 - 1 - 1 - 1 -	26-100 113-196 173-121 26-296						
1:11:11:11:11:11:11:11			20 - 1 - 1 - 2 - 1 - 2 - 1 - 2 - 1 - 2 - 1 - 2 - 1 - 2 - 1 - 2 - 1 - 2 - 1 - 2 - 1 - 2 - 2	284-100 162-194 87-11- 762-294						
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			24-118 24-136 21-156 21-163 21-163	264-100 162-196 87-131 263-296 939-1078						
			2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	262-296 252-296 939-1073						
			2 2 2 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3	163-196 67-131 263-296 939-1078						
			21 - 150 21 - 162 21 - 163	67-131 362-296 839-1078	1					
			21 - 10 - 10 - 10 - 10 - 10 - 10 - 10 -	262-296						
			2 2 2	939-1078						
			2 - 162 2 - 162	939.1078	374-361					
			2.10	939-1078						
			100		135-135					
			60-413	999-119	733.767					
			101.101							
		(US (ANEPV)								
			9:130							
	MINISTERNING AND PROPERTY.	HANNEL CATTISH VIRUSHICOVY	===	10.43						
		ï	8.5	131-157	62.1%					
		MEL CATFISH VIAUS) (CCV)	67-137							
		_	387:386							
		1	101:00 101:00							
		_	26-176							
		1	131-192	138-617	644.678	730.784	146-110	1111.1145		
	NE PROTECN	MEL CATFISH VIRUS) (CCV)	0.72	19-123						
Ī			69-309							
Ĺ			<u>5</u>							
1	STANDISE STORE OF PROJESH	7	=							
PVG65 115VII HYPOTH		~	16-580							
PVC46 HSVII HYPOTI			3	23.13%						
PVEST HSVII THYOU		╗	=	21410						
	HYPOTHETICAL GENE 67 PROTEIN	Т	1	301-546	1331-1369	1471-1341				
PVG12 HSVII HYPOTI	INTICAL GENE 48 PROTEIN	ī	165-281							
	HYPOTHETICAL GENG 73 PROTEIN	ī	27.0	111.157	913.949					
	HYPOTHETICAL GENE 15 PROTEIN	NEL CATRISII VIRUS) (CCV)	20.20	=						
ĺ	GENE S PROTEIN		ş					┪		
×	15.N	IN BEAUDETTE) (1	<u>=</u>	1233-1267	2119-2156	1100-3434	275313	3817:3856	3761-3795	
•	GL YCOPROTEIN HOU PRECURSOR	WH CYTOMEGALOVIAUS (STRAIN AD149)								Ī
	COPROTEIN PRECURSOR (MATRIX GLYCOP	CINE RESPIRATORY CORONAVIRUS (STRAIN IMI) 7004 / DR	2							
	CUPRDTED PRECURSOR (SPIKE GLYCOPRO	THE CORONAVIRUS (STRAIN F15	2	120-113	1901-(86	1363-1309				
1	ET OLYCOPROTEIN PRECURSON (SPIKE CLYCOPRO BOV	THE CORONAVINUS (STRAIN L9)	2	6	2					
ı	COPROTEIN PRECURSOR (SPIKE GLYCOPRO	THE CORONAVIAUS (STRAIN LY-131)	2	20.00	100	1363-1305				Ī
CVIII	COPROTEIN PRECURSOR (SPIKE CLYCOPRO	THE CORONAVILLIS (STRAIN MEBUS	90	830-03	100	1363-1303				
١.	COPROTEIN PRECURSOR (SPIKE GLYCOPRO	TOVE CONONA VIRUS (STRAIN QUEDEC)	200	100	993.1 I GB	11363-1303				

		Al Virunes Ino botteriophoget)					3	4664	3	j
١	A LIMOTH	100	T	T	B. 1.00	1263-1305	Γ		_	
III CEAPIE	CHARLES CON CONTRACT YCOPRO	VINE CORONAVIRUS ISTRAIN VACCINE)		1:	Γ					
١	ES CLYCOTICION TRECORDO CONTROL CONTRO	NAM CORONAVIRUS (STRAIN 229E)	Ï	Ť	110 (110				-	
	ES CLYCOPROTEIN PRECURSON ISPAN CONTO	THE FORONAVIRUS AGIV (STRAIN WILD TYPE 4) (ABIV-4)	Ì	Ī						
VCII CVAIAS	ES CLYCOPIOIEN PRECURSON ISTING CLYCOPIO	TIME CORONAVIAUS LOIV (STRATH ASS)	Ī	Ť						
- 1	ES OF YCOMOLEIA PRECURSON (STINE CE CO.	THE CORONAVIAUS LOIV (STRAIN BOIV / VALLANT CL-21	Ī	:						
l	ES CLYCOPROTEIN PRECUASOR ISPINE OF LOTTO	TOP CONCENTION AND AND	103.543		1			900		
	E) CI YCOPROTEIN PRECURSOR (SPIKE CLYCUPED	S SURVEYORD PROFESSION OF STREET	9110	441-413	613.73)	110-923	200	136		
I VON	ET CLYCOPADIEIN PRECURSOR (SPIKE GLYCOPAD	CON TAXABLE ON TAXABLE CONTACTOR CON	9116	197-903	691.735	119-923	1040-1166	1313-1314		
ı	ET AL VEOTROIE DA PRECUASOR (SPIKE GLYCOPRO	ICINE IRANSHISSIOLE GASTED CONTROL OF THE PROPERTY OF THE PROP	Ī	987-977	111.069	167-93	1031-114	1350-1317		
t	SOUND SECURSOR (SPIKE GLYCOPAG)	ACINE TRANSMISSIBLE GASTROEMIERUITA CONCRETATION	Ī	Τ	15.53	17.67	1036-1104	38-317		
- 1	ELULY COMPLETE PROCESSES OF VERYOR OF VERYOR	ACINE TRANSLIISSIBLE GASTROENTERITIS CORONAVIRUS IS	Ī	Ī		1	1174.6145			L
CVPRI	ET CLYCOPACTEIN PRECURSOR (STINE CETEOR	PENS BESPIEATORY COLONAVIAUS (STRAIN 641) 7004 / BRUT	1	Ī	4					
CVFRA	ES CLYCOPROSEIN PRECURSOR STILL OF LOTTO	THE SCHOOL TOBY CORNAVIBIES ISTRAIN BAM (PRCV)		466.500	M63-677	78				ļ
ı	ET CLYCOPADIEIN PRECUASOR ISPINE GLYCOPAD	SI SUSTANCIACION PROPERTY OF THE PROPERTY OF T	61.10	146-410	690-731	187.921	1038-1			1
2	FIGURE CLYCOPRO	CONF. TICANAMISTRICE CONTROLL STRUCK	61.102							1
!	PROPERTY OF THE LABORANTE GLYCOPROTEIN		Ī	1	695-736	103.036	<u>6</u>	135-1392		
- 1		LINE DATECTIOUS PENTONITIS VIRUS (STRAIN 19-11-0)	Ţ	1.						_
PVCL2:00'6	El G. TCUTAULEIN FRECUESON	AAN INSECTIOUS BRONCISTIS VIRUS (STRAIN 642)	62.16.	3						L
	E2 GLYCOPROTEIN PRECURSOR	THE PERSON OF A PARTIES AND ISTRAIN DEAUDETTE	137-478	772-904	1036-1070					ļ
	E2 GL YCOPROTEIN PRECUESOR	TATAL STATE OF THE	331.803	1037-1091						1
	ES CLYCOPROJEM PRECIMSON	TAN IN ECTIOUS BELOADERS AND LOS LOS LA PROPERTIES	417.478	112.404	1036-1090					1
1	TO SECTION OF THE PROPERTY OF	JAN IN ECTIOUS BRONCHITIS VIRUS (STILAIN RESEAR		Τ	1016-1000					_
Į	E. W. T. Cornelle Control of the Con	_		1	2					L
PVCL B HCAIVA	ET CLYCOPROTEIN PRECUASUR			120-163	717					ļ
1	GLYCOPACIEIN B PRECURSOR		3.5	128-163	437.478	451-415	45.17			1
	TO TO SECURE STATE OF THE SECURITY OF THE SECU			Γ						
1			M							L
VICE HISVIE	GLYCOPROTEIN B PARCUASUA		127-189							-
ı	GLYCOPROTEIN B PRECURSOR		27.689							1
١	CI VCOPROTEIN B PRECURSOR		40.00							_
ı	Section of the sectio	(2)								_
1			73.8W							L
	CLYCOPHOISIN B PRECUASOR		11.190							-
	GLYCOPROTEIN B PRECURSOR		117.871							
ł.	GLYCOPROTEIN B PRECURSOR	11011	15.	18:333						1
1	GLYCOPROTEIN B	Ï	10.01							-
	C: VCOBIOTEDI I PRECIMSOR			100 17						
	C. CrossOtton B. DeffCill Coll								L	_
COLD JISVIC	GLYLOROLEIN ST. PARCONSO.	ER)	004-191							Ļ
VOLE IISVE	GLYCOPROTEIN FRACTORSON		543-576	11.86						-
HSVE	CLYCOPHOTEIN B PRECURSOR		474-513	141.900						1
VCL B HSVEA	CLYCOPROTED PRECURSOR		\$42.576	38-11-						1
HSVER	GLYCOPHOTEN B PRECURSOR	SOUND INTERVENIENCE IN THE LINE OF THE PROPERTY OF THE PROPERT	473.576	196114						4
	TO VODE STEEL B PERCENSON			970				_		_
2	2 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	10								L
VGC HSVA		11RAIN RD-10)				1				Ļ
V.CLB HSVSA	CLYCOPIEIN B THE CARSON		140-211	404-403						ļ
PICE MICHINS	GLYCOPROTEDU & PRECURSOR	ATU CALITY	304-360	517-219	101.32	344-378	749.0			4
IIA I	GLYCOPROTEIN B PALCURSOR	STATES A PRICES	117.01							4
	CLASSOCIATION CILPELCURSOR	HINDSEN OUT		1	140 601	-				_
2				200		1	<u> </u>			
7.C.C.	CONTOURNE THE CONTOUR DESCRIPTION OF THE CONTOUR	HERPES SIADLEX VIRUS (TVPE 1/STRAIN 11)	2					\ \ +		ļ
LHSVIK	GLYCOPROTEIN C PRECURSOR	TATES AND SY VIRING 17 YPE 1/ STRAIN KOS)	469.310						1	\downarrow
NGIC IISV	GLYCOPROTEIN C PARCURSOR		\$2.5°							+
PUCIC HSV31	GLYCOPROTEIN C PALCUMSON	TOTAL STATE OF THE	41.477							1
DEVEL TISVAC	GI VCOPROTEIN C PRECURSOR	WEIDES SUOLES WAUS (TYTE 21 21 KAIN 199)	100				L			-
200	CL YCOPROTEIN GILL PRECURSOR	BOVING IGENESVINUS TYPE I (STILATH COOPER)				-				Н
200	ī	EQUINE IERPESVIRUS TYPE I (STRAIN ABIP) AND (STRAIN KEN	_			-				L
PLUIC HSVB	ī	HANDER'S DISEASE HEIDESYCHUS (STINADA BC-1)				+	\downarrow	+	_	Ļ
CHISMO	SECRETORY GLYCOTROLEIN OF STREET		63.97				$\frac{1}{4}$	1	1	ļ
	TARGET OF A CANDED TO MANAGEMENT						-	-	_	-
THANKS			2	_	_	_				I

Viele MVII	214414			A G L V	ABEAT	77187	487.18	7 7 7 7	ABEAT	172117
VELC PRVI		The state of the s			Name of the last					
	SECRETORY OF ICOMOTERS OF THE CHARGE	HAUSER / DECKE								
1000	CLYCOROLLEN GIRT PULCENSON		1 2 2							
200	C. T. C. C. C. C. C. C. C. C. C. C. C. C. C.	CABICAL A POCUM CIPIC CORAC CORP.	110-111							
TO HIS VEA	SUPPLIES OF SUPPLI	CONTRACTOR OF THE PARTY AND TH	100							
	- Control of the Cont	NEW YORK ON THE PARTY OF THE PA	100							
1000										
I BY	COLUMN THE CAROLINA	HERBER CRIM FW TRIES IN THE TO HEALTH								
- 1	CLYCUPROTEINE PRECURSOR	MEMORS SENTER VINCOLITY I								
MESVC	JUSION OF YCOPROTEIN PRECURSOR	BOVINE RESOURATIONY SYNCYTIAL VINUS (STRAIN ASSISTED)	146.302	34.343						
	I LEION CL YCOPROLEIN PRECLASUR	BOVINE RESPIRATORY SYNCYTIAL VIRUS (STRAIN COPENITAGE	- S	207.70	200					
1	PLEION OF YCOPROTEIN PRECURSOR		146.303	767-303	206-55					
ŀ	FUSION CLYCOMOTEN PACCUSIN		230-349	340-331	\$4E-601					
í	JUSTON GLYCOPHOTERN PRECURSOR	HUDIAN RESPIRATORY SYNCYTIAL VIRUS (SUBGROUP BISTRAL		161.302	\$06-549					
	I USIGN CL YCOPROTEIN PAECUASON		14:30	161.302	\$06.549					
	I USION CL YCOPHOTEIN PRECURSOR	HIDIAN RESPIRATIONY SYNCYTIAL VIRUS (SUBGROUP A / STRAI	116-202	167.301	506.343					
	FUSION GLYCOPHOTEIN PAECURSON		116.302	167-303	\$06.349					
1	FUSION OF YCOPROTEIN PRECURSOR	П	19:10	311-369	453.500					
	BUSINA OF VEOPROTEIN PRECUBSING	MEASUES VIRUS (STRAIN P.)-CAS	13:13	331-272	455.503					
٠	THE CONTRACT OF CO	ī		231-369	452.500					
1			ž	5.1.30	235.232	447.502				
		INITALIS VIBUS (STRAIN MILYAMARA VACCINE)	20.54	103-179	215-272	447.50				
CHE MANUS	PUSIUM CLYCOPROTEIN PRECURSOR	MUNIPS VIRUS (STRAIN AW)	X O	9:13	25.32	207.67				
470% JE	_	MUNITY VIRUS (STRAIN SOL)	×.6×	10)-130	235-272	641.502				
N. 27 120	JUSION GL YCOPKOTEIN PRECUM	3K1A/323	117-1117	111-111	426-512					
מרופא ביום	;=	NEWCASTLE DISEASE VIRUS (STRAIN BEAUDETTE CAS)	133-163	111-272	426-517					
PACEL NOVIR	=		117-163	111-111	26.35 26.31					
כבו אמאו	I USION GL YCOPROTEIN PRECURSOR	Ī	2		<u>=</u>					
יכון אסאר	FUSION CLYCOPROTEIN PRECURSUR	NEWCASTLE DISEASE VIRUS (STRAIN ITALILMAS)	=		3					
SCI PONI	FUSION CLYCOPROTEDY PRECURSOR	Ī	23.182							
אטרו אסאס	FUSION OF YCOPROTEIN PRECURSOR	Ī		201.20						
VGL NOV	FUSION OL YCOPROTEIN PRECURSOR	SLANDAR)								
אמין אסאום	FUSION OLYCOPROTERN PRECURSOR	NEWCASTLE DISEASE VIXOS (SIRAIN ILACA)	31.103	21.17	200					
2001	STORY OF VOICE OF STORY OF STORY	NEWCASTLE DISEASE VIRUS (STRAIN IN STERAS)	23.10		200					
ALIE PINE	PUSION CLYCOPROTED PRECURSOR	PHOCINE DISTENDER VIAUS	3-61	197.764	39.35	113.581				
VGLF PILL	FUSION CLYCOPROTEIN PRECURSOR	HUBSAN PARAINFLUENZA I VIRUS (STRAIN C29)	3:14	207-167	439.503					
NOLF PIZIE	FUSION GLYCOPROTEDN PRECURSOR		9:10	47-528						
WOLF PIRT	FUSION GLYCOPROTEIN PRECURSOR		13.183	117.533						
VGLT PID	FUSION GLYCOPROTEDN PRECURSOR	(STILAIN TOSHIBA)	93.18	477-528						
PYCLF PILIP	FUSION GLYCOPROTEIN PRECURSUR		117-183	107.241	456-518					
PYCHE RINDK	FUSION GLYCOPADTECN PRECURSOR	IN MIN 47869)	13.10	201-146	462-532					
PURE RINGE	FUSION CL YCOPROTEIN PRECURSOR	ADETE 0)	П	111-165	Ş					
CLF SENDS	FUSION GLYCOPROTEIN PRECURSOR		٦	274-765	44:506					
CLF SEND!	FUSION GLYCOPROTERN PRECURSOR	AUTANTSI	=	<u></u>	3					
CLF SENDII	FUSION GLYCOPROTEIN PRECURSOR		=		3					
20.0	FUSION CLYCOPROTEIN PRECURSOR	(5)								
2005	FUNDA GLYCOPROLEIN PRECURSOR	SENDAL VIEW COLORS								
100	TOTAL STANDARD SEASON STANDARD		98-186	5.5						
1.	FUSION GLYCOPROTEDY PRECURSOR	SDRAW VAUS (STRAIN W)	103.171	241.273	631.643					
2 10 10 10 10 10 10 10 10 10 10 10 10 10	PLANCE VEDPROTEIN PRECORSIN	TURKEY RIIINOTRACTIBITIS VIRUS	105-167	180-224	457.44					

							П	П		
PCCINE	אַרראַוֹטוּזּ	uses (no bacteriojitages)	ABGAL	AREAL	ARTAI	AREAs	4854	3	1	1
II. E Z.V.IC.			_							
1		FEBRUADEY SYNCYTIAL VIRUS (STRAIN COPENIAGE		Q-138					-	
		SCREEN TORY CYNEY ILAL VIRUS (SUBCACUP B / STRA)	10.01						-	
	ALVIOR SURFACE OLYCOPHOILING		2							
- 1			30.15							
PVCLO HRSV4			20.00							
			10.55							
		STATE OF CANCELLAL VIRUS (STRAIN ESB6256)	10 01							
132.7		CORPAR RESPINATION CONTRACTOR ISTRAIN REDIGIO	100							
125		CALAN ACTURATION OF STREET VISION OF STREET	10.00							
•		ILISTAN RESTRAINE STANCTION VIXOS COUCESCO.	30							
		HUNIAN RESPIRATORY SYNCYTIAL VIRUS (STRAIN AL)								
٠			Ī							
ŀ		SIGNA VIRUS	Ī	14.						
- 1		CONCIDIS YELLOW NET VIRUS	101-123							
	SPIKE GLYCOFROIEIN FRELURSOR		163.387							
		NIN	136-510							
ı			Ī	101.33	336-380	653-694				
PATER INCARA		ENTERNBANK VINUS (STRAIN DVS:4)		110.111	17.169					
1		REIAN CYTOMEGALOVINOS (STRAIN ADIEN)	١	403,140						
1		MAIAN CYTONIEGALOVIAUS (STRAIN TOWNE)	Ī							
ł		ELPES SINDLEX VIXUS (TYPE 1/STRAIN 17)								
- }		IFREE CEMPLEX VIRUS (1 YPE 17 STRAIN IU ENI	447.481							
1		SERVE CHANTER VIRILS (TYPE 6 / STRAIN CS)	937-406							
		TO CO STATE OF THE PARTY OF THE	10.00							
1		BOVINE IN FIGURE 1 17 C 1 (3) MAIN COLD	Ī	416-435						
l_		EQUINE (ERFESTRUS 17FE 1(3) KAIN 144)	Ī	403-441						
ı		EQUINE LETTES VITUS TYPE I (SI KAIN ABAT) AND LIBORATE	Ţ	137.461	216,233					
L		ELLESVIRUS SABIIDA (STRAIN I I)	ī							
J		AIDAINE CYTOMEGALOVIRUS (STIAIN SMITH								
		PSEUDORABIES VIRUS (STRATM KAPLAN)	207-4							
1	#C5#173#4 17 17 17 17 17 17 17 17 17 17 17 17 17	SEUDORABLES VIRUS (STRAIN MIA-3)	25.25							
PVGLM PRVID		PSEUDORABIES VIRUS (STRAIN IUCE)	36.36							
l		VARICELLA. ZOSTER VIRUS (STRAIM DURIAS)								
PVCI.1 HCMVA		CARACA POTOLEGAL OVIETS (STRAIN AD169)	Γ	113-159						
PVCLNI BUNGE	OVER PRECURSOR	STATE OF STA	19:75	465-137	1236-1263					
		BUNTAVIAUS CERCES SON AVE 1 341	Γ	916-950						
PVGLM BLOWSH		BUNTAVIAUS LA CACASA (1900)	197.17				•			
L		BUNYA VIRUS SNOW SINCE HARE	Ī	56.563	905.939					
1		BUNYALWELA VIRUS	Ī	310.1100						
	NI POL YPROTEIN PRECURSOR	DUGBE VIAUS							L	
1	NI POLYPROTEIN PRECURSOR	HANTAAN VIRUS (STRAIN B-1)								
PACE AS LIABILITY	LI POLYPROTEIN PRECUASOR	HANTAAN VIRUS (STILAIN HOLD)							_	
	LA BOS YOUNGED PRECINCOR	HANTAAN VIRUS (STRAIN LEE)	3							
A CENT	SOUTH PRESIDENT	HANTAAN VIRUS (STRAIN 16-118)	8							
ACI M INSA	TO THE CONTRACTOR OF THE CONTR	IMPATIENS NECROTIC SPOT VIRUS	61:18							
ACITY LA	M TOLITACION PARCONON	PROSPECT IIILL VIRUS	37-111							
VOLN TIV	M POLYPRUIEIN PRECENSOR	PUNTA TORO PREDOVIRUS	149.151							
PVGLM SEOUS	M POL YFIOTEIN PALLORSON	SECTO VIBILE ACTUALISM	121.19							
PVCLM SEOUR	M POLYPROTEIN PRECURSOR	1000 Care and a 200 care a 200 ca	694.728							
PVGI.N SEDUS	NI POLYPROTEIN PRECURSOR	SECOL VINCE CONTRACT	611.110							
PVCLN BEFV		SECOL VINOS (STRAIN SECTO)	11711	\$11-569						
PVGLP BEV	NONSTRUCTURAL GLYCOPAGIEIN GNS PRECURSO		19:07	2	622-656	1128-1236				
PVGLX PRVIL	PEPLONER GLYCOPROTEIN PRECURSOR	GENTE VINOS	420-461							
PVCLY ZENTA	SECRETED GLYCOPROTEIN GX	PEUDOIA IES VICUS (S I MALIT MALE)	301.349							
אמוג ראונט	GLYCOPROTEIN POLYPROTEIN PRECURSOR	IDMIN ALENAVIRUS							ĺ	

PCCENE	ALLAIOTIS	All Vierbes (no batteriophages)	11111	1111	AREAS	A H F.A 4	AREAS	AREAG	AREA?	AREAI
TILEBANG	LAGISTA		111.140	ī		Γ		ı	Ī	
PITILY LASS!	POLYPROTEIN PRECUAS	LASSA VIRUS (STRAIM GATAL)								
PVCLY LYCVA	GLYCOPAGIEIN POLYPROTEIN PRECURSOR		1							
PVGLY LYCVW	GLYCUPROTEIN POLYPROFEIN PRECURSOR	5	1	Ī					Ī	
PVGLY MOPE!	GLYCOPROTEIN POLYPROTEIN PRECUASOR	LYPHICCYTIC CHONOMENINGITIS VIRUS (STRAIN WE)	26-15	797-161						
PUGLY PIARY	GLYCOPROTEIN POLYPROTEIN PRECURSOR	MOPEIA VIRUS	1							
PVGLY TACV	GLYCOPROTEIN POLYPROTEIN PRECURSOR	VIRUS	34-33							
L	CL VCOPROTEIN POLYPROTEIN PRECURSOR	TACALUE VIRUS	115-363							
ı	CL VIOPROFEIN POLYPROFEIN PRECURSOR	PACARIBE VIRUS (STRAIN VS)	301-151	111-416						
	CONTRACTOR NO VERNICAL PROPERTY PROPERTY CO.	TACALIBE VIRUS (STRAIN V?)	102-150	311-118						
	SCHOOL STATE OF STATE	VL 11501)	103-151	313-416						
			335.669							
A CONTRACTOR OF THE PARTY OF TH	GENORIE POLYROIEIN IS		167.301							
PUCINAL CPSAIV	GENOVIE POLYPROTEIN NI	COWPLA MOSAL VIRUS								
PVCIND ACELV	CHONE POLYPROTEIN N		72.748	74						
PVC.P8 EBV	GENOMIE POLYPROTEIN MI		137-871	417-946						
PUCP EROV	PROBABLE MENIBRANE ANTIGEN OP15	EPSTEIN-BALR VIRUS (STRAIN B95-1)	94-149				•			
	TO SULL TO ALL TO ALL THE PARTY OF THE PARTY	BOLA VIRUS	160-111	134.368	469.303					
	CONTINUE WATER CONTINUE OF THE PARTY OF THE	DESCRIPTION AND SOURCE	362-386							
ACL MABY	STRUCTURAL OF TOWNOISIN TRECO-SOR		143.104							
MIRES VACCE	STRUCTURAL IN TECHNOLEIN PIECURSOR									
PVIIOZ VACCV	LATE PROTEIN 912	VACCINIA VIRUS (STRAIN LOPENIAUER)								
PVIIO? VARV	LATE PROTEIN H2	VACCINIA VIRUS (STRAIN WR)								
PVS101 VACCC	LATE PROJEIN ITS	AARIOLA VIRUS	51-93							
1000	2000 E	VACCINIA VIRUS (STRAIN COPENIAGEN)	111-115							
		VACCEMIA VIBILE LET BATH WITH	===							
PY III VARV	FRUITINIII		134.301							
PVIEL LSV	PROTEINHS	AMOULA VIACO								
PV118P VACCC	PROBABLE HELICASE									
PVIIRE VACCV	HOSE RANGE PROTEIN	ENHAGEN)	10.2							
PVIB) VACCC	HOST RANGE PROTEIN		216-379							
PVIOT VACCV	PROJECTION	ENHAGEN)	Ì	210.744						
PVIOT VARV	PROJECT	VACCINIA VIRUS (STRAIN WR)	٦	20.74						
PVID& VACCV	PROJECTION	VANIOLA VIRUS	200	210.74						
PVICE VARV	PROTEIN 16	VACCINIA VIRUS (STRAIN WR)	18-92							
PVIOT VARV	PROJEINIE	VARIOLA VIRUS	18-92							
PVIDS VACCC	PROTECTION	VARIOLA VIRUS	173-407							
PVIDS VACCV	PUTATIVE IMA IELICASE ID	ENIAGEN	348-519							
VISE VARV	PUTATIVE RMA (CELICASE 18	VACCINIA VIXUS (STAAIN WA)	\$42.529							
PVIET INCHA	PUTATIVE ANA PELICASE 18		341.589							
PVIET HOVY	SEED DOCEDIATE EARLY PROTENT	IDMAN CYTONEGALOVIAUS (STRADY AD169)	11.113		161.402	416-450				
PVIET MEMVS	35 KD INDIEDIATE EASTY PROTEIN I	HUMAN CYTOMEGALOVIRUS (STRAIN TOWNE)	11-113	171.105	168-402	416-450				
PVIEZ NOVOP	INDIEDIATE EARLY PROTEIN I		144.297							
PVIEW MOVAC	INDICOLATE EALLY PROTEIN IE.	Ų,	94-118	105-195						
PVIF CAEVC	DOCEDIATE EASE, RECULATORY PROTEIN IE.N	S)	177-407							
PVIT BIVE	WILDN DO ECTIVITY FACTOR		19-61							
1000	CHICK THE CTIVITY FACTOR	Γ	20.00							
200	SCHOOL DESCRIPTION OF PACIFICA	Γ	12-60							
1000	VIETON DATECTIVITY FACTOR	3	₹	62.56						
	VIETON PARECTIVITY BACTOR	INDIAN INMINODEFICIENCY VIRUS TYPE I (BHIO.BAU.HXB), PV	7	63.06					•	
NAME OF TAXABLE	MARION PARECTIVATY FACTOR	HABLAN BARANDEFICIENCY VIRUS TYPE I (BHS ISOLATE)	7	23.86						
	VIEDN METHOTY SACTOR	INDIAN DOLLNODE FICENCY VIRUS TYPE I (ELI ISOLATE)	=	91.19						
TANKS IN	VIEW INTECTIVITY PACTOR	HIDALAN BUNDARDEFICIENCY VIRUS TYPE I (MCSF ISOLATE)	=	94-79						·
101121	VIEWN INFECTIVITY FACTOR	INDIAN INDIANODESICIENCY VIRUS TYPE I (NAL ISOLATE)	1.16							
PVIT HVINS	VILLON DO ECTIVITY PACTOR	HIDIAN DALINCOEFICIENCY VIRUS TYPE I (NOT ISOLATE)	77	94-29						
PULL HOINE	VINION DIRECTIVITY FACTOR.	HUNGAN INGRUNDOEFICIENCY VIRUS TYPE I (NEW YORK-5 150L 1-43	143	94.69						
- 11 11 L										

rctive	ALLNIOTIS	Ī	AREAL	AREA? AREA?	Т	AREA	ABIAJ	ABEA 6	AREA?	1415
U.L. KANIE	EROIGIE.	WIN 12 10 10 10 10 10 10 10 10 10 10 10 10 10	Ī	Γ	Γ	Ī	Γ			
_	CINION INTECTIVITY FACTOR	HUNIAM MOLUNDE FILERAL TOTAL THE TOTAL TOTAL	Ī	3	İ					L
VIP IIVIOY	VIBION INTECTIVITY FACTOR	HIGHAN INCHADOL PICIENCY VINUS LYPE I LAIM INCANCE			İ	İ			-	L
20.21	VIRION IN ECTIVITY FACTOR	HUNIAM IS BILL MODEFICIENCY VINUS TYPE I (DVI ISOCATI)			 	İ				
15121	VIRION IN ECTIVITY FACTOR	HINDIAN INDICHORERCIENCY VIRUS TYPE I (PFAIAT ISTATIC)		<u> </u>		İ				
121/1	VIRGO IN ECTIVITY FACTOR	HUNIAM INCHUNDOEFICIENCY VIRUS TYPE I (STRAIN UGANDAN	Ì							
17176	VILION IN ECTIVITY FACTOR	HIDIAN BINLINGDEFICIENCY VIRUS TYPE I (ZLCDC-Z) I ISOLA			1	1				
10.3	VIRION IN ECTIVITY FACTOR	SIGNIAN INDICACOEFICIENCY VIRUS TYPE I (ZAIRE & ISOLATE)	Ì	2.2	†	Ť				
-	WIERWINSECTIVITY FACTOR	HUBIAM ISLIUMODEFICIENCY VIRUS TYPE 2 (ISOLATE DIOL.?)	19.13		1	Ť				
	STREET STREET STREET	INDIAN INDIANOBERCIENCY VIRUS TYPE 3 (150LATE MIS-2)	157-193		1	1				
ı		HILLIAM INDIUNODEFICIENCY VIRUS TYPE 2 (ISOLATE ROD)	161.197							
3		DOUGH FAITIVIBUS (STRAIN SA.OSIVV)	-							
İ		ESSESSION AND INCOME FILTENCY VIETIS (AGAILS) ISOLATE)	Ī	150.701						
	CINION IN ECTIVITY FACTOR	THE PERSON NAMED AND PARTY OF THE PERSON NAMED IN CO. LANSING.	13.51							
PVIF SIVAI	VIRION INTECTIVITY FACTOR	SINIJAM INDICACOLE ALLE MALT VINCE (ACMIN) INCA ILL	Ī							L
	VINION IMPECTIVITY FACTOR	SINIAN INDICATOR ICLENCY VINUS HOULAND AND AND AND AND AND AND AND AND AND	Ī			İ				
	VIRION INTECTIVITY FACTOR	SINITAN INTOMODE REIENCY VINUS (TYO. I ISOLATE)			1		Ī			
	VIRION INSECTIVITY FACTOR	CHINDANZEE INDICHODEFICIENCY VIRUS	=	1						
١	VIRION INSECTIVITY FACTOR	STATION INDUNDREFICIENCY VIRUS (ISOLATE GD!)	=							
1	PROPAGILE TATEGRAL MENDRANE PROTEIN	HERPES SINDLEX VIRUS (TYPE I / STRAIN 17)	٦		1					
	NISCORD SAME AND SAME	EQUINE HERPESVIRUS TYPE 1 (STRAIN ABAP)	141-182	331.369						
ALL MANY		III TAPE SVIRUS SATAITAL (STRAIN !!)	80-128							
OAZA ANIA	INTELLIGIA MENDANCE CANDIDER	VALIFER I A. POSTER VIRIS (STRAIN DUNIAS)	107.151	155-139 247-301	<u> </u>					
VIM SSVI	a I	CAR COLONIA VIBIL INTERACTION SCVI	200	138.172	- 					
VB1 VACCC	PROBABLE INTEGRASE	CACCACACACACACACACACACACACACACACACACAC	22.54		<u> </u> 					
VIOI VACCV	PROTEIN		356	-	-					
PUIDI VARV	PROTECNI	VACCINIA VAUS (STRAIM WR)		1						L
PVK0J VACCC	PROTECHÍ	VALOLA VIAUS			+	1				
VIND VACEV	PROTETNKY	VACCINIA VINUS (STICATIN CUTENIAGEN)		l	\dagger	T	Ī			
VKO7 VACCV	PROJEINKS	VACCINIA VIRUS (STRAIN WR.)			\dagger	T		Ī		
VL03 VACCC	PROTEIN K?	VACCEMIA VIRUS (STRAIN WAL AND (STRAIN COTEMIAGEN)			†	1				
PVL03 VACCV	PROTEIN L3	VACCINIA VIRUS (STRAIN COPEMIAGEN)		1	+		T	Ī		
PVL02 VARV	PROTEINLE	(STAAIN WA)			+	1		Ī		
PYLI CIUPVK	PROTEINLE		T							
WI FPM	PROBABLE LI PROTEIN	AFILLONIAVIRUS (STRAIN KANS	2		+	1				
PVL I ID VOS	PROBABLE LI PROTEIN	AVIAN PAPELICIMAVIRUS FPV-L	8			1				
V: 1 15 VOS	PROBABLE LI PROJEIN	HEMAN PAPILLONAVIRUS TYPE S	15-19		1	1				
ALI IDVIA	PROBABLE LI PROJEIN	IRBIAN PAPILLONIA VIRUS TYPE 8	20.5		1					
VLI HPV47	PROBABLE LI PROTEIN	INDIAN PAPILLONIA VIRUS TYPE IA	145-179		1	1				
W.I PAPVD	PROBABLE LI PROTEIN	HUMIAH PAPILLONIAVIRUS TYPE 47	153-101		1	1				
WLI REOVO	PROBABLE LI PROTEIN	DEER PAPILLOMAVIAUS	1		1	1				
VL2 IPV03	MAJOR CORE PROTEIN LANGEDA I	REDVIAUS (TYPE) / STRAIN DEARING)	٦	117111	1		Ī			
PVL2 IPVOI	PROBABLE L2 PROTEIN	HEMIAN PAPILLOMAVIRUS TYPE	34:33		1	Ì				
VL2 IDVIG	PROBABLE LI PROTEIN	INDIAN PAPIL LOMIAVIRUS TYPE I	356-342		1					
VIAGI CIA	PROBABLE LT PROTEIN	HUDIAN PAPILLOMAVIAUS TYPE 16	25.22	<u> </u> 		Ì		ĺ		
VI.2 HPVII	PROBABLE LI PROTEIN	HUSIAN PAPILLOMIAVIRUS TYPE IA	165.37		-	Ì				
PVL 3 IDV33	PROGRADIE L'1 PROTEIN	HUNIAN PAPIL LONG VINUS 1YPE 31	316-376	<u> </u> 		1				
PVI 1 10V47	PROBABLE LI PROTEIN	HUNLAN PAPILLONIAVIRUS TYPE 15	((;2)							
PVL2 10 VSI	PROBABLE LI PROTEDA	HUDILM PAPILLONIAVIRUS TYPE 47	341-375			1				_
PVC. HVSB	PROBABLE LY PROTEIN	HUBLAN PAPIL LONG VIRUS 1 YPE 51	107		1		Ī			
PM S MOVE	PROBABLE LY PROTEIN	HUNCAN PAPILOMANTRUS TYPE SD		-						
PVL 3 REOVI	NUMOR CORE PROTEIN LANGED 1	ALOVIRUS (TYPE 1 / STRAIN DEAUNG)	<u></u>		\dagger					
MI REOM	MINOR CORE PROTEIN LANGIDA 3	AEGVIAUS (TYPE 2/STACH US/ORES)	Ŧ	277	1000					ļ
יאומי מאו	MINOR COLE PROTEIN LANGEDA 1	REDVAUS (TYPE I / STEAM LAND)		T						
	Take and the	TIPULA IRIDESCENT MRUS		947-14	4					

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100	141440714	Ad Vigures (no harterlank sheet)								
FRE MARIE	PROTEIX		AREAL	ANEAL	ARGAZ	AREA 4	AREAS	ASEA	AREA 7	ABEAI
LVAIL REOVE	PROTEININI	DIENIAGEN	l	Г		Г	Г			
PVNIII REOVU	AIINOR VIRION STRUCTURAL PROTEIN NU.		217.331							
PVTIII REOVO	MAJOR VIRION STRUCTURAL PROTEIN AID-TAIL-IC	NO.		619-663						
PUNI REDVI	U-1A(U-1C			618-662						
TVAIL REOVE	U.IAIU-IC	REOVINUS (1 YPE 1/ STRAIN DIJIONES)		618-662						
PVAI) REOVD	U.IARU.IC			61B-442						
PVALAZ BRSVA	ALAIGA NONSTRUCTURAL PROTEIN MIU-NS			11.11	523-558	919-040				
PLAIAT HRSVA	NIATRIX GLYCOPROTEIN NIZ	100	41.90							
PUNIAN TRIV	MATRIX CLYCOPROTEIN MI	VIRUS (STRAIN A2)	43.90							
PLAIAT COVO	MATRIX GLYCOPROTEIN NIZ	IURKEY RIIINOTRACIIEITIS VIRUS	76-70							
PLAINT INCH	MATRIX PROTEIN	CANINE DISTRICTER VIRUS (STRAIN ONDERSTEPODAT)	193.334							
PLAIAT NIVA	MANNIK INI PROTEIN	INFLUENZA C VIRUS (STRAIN CILISO)	91116	11.20						
PISKIT MOVO	NIA 18 IX PROTEIN	JA (4.) 21	110-136							
PANAT PIS	MATRIX PROTEIN	AIN BEAUDETTE CASS								
PVSIAT PISH	MATRIX PROTEIN			204-252						
PUNIAT RABVA		RUS (STRAIN KIRL 1985)		204-252						
PUNAT RABVE			66.103							
PINIAT RABVE		(i)	101.69							
PUNIAT RABVE	NA TRIX PROTEIN		101.49							
PINIT RABIT		IGASIARA REESID	[01:69							
PLAINT RABYS			101.60							
PLYILL SYNV		RABIES VIRUS (SIRAIN SAD BIO)	101.10							
PVILAT VSVIC	MATRIX PROTEIN	SONCHUS VELLOW KET VIRUS	02.45							
אינו כיסאו		VESICULAR STONATITIS VIRUS (SCRUTYPE INDIANA / STRAIN ()	112-801							
PISIE CVPFS			П							
PINEL CIPPU			Ĩ	13.257						
PUNET CUPRI	EI GI YCOPROTEIN PRECUASOR	AVIRUS (S	181.111							
PLYE CVIKE		HAUS ISTRAIN RAID								
PLNE! FPV				19:309						
PV3E 18V6	PRECURSOR	146	_							
7,121,13/1			11-53	177-218						
7 XE1 18VE		_	Ī	=						
7.0E1 09VK	EI CLYCOPROTEIN	1	Ť	===						
	7.5.00	US IS I WALL IN BEST OF		Ì			Ī		1	
F.1112			1	110.114			Ì	Ť	1	
1000	N 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	CAIR III ONE RADIAM VIRILE (STRANDOIL	Ť	7			Ì	Ť		
PA UP CALIVE			Ī	ğ	Ī		1	T		
PI VIP CANIVS		200	Ī	18.334	 					
PYND CANVW		SPOURGE	187-254 21	170-124						
PINE CERV		RAIN W260)	1	10.334						
PLAIP FAIVO			217.246				_			
PLYID SOCKIV			117.251							
li		_								
il		DUCK IEPATITIS B VIRUS (BROWN SHANGICAI DUCK ISOLATE S	П	190-761						
		_	T	\$.						
			Ť	20.23		j				
10003		MOINI DUCK ISOLATE ST	ī	2						
1001		ITIS VIRUS	10.74	j				1		1
PLYSA WIVE			10.50	1						
PVALSA WHYSS			777-872	1				1		
PITISA WILVI	INLUDR SUIT ACE ANTIGEN PRECURSOR	WOODCHOOK REPAILITS VIRUS 39	113-243	1]		1	1	1	7

1111	FROTEIN									
1			13.23							
	TATACE ANTIGEN PRECUISOR	WOOD HULL AND STRUCTURE OF THE STRUCTURE	100							
	PROBABLE MAJOR SURFACE ANTIGEN PRECURSOR		110						-	
I	MATERIA PROTEON 1		!	11.111						
1	VIATRIX (NII) PROIL IN	INITIAL CITATA A VIII O CONTRACTOR CONTRACTO	11.11	111.233						
1	MATRIX MIT PROTEIN		İ							
WIN 1111	NA TRIX (MI) PROIL IN	INTUENZA A VIRUS (STRAIN AC ASSE DESCRIPTION OF ANY STRAIN	i	25.22						
VIII INTE	VIATRIX (MI) PROICIN		47.126	200						
FULL CUPE	MATRIX (MI) PROTEIN	NI LOS NA VINCENTA NI CONTRACTOR	i	74.222						
	NATE OF PROPERTY		Ī	14.221						
	V. 100 PRO 100		İ	100						
	N. T. C. C. C. C. C. C. C. C. C. C. C. C. C.		I							
			Ì	*						
VIII IVEK	MATRIX (MI) PROTEIN	_	_	76.20						
	NATRIX (SII) PROTEIN	$\overline{}$	93-126	134.223						ļ
Ì	MATRIX (MIL) PROTEIN			74-332						
ı	VIAIDIX (ALL) PROTEIN	TATOLOGICAL STREET		134-111						
ı	NATHER INIT PROTECT		Ī	74.333		L				
1	NATER AND PROJECT		Ī,							
L	NAT TO VALLE BEOLE (N	- 1								
CVBVI INC	709100111111111111111111111111111111111	BOWING WILD. TYPE II	3.50							
NAIL INBUE	NIA INI A (ALL) TROUGHT	MILLENZA B VIRUS (STRAIN BA EU/O)	35.30							
	NIA IRIA (NII) TROIGUE	MELITENZA B VIRUS (STRAIN DISINGAPORE/12/19)	200							
PANIE INBAC	NIATRIX (NIII PEOTE 13	NET TENZA B VIRUS (STRAIN BIANN ALBONING ICOLD ADAPTE	133-164							ļ
PANIE INDA	PROBADIR NA INIX (PLI) PROFESS	BOWING WILD TYPE!	133-184							
WILE INDIE	PROBABLE MATRIX (PLZ) PROTEIN	TANA & VIETT CTRAPA BILEE/40)	13:11							
VALES INDS	PROBABLE MATRIX (NII) PROTEIN	NATIONAL PURITY (STRAIN BISINGAPORE/12/19)	133-164							
PWITE MYXVL	PROBABLE MATRIX (A11) PROTEIN	ANNOTATION OF THE AND ANNE	01-91	49.107						
VY-SOL VACCC	N-TI PROTEIN	VALLENIA VIBLIS (STRATH COPENIAGEN)	H-113							
VINDS VACCY	PEOTE IV N	CACCINIA CIBLIS ISTRAIN WRI	64-113							
PVX34 ROTES	PROTEIN	DOVA CHINE CARLED C (STEAM SHINIOKU)	5							ļ
איאוז אסזויי	MONSTRUCTURAL PROTEIN NSTA	SOUTH POLICE CONTINUES CON	=	131-169						
VNCA AAVI	NOWSTRUCTURAL PROTECH HS14		577.16	13.11						
PANCA RSV	DNA KEPLICATION PROTEIN	U VIRUS C	39.163			_				
PANCH PAVEO	MAJOR HONCAPSID PROTEIN	NICE STAPE VAUS	36.18							
PINCE ADVO	PROBABLE MONCAPSID PROTECN NP	BOYINE PARVOVINUS		18.104						
PANCE AFDEV	NONCAPSID PROTEIN MS-1	ALEUTIAN MINK DISEASE PAR COVINCIS IS INAIN UP		15	115.640	115.760	780.849			
	NOW A PROTECT NS-1	AEDES DENSONUCLEOSIS VIRUS (STRAIN GRV 001 001)								
	MANY APRIL PROJECT NS: 1	FELTINE PANLEUXOPENIA VIRUS (STRAIN 193)								
	ACAD ABOUT IN MS. I	HINK ENTCHITS VINUS (STRAIN ABASIIIR!)					1			
AND STATE	NOW APRID PROTEIN MS-1	LIULINE KINUTE VIRUS (STRAIM XIVALI)								
200	NOW APSID PROTEIN NS.1	KIDADAE KIRATE VIRUS								
	PROBABLE MONCAPSID PROTEIN MS!	SOVINE PARVOVIRUS								L
	LANK APRID PROTEIN NS. I	CANINE PARVOVIRUS (STRAIN N)								L
200	ACAMON PROTEIN NS.	HUNIAM PARVOVIRUS BIP	2							L
2	AND A PROPERTY NS	HANISTER PARVOVIRUS HI								
EAVA SONA	STATE OF THE PROPERTY OF THE P	PORCINE PARVOVIRUS (STRAIN NADL-2)	4:37	01.710						
	LONG TELEFORET PROTECT NSI	BLUETOHOUR WRUS (SEROTYPE 18/150LATE USA)	-							
	MONEY COUNTY PROTEIN NS	DEUTONGUE VIRUS (SEROTYPE 11/1SOLATE USA)	2			$\Big $		-		Ļ
1	SA PROTEIN AS	BLUETONGUE VIRUS (SEROT VPE 17 ISOLATE AUSTRALIA)	107.141							L
LANSI BIAIS	SUPPLIES AT PROTEIN NS	BLUETONGUE VIRUS (SEROTYPE I/ ISOLATE SOUTH APRICA)	10.10			1	1			L
NASI BIASO	SN X25CEA TY BILLIANS	BLUETONGLE VIRUS (SEROTYPE 10/150LATE AUSTRALIA)					1			
NA CONTRACTOR	NOTICE IN LANGE OF THE PROPERTY OF THE PROPERT	EPIZOOTIC IEMORULAGIC DISEASE VIAUS (SEROT YPE 1 I STRA								L
NAS: AAM	NOW THE PROPERTY OF THE PARTY O	DOLLENZA A VIRUS (STRADI AJAM ARBORANO)								ļ
PVNSI IACAO	MONSTHUCTURAL PROTEIN TO	MATICIENZA A VIBUS (STRATH ACAMELAIONGOLIAN)	17.31			-				4

PCCANE	ACLAICTIS	All Virutes (no batteriophages)	AREA! AREA!	ABEAD	ABEA4	ABEAS	AMELL	AREAI	AREAI
PVNS IACK	NONSTRUCTURAL PROTECN NST	INCLUENZA A VIRUS (STRAIN ACHICRENGERNANY PUM)					Г	П	
PINST JADAZ	HOMSTRUCTURAL PROTEIN WS!	BOLLIENZA A VIRUS (STRAIN ACHICKENDAPANIA)	01-97						
VNSI IADEI	MONSTRUCTURAL PROTEIN MS!	INSTUTENZA A VIRUS (STRAIN ADUCKVAL BERTAMOTA)	19-81					-	
PYNSI IADUS	NONSI RUCTURAL PROTEIN WSI	INPLUENZA A VIRUS (STRAIN ANDUCKENGLAND/1/34)	7-10						
VNSI IAFOAS	NOVSTRUCTURAL PROTEIN WST	INTLUENZA A YIRUS (STRAIN A/DUCKUKRAINE/M3)	91						
PVNS TAFOW	PONSIBUCTURAL PROTEIN NS	INTLUENZA A VIAUS (STRAIN AGORT MONANOUTIVIAT)							
1	MONSTRUCTURAL PROJECT MAST	SOUTH OF A COUNTY AND A STORY OF STREET ASSESSMENT OF STREET							
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PWKS IANIAA	MONSTELECTURAL PROTECURASI	INTLUENZA A VIALIS (STRAIN AL ENINGRADISU)	10.31						
SI IARIAN	NONSTRUCTURAL PROTECN NSI	INTUENZA A VIAUS (STRAIN AALAL LARDVAL BERTANDIA	4.0						
PVS:SI IMMO	NOWS IN UCTURAL PROTEIN WS!	738	19:51						
SI LAITH	NONSTRUCTURAL PROTECT NS	INTLUENZA A VIRUS (STRAIN AMIALLARDNEW YORKABIAM	16.51						
	NONSTRUCTURAL PROTEIN NS!	INTLUENZA A VIRUS (STRAIN ABIYNAIMANEDA-TIIAVI)	06-90						
ı	NOWSTRUCTURAL PROTEIN NS!	INCLUENZA A VIRUS (STRAIN APINTALVAL BERTALISM	19:03						
PWS1 (4.91)	MONS IRUCTURAL PROFESS NS	INTLUENZA A VIRUS (STRAIN APINTALVALDERTA/17179)	49-13						
	NONSTRUCTURAL PROTEIN NS!	INCLUENZA A VIRUS ISTRAIN APINTAL/ALBERTA/261/71	4:0						
PINSI INPUE	HONSTRUCTURAL PROTEIN NSI	INTLUENZA A VIRUS (STRAIN APINTALDALBERTAJ)1179)	4.03						
	HONSTRUCTURAL PROTEIN NS!	INFLUENZA A VIRUS (STRAIN APUERTO RICO4034)	19:13						
PYPS! IATEC	HOMETRUCTURAL PROTEIN NS!	INTLUENZA A VIAUS (STRAM A/TURKEY/BETISLEHEN-GLILITII4	11.11						
SI LATER	NONSTRUCTURAL PROTEIN NST	INTLUENTA A VIRUS (STRAIN ACTURKEYCANADANI)	19:11						
PVNSI IATRS	HONS FRUCTURAL PROTEIN NS!	INFLUENZA A VIAUS (STRAIN ACTURIX EYORE GON/11)	19.61						
1	NONSTRUCTURAL PROTEIN NS!	INTLUENTA A VIRUS (STRAIN ATERWSOUTH AFRICARI	16-10						
	HONSTRUCTURAL PROTEIN NS!	INTLUENZA A VIRUS (STRAIN ATERNTURKNENIA/1972)	(1.0)						
H	HOWSTRUCTURAL PROTEIN NS!	Ī	49.01						
	NOMSTRUCTURAL PROTEIN MSI	INTLUENZA B VIRUS (STRAM BVANN ARBOR/1966 COLD.ADAPTE	10:13						
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- [MONSTRUCTURAL PROTEIN NS	B VIAUS (STRAIN BAIONG KONGALTS), AND (STRAIN	10):17					1	
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THE E	MONSTRUCTURAL PROTEIN MS	B VIXUS (STRAIN GALDAR)						Ì	
VASI DESTE	MONSTRUCTURAL PROTEIN MSI		21:01:				Ì	Ī	
VARM (SAA)	MONSTRUCTURAL PROTEIN TO	DALLENCY BY VIEW (STRAND SPICE TEACHER)	// // //						
TAKE DOS	NONSTRUCTURAL PROTEDURS:		Τ						
VHSI INBSI	HOMSTRUCTURAL PROTEIN HSI	FORESTRYS	6:10				Ī	Ī	
VNSI DIBVI	NOWSTRUCTURAL PROTEIN WS!	INTLUENZA B VIRUS (STRAIN BYSINGAPOREMA)	10.17						
PVNSI DIBYA	HOWSTRUCTURAL PROTEIN MS!	DIGLUENZA B VIRUS (STRAIN BIVICTORIANI)	113.177						
VNS1 AHSV9	HONSTRUCTURAL PROTEIN HSI		143-179						
PVNS2_BTV17	NONSTRUCTURAL PROTEIN NST		67.101						
VNS2 BTVIX	NONSTRUCTURAL PROTEIN MS?	SLUETOWOUE VIRUS (SERDITYN 177 ISOLATE USA)				ļ			
PANEL CAMON	NOME THE PROPERTY AND AND AND AND AND AND AND AND AND AND	N BAD	11.101				Ī		Ī
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VHS2 IAANA	HOMSTRUCTURAL PROTEIN NS2	-	Ī						
PVNS2 IAANN	MONSTRUCTURAL PROTEIN NS2	-	16:01						
PVNS3_LACHT	NONSTRUCTURAL PROTEIN NS2	WHEEL AND (STRAIN	14.93						
VNS1_IACKO	HONSTRUCTURAL PROTEIN NS2		16-91						
VNS2 IACKI	NOMSTRUCTURAL PROTEIN WS?	INTLUENZA A VIRUS (STRAIN ACHICKENGERAIANYAVVV)	14:39						
VNS2 IADA2	NONSTRUCTURAL PROTEIN NST		8						
PVNS1 IADEI	NONSTRUCTURAL PROFETN NS1		£.						
WNS1 [ADU]	MONSTRUCTURAL PROTEIN NS	DOLUGUZA A VILUS (STRAIM ADUCEZENOLAMOVIZA)	8:						
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HONSTRUCTURAL PROTEIN? CANING ENTERIC CORONAVIRUS STRAIN PATES 1-42		NONCIBILITIES PROJECT NS4	ALCE STRIPE VIRUS	2		1		<u> </u>		
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NOW INCLUDAL PROTEIN C HIBAARY BALLAND (LURA) VINUS (STAIN NILL 1911) 11-115	PVNSC PING	NONSTRUCTURAL PROTEIN C	ILIBIAN PARAINFLUENZA I VIRUS ISTRAIN CL. VVI	Ť	<u> </u>					
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NOW! BUCHTUAL PROTEIN C	20V35 25W14	KONSTRUCTURAL PROTEIN C	SENDAL VIRUS (STRAIN HAURE)							
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HOSS SECTURAL PROTECT N.S. BLOWA AVRIAGE A CROSS (TOCATE L.Y.)	PVNST BLRG.	NOWS TRUCTURAL PROTEIN NS.S	BUNYAVRUS GERMISTON							
NORSTRUCTURAL PROTEIN N.S. LACADA VARIOS A. CROSSE	PVKET BLAGE	NOWSTRUCTURAL PROTEIN NS.S	BUNYAVIRUS LA CROSSE (ISOLATE L74)		<u> </u>					
MONSTRUCTURAL PROTEIN MS 1 INCOURN VRUS MONSTRUCTURAL PROTEIN MS 1 IOSCANA VRUSTOS) MONSTRUCTURAL PROTEIN MS 1 UNIUNEAU VRUSTOAM PARAM EAPLANG PRY PROPABIL MUCLEAR ANTIGEN PRINCE MINISTER STRAIN FORMANISMS (CHAIN FORMANISMS)	VAN TANK	NOWSTRUCTURAL PROTEIN NS. S	BUNYAWAUS LA CROSSE			 				
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PROBABLE MUCLAL ANTIGEN PREDOCABES VICUS (STANIN KANAMULA)	PANTA PRINKA	NONSTRUCTURAL PROTEIN NS-S	UNKUNEMI VIRUS (DUK)	11.71						
FARING STRAIN DOLLARY (STRAIN DOLLARY)	INVIE DIVI	PROBABLE MICLEAR ANTIGEN	PSELEGOLABEES VIRUS (STRAIN KALLAD) (PRV)	1						
MAKE TOPROTEIN	700	MAKEROPROTEIN	DIION VIRUS (STRAIN INDIANUMINAL) (DIIO)	100.00						

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MACLIGATION MACLIGATION	MUC IABLA		INTLUENZA A VIRUS (STRAIN NAMN AUDONAMO)		37-401					-	
NUCLICIPATION NUCLICITY	NUC INBUD	MACLEOPROTEIN	=		37-406						
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WKLIGDROTTH WKLIGRALA WING STAMP ADDECESSION-OFF WHIN WKLIGDROTTH WKLIGDROTT	NUC IACKP	MUCLEOPROTEIN			1	7708					
WICLIOPROTERN	NUC INDAU	NUCLEOFROTEIN	-			157-408					
MACLEDBOTTEN MOTUREA A VINUS STRAIN ADDICACEMICANOM 141 14	NUC INDEE	MUCLEOPROTEIN	DIFLUENZA A VIRUS (STRAIN ANDUCIOAUSTRALIA/14940)			157-408					
MACLEGROUGH MOTUREA A YNUL (STAIN ADDICAGESCANO) 141	NE IADEZ	MICLEOPROTEIN				157.404					
WATEGORIEM DOGLURRA A VIRIGE IS IN A ADDICATED AND 1-4 99-114 1-4	AUC IADEI	MUCLEOPROTEIN	Ē			960-408					
WALEGORGIEN DOGLERNA A VILLE (I I IAM ADDECARGATANI) 1-41	NUC IABE2	NUCLEOPHOTEIN	Ī	Γ		187-408					
WATEGOROTERN NOTEGOROTERN 1-11	MIC INDIO	NOCI EGYROTEIN				187-408					
VACTEGROTER WELLERA A VILLS (STAIN ADDICEASURED MENT) 1-41	NUC IABNIZ	NACL EDPROTEIN	INTLUENZA A VIRUS (STRAIN ADUCKATIONG KONGINS)			137.404					
NUCLEGROTERN DELLURA A VILLES STRAIN ADDUCKARAMISON 1-1 1-	NUC IADAIA	NUCL EOPROTEIN	INTUENZA A VINUS ISTRAIN ADUCKAIENDHISMINA			157-408					
WICKLEDPROTEIN WILLIAMA A VIRUS STRAIN ADDUCKORADSTONS) 1-1 11-149 WICKLEDPROTEIN WILLIAMA A VIRUS STRAIN ADDUCKORADSTONS) 1-1 11-149 WICKLEDPROTEIN WILLIAMA A VIRUS STRAIN ADDUCKORADSTONS 1-1 11-149 WICKLEDPROTEIN WILLIAMA A VIRUS STRAIN ADDUCKORADSTONS 1-1 11-149 WICKLEDPROTEIN WILLIAMA A VIRUS STRAIN ADDUCKORADSTONS 1-1 11-149 WICKLEDPROTEIN WILLIAMA A VIRUS STRAIN ADDUCKORADSTONS 1-1 11-149 WICKLEDPROTEIN WILLIAMA A VIRUS STRAIN ADDUCKORADSTONS 1-1 11-149 WICKLEDPROTEIN WILLIAMA A VIRUS STRAIN ADDUCKORADSTONS 1-1 11-149 WICKLEDPROTEIN WILLIAMA A VIRUS STRAIN ADDUCKORADSTONS 1-1 11-149 WICKLEDPROTEIN WILLIAMA A VIRUS STRAIN ADDUCKORADSTONS 1-1 11-149 WICKLEDPROTEIN WILLIAMA A VIRUS STRAIN ADDUCKORADSTONS 1-1 11-149 WICKLEDPROTEIN WILLIAMA A VIRUS STRAIN ADDUCKORADSTONS 1-1 11-149 WICKLEDPROTEIN WILLIAMA A VIRUS STRAIN ADDUCKORADSTONS 1-1 11-149 WICKLEDPROTEIN WILLIAMA A VIRUS STRAIN ADDUCKORADSTONS 1-1 11-149 WICKLEDPROTEIN WILLIAMA A VIRUS STRAIN ADDUCKORADSTONS 1-1 11-149 WICKLEDPROTEIN WILLIAMA A VIRUS STRAIN ADDUCKORADSTONS 1-1 11-149 WICKLEDPROTEIN WILLIAMA A VIRUS STRAIN ADDUCKORADSTONS 1-1 11-149 WICKLEDPROTEIN WILLIAMA A VIRUS STRAIN ADDUCKORADSTONS 1-1 11-149 WICKLEDPROTEIN WILLIAMA A VIRUS STRAIN ADDUCKORADSTONS 1-1 11-149 WICKLEDPROTEIN WILLIAMA A VIRUS STRAIN ADDUCKORADSTONS 1-1 11-149 WICKLEDPROTEIN WILLIAMA A VIRUS STRAIN ADDUCKORADSTONS 1-1 11-149 WICKLEDPROTEIN WILLIAMA A VIRUS STRAIN ADDUCKORADSTONS 1-1 11-149 WICKLEDPROTEIN WILLIAMA A VIRUS STRAIN ADDUCKORADSTONS 1-1 11-149 WICKLEDPROTEIN WILLIAMA A VIRUS STRAIN ADDUCKORADSTONS 1-1 11-149 WICKLEDPROTEIN WILLIAMA A VIRUS STRAIN ADDUCKORADSTONS 1-1 11-149 WICKLEDPROTEIN WILLIAMA A VIRUS STRAIN ADDUCKORADSTONS 1-1 11-149 WICKLEDPROTEIN WILLIAMA A VIRUS STRAIN ADDUCKORADSTONS 1-1 1	NUC INDEA	NUCLEOPROTEIN				157-406	_				
WCKLEGPROTERN	NUC IADUS	MUCLEOPROTEIN				157.408					
NUCLEOPEOTERN NUCLEOPEOTER	NUC IAENS	NUCLEOPROTEIN		Ī	200						
WALLEOPROTEIN	NUC INTON	NUCLEOPROTEIN	INTLUENZA A VIRUS (STRAIN AENGLANDVINSS)		8						
NUCLEOPROTEIN NOTLERA A VIRUS STAND AGGET VALANDS DATE	NUC IAFOW	MUCLEOPROTEIN		Ī	2.68						
NCCLEGRACIEN NFLLERIZ A VIRLIS (STAIN ACRUL PLACIE VIRLEACOSCAL 143 111-114	NUC IN PO	MUCLEOPROTEIN									
NICLEOPROTEIN NICLEREA A VRUS (STAM AGONT PAGGE VRUDADOSTICE 42 19-154	SUC INTR	MUCLEOPROTEIN	_			137-408					
NUCLEOROTEN	NUC INCRE	NUCL EOPROTEIN	_		Ī	90-09					
HILLERY A VIRUS STRAIN ACEL LALANT AND STRAIN 1-4 131-449 MACLEGPROTEIN MELLERY A VIRUS STRAIN ACEL LALANT AND STRAIN 1-1 1-1 1-1 MACLEGPROTEIN MELLERY A VIRUS STRAIN ACEL LALANT AND STRAIN 1-2 1-1 1-1 MACLEGPROTEIN MELLERY A VIRUS STRAIN ACEL LALANT AND STRAIN 1-2 1-1 1-1 MACLEGPROTEIN MELLERY A VIRUS STRAIN ACEL LASTACHARD STRAIN 1-2 1-1 1-1 MACLEGPROTEIN MELLERY A VIRUS STRAIN ACEL LASTACHARD STRAIN 1-2 1-1 1-1 MACLEGPROTEIN MELLERY A VIRUS STRAIN ACEL LASTACHARD STRAIN 1-2 1-1 MACLEGPROTEIN MELLERY A VIRUS STRAIN ACEL LASTACHARD STRAIN 1-2 1-1 MACLEGPROTEIN MELLERY A VIRUS STRAIN ACEL LASTACHARD STRAIN 1-2 1-1 MACLEGPROTEIN MELLERY A VIRUS STRAIN ACEQUINCAL LAND STRAIN 1-2 1-1 MACLEGPROTEIN MELLERY A VIRUS STRAIN ACEQUINCAL LAND STRAIN 1-2 1-1 MACLEGPROTEIN MELLERY A VIRUS STRAIN ACEQUINCAL LAND STRAIN 1-2 1-1 MACLEGPROTEIN MELLERY A VIRUS STRAIN ACEQUINCAL LAND STRAIN 1-2 1-1 MACLEGPROTEIN MELLERY A VIRUS STRAIN ACEQUINCAL LAND STRAIN 1-2 1-1 MACLEGPROTEIN MELLERY A VIRUS STRAIN ACED STRAIN ACE	NUC IAGUI	NUCI EOPROTEIN	(81.07)		Ī	137-406					
MUCLEGROTEIN MELLERZA A VIRUS (STAND ACGLICALATAROTIST)	NUC INGUS	MUCL EOFROTEIN		Ī	2.48						
MACLEGROTEIN MELLERZA A VRUS (STANIN ACULLALARACUISATI) 143 141	NUC IAGUI	MUCLEOFROTEIN	1	Ī]						
MUCLEOROTEIN	NUC IAGO	MACLEDIROTEIN	1		Ī	5 40	Ĩ				
MUCLEOROTERN	MUC INGUA	HUCLEGPROTEIN	j		ĺ	37-409					
MICLEGREGIEN MOTLEREA A VIRUS STAND ACCULANISMESOT ANIAND 141 191-199	NUC INGURI	MUCLEOPROTEIN	÷	Ī	Ī	37-406					
MACLEGRADIEN PRELIENZA A VIRUS (STAJIN AGULCASINNESOTANTSO) 143 19-154	MUC INCIN	MICLEOPROTEIN	7		Ī	37.400					
MUCLEGRADIEN MELLERZA A VIRUS ISTANIA ANGROGAZION 143 1419 141	MC IAIIC	MUCLEOPROTEIN	rESOT A/945/80)		Ī	57.400					
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MUCLE COPROTEIN MUCLE COPR	MUC IAIGO	MUCLEOPROTEIN				2 3					
MACLE GORGIEN METURIZA A VIRUS (STAMIN AND MONEYINS) 1-1 131-409	NO. IADRI	MUCLEUROILIN			Ī	200					
MICLE GORDIERN MET LENZA A VIRUS (STALIN ANONG KONGATA) 1-41 131-409 MICLE GORDIERN MET LENZA A VIRUS (STALIN ANONG KONGATA) 1-41 131-409 MICLE GORDIERN MET LENZA A VIRUS (STALIN ANGLOVATA) 1-42 131-409 MICLE GORDIERN MET LENZA A VIRUS (STALIN ANGLOVATA) 1-43 131-409 MICLE GORDIERN MET LENZA A VIRUS (STALIN ANGLOVATA) 1-43 131-409 MICLE GORDIERN MET LENZA A VIRUS (STALIN ANGLOVATA) 1-43 131-409 MICLE GORDIERN MET LENZA A VIRUS (STALIN ANGLOVATA) 1-43 131-409 MICLE GORDIERN MET LENZA A VIRUS (STALIN ANGLOVATA) 1-43 131-409 MICLE GORDIERN MET LENZA A VIRUS (STALIN ANGLOVATA) 1-43 131-409 MICLE GORDIERN MET LENZA A VIRUS (STALIN ANGLOVATA) 1-43 131-409 MICLE GORDIERN MET LENZA A VIRUS (STALIN ANGLOVATA) 1-43 131-409 MICLE GORDIERN MET LENZA A VIRUS (STALIN ANGLOVATA) 1-43 131-409 MICLE GORDIERN MET LENZA A VIRUS (STALIN ANGLOVATA) 1-43 131-409 MICLE GORDIERN MET LENZA A VIRUS (STALIN ANGLOVATA) 1-43 131-409 MICLE GORDIERN MET LENZA A VIRUS (STALIN ANGLOVATA) 1-43 131-409 MICLE GORDIERN MET LENZA A VIRUS (STALIN ANGLOVATA) 1-43 131-409 MICLE GORDIERN MET LENZA A VIRUS (STALIN ANGLOVATA) 1-43 131-409 MICLE GORDIERN MET LENZA A VIRUS (STALIN ANGLOVATA) 1-43 131-409 MICLE GORDIERN MET LENZA A VIRUS (STALIN ANGLOVATA) 1-43 131-409 MICLE GORDIERN MET LENZA A VIRUS (STALIN ANGLOVATA) 1-43 131-409 MICLE GORDIERN MET LENZA A VIRUS (STALIN ANGLOVATA) 1-43 131-409 MICLE GORDIERN MET LENZA A VIRUS (STALIN ANGLOVATA) 1-43 131-409 MICLE GORDIERN MET LENZA A VIRUS (STALIN ANGLOVATA) 1-43 131-409 MICLE GORDIERN MET LENZA A VIRUS (STALIN ANGLOVATA) 1-43 131-409 MICLE GORDIERN MET LENZA A VIRUS (STALIN ANGLOVATA) 1-43 131-409 MICLE GORDIERN MET LENZA A VIRUS (STALIN ANGLOVATA) 1-43 131-409 MICLE GORDIERN MET LENZA A VIRUS (STALIN ANGLOVATA) 1-43 131-409 MICLE GORDI	100	MACEUMOIEUM		Ī		1					
MACLEGRADIEN METCHAZA A VIRUS (STALIN ANEQUINEPRADUE/1744) 14-14 111-401	NA INDE	Mini Bostolson		Ì	1.409	Ī					
NICLEGRAGIEN NICLERA A VILUS (STACH AKTEVISKY) 1-21 19-194 NICLEGRAGIEN NICLERA A VILUS (STACH AKTEVISKY) 1-21 11-495 NICLEGRAGIEN NICLERA A VILUS (STACH AKTEVISKY) 1-21 11-495 NICLEGRAGIEN NICLERA A VILUS (STACH AKTEVISKY) 1-21 11-495 NICLEGRAGIEN NICLERA A VILUS (STACH AKTACHAS) 1-21 19-1145 NICLEGRAGIEN NICLERA A VILUS (STACH AKTACHAS) 1-21 13-1495 NICLEGRAGIEN NICLERA A VILUS (STACH AKTACHAS) 1-21 13-1495 NICLEGRAGIEN NICLERA A VILUS (STACH AKTACHAS) 1-21 13-1495 NICLEGRAGIEN NICLERA A VILUS (STACH AKTACHAS) 1-21 13-1495 NICLEGRAGIEN NICLERA A VILUS (STACH AKTACHAS) 1-21 13-1495 NICLEGRAGIEN NICLERA A VILUS (STACH AKTACHAS) 1-21 13-1495 NICLEGRAGIEN NICLERA A VILUS (STACH AKTACHAS) 1-21 13-1495 NICLEGRAGIEN NICLERA A VILUS (STACH AKTACHASTORAFE VIRS) 1-21 13-1495 NICLEGRAGIEN NICLERA A VILUS (STACH AKTACHASTORAFE VIRS) 1-21 13-1495 NICLEGRAGIEN NICLERA A VILUS (STACH AKTACHASTORAFE VIRS) 1-21 13-1495 NICLEGRAGIEN NICLERA A VILUS (STACH AKTACHASTORAFE VIRS) 1-21 13-1495 NICLEGRAGIEN NICLERA A VILUS (STACH AKTACHASTORAFE VIRS) 1-21 13-1495 NICLEGRAGIEN NICLERA A VILUS (STACH AKTACHASTORAFE VIRS) 1-21 13-1495 NICLEGRAGIEN NICLERA A VILUS (STACH AKTACHASTORAFE VIRS) 1-21 13-1495 NICLEGRAGIEN NICLERA A VILUS (STACH AKTACHASTORAFE VIRS) 1-21 13-1495 NICLEGRAGIEN NICLERA A VILUS (STACH AKTACHASTORAFE VIRS) 1-21 13-1495 NICLEGRAGIEN NICLERA A VILUS (STACH AKTACHASTORAFE VIRS) 1-21 13-1495 NICLEGRAGIEN NICLERA A VILUS (STACH AKTACHASTORAFE VIRS) 1-21 13-1495 NICLEGRAGIEN NICLERA A VILUS (STACH AKTACHASTORAFE VIRS) 1-21 13-1495 NICLEGRAGIEN NICLERA A VILUS (STACH AKTACHASTORAFE VIRS) 1-21 13-21495 NICLEGRAGIEN NICLERA A VILUS (STACHASTORAFE VIRS) 1-21 13-21495 NICLEGRAGIEN NICLERA A VILUS (STACHASTORAFE VIRS) 1-21 13-21495 NICLEGRAGIEN NICLERA A VI	NUC IANTE	NUCLEOPROTEIN		Ĺ	7.40						
MICLEGORGIEN METUREZA A VIRUS (STRAIN AKERVISTY) 142 111-409 MICLEGORGIEN METUREZA A VIRUS (STRAIN AKERVISTY) 143 111-409 MICLEGORGIEN METUREZA A VIRUS (STRAIN ARACLIARDAREW YORKSTOOTI) 143 141-409 MICLEGORGIEN METUREZA A VIRUS (STRAIN ARACRASISCHI) 141 141-114 MICLEGORGIEN METUREZA A VIRUS (STRAIN ARACRASISCHI) 141 141-114 MICLEGORGIEN METUREZA A VIRUS (STRAIN ARACRASISCHI) 141 141-114 MICLEGORGIEN METUREZA A VIRUS (STRAIN ARACRASISCHI) 141 141-114 MICLEGORGIEN METUREZA A VIRUS (STRAIN ARACRASISCHI) 141 141-114 MICLEGORGIEN METUREZA A VIRUS (STRAIN ARACRASISCHI) 141 141-114 MICLEGORGIEN METUREZA A VIRUS (STRAIN ARACRASISCHICARIEZISCHI) 141 141-114 MICLEGORGIEN METUREZA A VIRUS (STRAIN ARACRASISCHICARIEZISCHI) 141 141-114 MICLEGORGIEN METUREZA A VIRUS (STRAIN ARACRASISCHICARIEZISCHI) 141 141-114 MICLEGORGIEN METUREZA A VIRUS (STRAIN ARACRASISCHICARIEZISCHI) 141 141-114 MICLEGORGIEN METUREZA A VIRUS (STRAIN ARACRASISCHICARIEZISCHI) 141 141-114 MICLEGORGIEN METUREZA A VIRUS (STRAIN ARACRASISCHICARIEZISCHI) 141 141-114 MICLEGORGIEN METUREZA A VIRUS (STRAIN ARACRASISCHICARIEZISCHI) 141 141-114 MICLEGORGIEN METUREZA A VIRUS (STRAIN ARACRASISCHICARIEZISCHI) 141 141-114 MICLEGORGIEN METUREZA A VIRUS (STRAIN ARACRASISCHICARIEZISCHICA	PUC IAKIE	MUCLEOPROTEIN	Ī			\$7-406					
MUCLEOPROTEIN NPELURIZA A VRUS (STANIM AALENINGALDISAT) 142 113.409 MUCLEOPROTEIN NPELURIZA A VRUS (STANIM AALALARDNEW YORKASTOTI) 143 14114 MUCLEOPROTEIN NPELURIZA A VRUS (STANIM AALACARASENSAT) 141 14114 MUCLEOPROTEIN NPELURIZA A VRUS (STANIM AARACALASENSAT) 141 14114 MUCLEOPROTEIN NPELURIZA A VRUS (STANIM AARACALASENSAT) 141 14114 MUCLEOPROTEIN NPELURIZA A VRUS (STANIM AALACARASENSAT) 141 14114 MUCLEOPROTEIN NPELURIZA A VRUS (STANIM AALACARASENSAT) 141 14114 MUCLEOPROTEIN NPELURIZA A VRUS (STANIM AALACARASENSAT) 141 14114 MUCLEOPROTEIN NPELURIZA A VRUS (STANIM AALACARASENSATSENSAT MUCLEOPROTEIN NPELURIZA A VRUS (STANIM AALACARASENSATSENSAT MUCLEOPROTEIN NPELURIZA A VRUS (STANIM AALACARASENSATSENSAT MACLEOPROTEIN NPELURIZA A VRUS (STANIM AALACARASENSATSENSAT MACLEOPROTEIN NPELURIZA A VRUS (STANIM AALACARASENSATSENSAT MACLEOPROTEIN NPELURIZA A VRUS (STANIM AALACARASENSATSENSAT MACLEOPROTEIN NPELURIZA A VRUS (STANIM AALACARASENSATSENSAT MACLEOPROTEIN NPELURIZA A VRUS (STANIM AALACARASENSATSENSAT MACLEOPROTEIN NPELURIZA A VRUS (STANIM AALACARASENSATSENSAT MACLEOPROTEIN NPELURIZA A VRUS (STANIM AALACARASENSATSENSAT MACLEOPROTEIN NPELURIZA A VRUS (STANIM AALACARASENSATSENSAT MACLEOPROTEIN NPELURIZA A VRUS (STANIM AALACARASENSAT MACLEOPROTEIN NPELURIZA A VRUS (STANIM AALACARASENSAT MACLEOPROTEIN NPELURIZA A VRUS (STANIM AALACARASENSAT MACLEOPROTEIN NPELURIZA A VRUS (STANIM AALACARASENSAT MACLEOPROTEIN NPELURIZA A VRUS (STANIM AALACARASENSAT MACLEOPROTEIN NPELURIZA A VRUS (STANIM AALACARASENSAT MACLEOPROTEIN NPELURIZA A VRUS (STANIM AALACARASENSAT MACLEOPROTEIN NPELURIZA A VRUS (STANIM AALACARA AALACARA AALACARA AALACARA AALACARA AALACARA A VRUS (MACLEOPROTEIN AALACARA AALACARA AALACARA AALACARA AALACARA AALACARA AALACARA AALACARA AALACARA AALACARA AALACARA AALACARA AALACARA AALACARA AALACARA AALACARA AALACARA AALACARA AALACARA	MIC INEN	NUCL EGPROTEIN			13-409						
HOLLERYA A VRUS HOLLERYA A VRUS HAT HAT HAT	NUC IABIAA	MUCL EOPROTEIN			П						
HIGH EOPEOTERN HIGH LENEA A VELUS (STACK A AND LASTAN AND LAST	NUC INDOM	MUCI EDPROTEIN	=			37.408					
MUCLEOPROTERN MPLUERZA A VRUS (STALIN AAGMASWEDENRA) 1-43 94-154	אנואראן אנואר	MUCLEOPROTEIN	_;			53-404					
MUCLEOROTEIN NPG LIERZĂĂ VIRLS (STIAND ANEW IRASEVANS) 143 96-154 MUCLEOROTEIN NPG LIERZA A VIRUS (STIAND ANTINOSI) 143 151-149 MUCLEOROTEIN NPG LIERZA A VIRUS (STIAND ANDIOWNI) 143 151-149 MUCLEOROTEIN NPG LIERZA A VIRUS (STIAND APARIO MICORALS) 143 151-149 MUCLEOROTEIN NPG LIERZA A VIRUS (STIAND APARIO MICORALS 141 151-149 MUCLEOROTEIN NPG LIERZA A VIRUS (STIAND ANDIOWNI) 141 151-149 MUCLEOROTEIN NPG LIERZA A VIRUS (STIAND ANDIOWNI) 141 151-149 MUCLEOROTEIN NPG LIERZA A VIRUS (STIAND ANDIOMENTEW TEAST 141 151-149 MUCLEOROTEIN NPG LIERZA A VIRUS (STIAND ANDIOMENTEW TEAST 141 151-149 MUCLEOROTEIN NPG LIERZA A VIRUS (STIAND ANDIOMENTEW TEAST 141 151-149 MUCLEOROTEIN NPG LIERZA A VIRUS (STIAND ANDIOMENTEW TEAST 141 151-149 MUCLEOROTEIN NPG LIERZA A VIRUS (STIAND ANDIOMENTEW TEAST 141 151-149 MUCLEOROTEIN NPG LIERZA A VIRUS (STIAND ANDIOMENTEW TEAST 141 151-149 MUCLEOROTEIN NPG LIERZA A VIRUS (STIAND ANDIOMENTEW TEAST 141 151-149 MUCLEOROTEIN NPG LIERZA A VIRUS (STIAND ANDIOMENTEW TEAST 141 151-149 MUCLEOROTEIN NPG LIERZA A VIRUS (STIAND ANDIOMENTEW TEAST 141 151-149 MUCLEOROTEIN NPG LIERZA A VIRUS (STIAND ANDIOMENTEW TEAST 141 151-149 MUCLEOROTEIN NPG LIERZA A VIRUS (STIAND ANDIOMENTEW TEAST 141 151-149 MUCLEOROTEIN NPG LIERZA A VIRUS (STIAND ANDIOMENTEW TEAST 141 151-149 MUCLEOROTEIN NPG LIERZA A VIRUS (STIAND ANDIOMENTEW TEAST 141 151-149 MUCLEOROTEIN NPG LIERZA A VIRUS (STIAND ANDIOMENTEW TEAST 141 151-149 MUCLEOROTEIN NPG LIERZA A VIRUS (STIAND ANDIOMENTEM A	AUC IANE	MUCLEOPROFEIN				17-401					
NUCLEORDIEN PRÉLIERZA A VRUS (STRAIN ANTIMON) 143 153-409 NUCLEOROTEIN PRÉLIENZA A VRUS (STRAIN ANDIOVAS) 1-41 151-409 NUCLEOROTEIN PRÉLIENZA A VRUS (STRAIN ANDIOVALSTENT) 1-42 151-409 NUCLEOROTEIN PRÉLIENZA A VRUS (STRAIN ANDIOV TURNSTONENTENT (AT 151-40) 1-41 151-409 NUCLEOROTEIN DEFLUENZA A VRUS (STRAIN ANDIOV TURNSTONENTENT (AT 151) 1-61 96-154 MACLEOROTEIN DEFLUENZA A VRUS (STRAIN ASTRAINSTONENTENT (AT 151) 1-61 96-154	PAUC_IANT6	MUCLEOPROTEIN				157-401					
HUCLEGREGIEN POPTLERZA A VRUS (STRAIN AND STEENS) 1-41 151-109 HUCLEGREGIEN POPTLERZA A VRUS (STRAIN AND STEENS) 1-41 16-114 HUCLEGREGIEN POPTLERZA A VRUS (STRAIN AND STEENS) 1-41 15-114 HUCLEGREGIEN DOFTLERZA A VRUS (STRAIN AND STEENS) 1-41 15-114 HUCLEGREGIEN DOFTLERZA A VRUS (STRAIN AND STEENS) 1-41 15-114 HUCLEGREGIEN DOFTLERZA A VRUS (STRAIN AND STEENS) 1-41 15-114 HUCLEGREGIEN DOFTLERZA A VRUS (STRAIN AND STEENS) 1-41 15-114 HUCLEGREGIEN DOFTLERZA A VRUS (STRAIN AND STEENS) 1-41 15-114 HUCLEGREGIEN DOFTLERZA A VRUS (STRAIN AND STEENS) 1-41 15-114 HUCLEGREGIEN DOFTLERZA A VRUS (STRAIN AND STEENS) 1-41 15-114 HUCLEGREGIEN DOFTLERZA A VRUS (STRAIN AND STEENS) 1-41 15-114 HUCLEGREGIEN DOFTLERZA A VRUS (STRAIN AND STEENS) 1-41 15-114 HUCLEGREGIEN DOFTLERZA A VRUS (STRAIN AND STEENS) 1-41 15-114 HUCLEGREGIEN DOFTLERZA A VRUS (STRAIN AND STEENS) 1-41 15-114 HUCLEGREGIEN DOFTLERZA A VRUS (STRAIN AND STEENS) 1-41 15-114 HUCLEGREGIEN DOFTLERZA A VRUS (STRAIN AND STEENS) 1-41 15-114 HUCLEGREGIEN DOFTLERZA A VRUS (STRAIN AND STEENS) 1-41 15-114 HUCLEGREGIEN DOFTLERZA A VRUS (STRAIN AND STEENS) 1-41 15-114 HUCLEGREGIEN DOFTLERZA A VRUS (STRAIN AND STEENS) 1-41 15-114 HUCLEGREGIEN DOFTLERZA A VRUS (STRAIN AND STEENS) 1-41 15-114 HUCLEGREGIEN DOFTLERZA A VRUS (STRAIN AND STEENS) 1-41 15-114 HUCLEGREGIEN DOFTLERZA A VRUS (STRAIN AND STEENS) 1-41 15-114 HUCLEGREGIEN DOFTLERZA A VRUS (STRAIN AND STEENS) 1-41 15-114 HUCLEGREGIEN DOFTLERZA A VRUS (STRAIN AND STEENS) 1-41 15-114 HUCLEGREGIEN DOFTLERZA A VRUS (STRAIN AND STEENS) 1-41 15-114 HUCLEGREGIEN DOFTLERZA A VRUS (STRAIN AND STEENS) 1-41 15-114 HUCLEGREGIEN DOFTLERZA A VRUS (STRAIN AND STEENS) 1-41 15-114 HUCLEGREGIEN DOFTLERZA A VRUS (STRAIN AND STEENS) 1-41 15-114 HUCLEGREGIEN DOFTLERZA A	AUC IAOIU	MUCLEOPROTEIN			27-08						
HUCLEORDIEN RELEGRA VRUS (STRAIN ARMONALSERY)) 141 151-169 NUCLEORDIEN POELEKZA A VRUS (STRAIN ARMONY TURNSTONEANY TASS 41 151-169 NUCLEORDIEN DETLERZA A VRUS (STRAIN ARMONY TURNSTONEANY TASS 41 151-169 NUCLEORDIEN POELEKZA A VRUS (STRAIN ARMONY TURNSTONEANY TASS 41 151-161	MIC, INPAR	NUC! EOPROTEIN	INTLINENZA A VIRUS (STRAIN AOHIO/413)	Ī	Ī						
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MUCLEORIOTEN DE LIERA A VILUE (STADA ASEALAMASSICHUSETTEIN) 1-41 96-134	ACC LARUD	MUCLEOPROTEIN		Ī	T						
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PVACC IATE	NUCLEORISM	19/10)		١	37.446			İ		
PUNIC INTEN	NIXI FOR FOLISIN	틹		١	33.40				1	
PYNUC IATEO	MUCLIFORM	DIFLUENZA A VIRUS (STRAIN ATURKEYONTARIO/77)2/46)		٦	131-401					
PVMUC IATAS	MICHOLOGIC		Ī	٦	360-406			Ì		
PVARIC LATRY	MUCLEOFICIE		2	٦	137.409			İ		
PUNC IATX7	MUCLEORIGIES		7	37.40				Ì		
7.NC 14.00	NUCLEOPROTEIN	3	1-42	17.400					Ī	
PVMIC IAUSS	NUCLEOPROTEIN	INTELENZA A VIRUS (STRAIN AUSSIVOVI)	1-43	127-408						
PUNIC IAVI6	NUCLEOPROTEIN	(89)	357-406							
PUNDE IAWIN	MUCLEOPROTEIN	THE CONTRACT OF THE STATE AND ADDRESS OF THE STATE OF THE	7	M-154	157.406					
PVNUC JAWIE	MICLEOPROFEIN	SETTINGEN & MAIN OF BANKAL BRACIFIC OCEANING	₹.	96-154	157-408					
PUNIC IAWIL	MICLEOPROTEIN	STATE OF THE STATE AND AND SAITHOUS	7	357.409						
PUNIC IAWIS	MICLEOPROTEIN	THE COUNTY OF THE PARTY OF THE	3	12-124	357-401					
PUNC IAER	MUCLEOPROTEIN	INCOCACA CITE SEE AND ACTUAL CONTRACTOR OF THE C	-	¥.5×	157-408					
PVNUC IAZ41	MUCLEOPROTEIN	INCOLNEY A VINCE AND A WIND AND AND AND AND AND AND AND AND AND A		7.3	127-404					
PYNUC IAZCA	NUCLEOPROTEIN	TO LUCKEN A VINCE (21 CAN A A WINGER A NUMBER OF 17 CAN		157-409						
PVNUC IAZDA	MUCLEOPROTEIN	INCLUENCE A VINUS (STRAIN ASSAURED AND INCLUSION AND INCLU	Ι	357-409						
PVAILC IAZGE	NUCLEGPROTEIN	INCLUENCE A VINCE (STACK MANAGEMENT AND CONTRACTOR OF THE CONTRACT		<u> </u>	13.408					
PVNIC JAZIII	MUCLEOPROTERM	INTERPRETATION OF THE PROPERTY	Ī	157-409						
PVNUC IAZIII	MUCLEOFROTEIN	INFLUENCY A VINOS (STRONG PORTING FOR THE PROPERTY OF THE PROP	Γ	¥-134	157-408					
PVNUC IAZIII	NICLEOPROFEIN	INT UENCA A VICUS (STRAIN POST MEDIANO POLICIOSO)	Ī	25.134	117-408					
PYNIC IAZII	MUCLEDPROTEIN	INTELLECT A VIRUS (STRAIN AD WINCH RAND AGAIN	T	2	157-408					
PWRIC IAZIZ	NUCLEOPROTEIN	INTLUENZA A VIRUS (STICAIN ASSAINCIO MALINA)	Ī	Γ	107-701					
PVADIC IAZII	NICLEOPROTEIN	INFLUENZA A VIRUS (STRAIN ASWORE/IOWAITPINT)		Ī	107 501					
PVNUC 1AZII	NUCLEOPROTEIN	Dricenza a virus (Strath Aswinenoways)			153.401					
PYNUC 1AZ11	MUCLEGRAGIEIN	INTLUENZA A VIRUS (STACIN ASWINDLIAL 1919) 10)		10.10	157-401					
PYRUC 1A211	MUCL EOPROTE IN	THE LUENZA A VIRUS (STRAIN AS WINDER AT VIRUS	I	3	157-408					
PVNUC IAZM	MUCLEOPROTEIN	INCLUENZA A VICOS (SI KAIM ASS WINZELLAZIONE)		131.75	151-408					
PVNUC 1AZIA	MUCLEOPROTEIN	DELLENZA A VILUS (STRAIN ASSWINGTIAL TASWIN	T	1	131-404					
PYNUC IAZKIA	MUCLEOPROTEIN	INFLUENZA A VIAUS (STRAIN ACS WINES/ANELSOCIOCAL)	T	21.2	151-408					
PVNUC IAZNE	MUCLEOPROTEIN	INTILIENZA A VIRUS (STRAIN ASWINEALATON)		2 3	157.488					
PVINIC IAZON	MUCLEOPROTEIN	DALLENZA A VINUS (STRAIR ASWINGSMETHER LANDS) DASS	Ī		19751					
PVNUC IAZON	NUCLEOPROTEIN	DOLUERZA A VIRUS (STRAIN ASWINGAMOLICES)		¥	327408					
PUMIC INZTE	MUCLEOPROTEIN	INCLUENCE A VINCE COLLAND AS WINE THE WAS COPENANT	7	3.5	1740					
PVMIC IAZWI	MUCLEOFROTEIN	INTEGRAL A VINCE SETTING AND AND AND AND AND AND AND AND AND AND	77	26.154	157-406					
PVNIK IAZWI	NUCLEOPROTEIN	SACTOR NAME OF THE PARTY AND ASSESSED ASSESSED.	3	2.13	157-401					
PVINC DIBAA	MUCLEOPKOTEIN	THE PARTY OF CHAIR AND AND AND AND AND AND AND AND AND AND	15.143	410-514						
PVXUC INBAC	NUCLEOPROTEIN	8		115-020						
PURIC INDAD	MUCLEUMOIEIN	DATICENZA B VIRUS (STRAIN BANN ALBONING (WILD-TYPE))	19:145	410-514						
PVINC INSLE	MUCLEURAUEIN	INTELLENZA & VIXUS (STRATH BAED40)	75-146	110-311						
PVRUC INSS	PUCLEURICA CONTRACTOR	BIFLUENZA & VIRUS (STRAIN BASINGA-NORE/22279)	13.142	100						
ANGE INC.	MOLECUSO LESS	INTEUENZA C VIRUS (STRAIN CCALIFORNIA/16)	11.103	406.467						
AND MAN	NOCT ECHANGE	NAMBURG VIRITS (STRATIN MUSOKE)	173.203	333-403						
PVNUC NABVI	NO. LECTRO SELV	MAJEURO YIRUS (STRAIN POPP)	173-207	11.407						
ארנור	ACTES OF	VACCINIA VIDUS (STILAIN COPENHAGEN)	100	2	Ž. 12	2		1		
100	1000	VALIDLA VIRUS	2:5	2		381-613				
A CONTRACTOR	IS NO PROTEDU	FOXTAL MOSAIC VINUS	111-117							
200	N TO MOTO	NARCISSUS MOSAUC VIRUS (PRIV)	119-137							
	116 KD PROTEIN	PAPAYA MOSAIC POTEXYIRUS (PMV)	2		76					
	223 KD PROTED	POTATO VIRUS M (STRAIM RUSSLAN) (PVA))	207	200						
	10 00 00 00 00 00 00 00 00 00 00 00 00 0	POTATO VIRUS X (PVX)	216-350							
NOK LANG										

N CLNC	ALLINOIS	All Vieutet (no batteriophoges)	, , , ,							
NOT ENTE	1	POTATO VIREIS X 1878 AIM CRITPUXI	} }:	2		4	7	1	4	1
PLOR! WENT	1	STANDED YOUR YELD WITHOUT ASSOCIATED VIRIS (SAIVE	161.107	911.844						
PLUR WCNVO	14) KD PROTEIN	WIGHE CLOVER MOSAIC VIEWS STRAIN IN WICHY	1240-1218							
PLPIO XPVAC	i i	WHITE CLOVER MOSAIC VIRUS (STRAIN D) (WCNIV)	1340-1289							
PI PIG MP10P	÷	AUTOCRAPIA CALIFORNICA MUCLEAR POLYIGDROSIS VIRUS (=							
P. PIG BASOV	PIOPROIEN	ORGYIA PSEUDOTSUGATA NRILTICAPSID POLYIEDROSIS YIRUS	3.5							
7. P10. BGDV	PROTEINSIO	RICE DLACK STREAKED OWARF YIRUS (ADSDV)	139.111	305.439	506-556					
P. P. 10 W. IV.	NONSTRUCTURAL PROTEIN PASIO	ACE GALL DWARF VIRUS (RCDV)	16.273							
VOI INV	NONSTRUCTURAL PROTEIN PUSIO	WOUND TUNIOR VIRUS (WTV)	130-234							
VIW HIGH	NONSTRUCTURAL PROTEIN PHS!!	NCE DWARF VIRUS (RDV)	23.60	333.314						
7.F.2. 45V	MONSTRUCTURAL PROTEIN PHS11	WOUND FUNIOR VIRUS (WIN)	Ž							
7 E E	NOWSTRUCTURAL PROTEIN PIL	RICE DWARF VIRUS (RDV))	160.11							
Pris WINE	NONSTRUCTURAL PROTEIN PHST	WOUND TUNIOR VIRUS (WTV)	101.73							
P. P. 10 115\ED	NOVSTRUCTURAL PROTEIN PUSES	WOUND TURIOR VIRUS (STRAIN M) (WTV)	£.18							
MIN IKNYA	CAPSID ASSENIBLY AND DNA MATUR VIION PROTE	EQUINE HERPESVIRUS TYPE I (STRADY ABAP) (EIIV-1)	18-31	-						
Presi itsveu	PROBABLE CAPSID PROTEIN 1723	HILDIAN CYTOMEGALOVIRUS (STRAIN AD167)	41-12	146-180						
PV P. 14 F 110 V		HERVES SINITLEX VIRUS (TYPE 6/STRAIN UGANDA-1102)	=							
F 126 H 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	ATT NIBRANE - ASSOCIATED STRUCTURAL PROTEIN V	EBOLA VIRUS	66.700							
PY PEG IISVSA	CAPSID PROTEIN VP16	EQUINE HERPESVIRUS TYPE I (STRAIN AB4F) (CIIV-1)	12.00							
PL P36 NPVOP	CATSIO PROTEIN VP26	HE WE SYIAUS SAISIN (STRAIN II)	17:10							
0.27 529.4	P36 PAOIEIN	ORGYIA PSEUDOTSUGATA NAM, TICAPSID POLYHEDROSIS VIRUS	111.150							
PV F7 AIISV	CAPSID PROTEIN VP26		17:0							
P. F. BIVIO	OUTER CAPSID PROTEIN VP3	KAIN VACCI	100	20.30	£0.483	14.662	641.730	976-1056		
PINE BIVE	OUTER CAPSID PROTEIN VP3		100.00	Ī						
P. P. BIVII	DUTER CAPSID PROTEIN VP2			18.55						
P. P. BTVIS	OUTER CAPSID PROTEIN VP2	ī	===	61.30			T			
P. P. E. E. P. V.	OUTER CAPSID PROTEIN VP2	1 AJ MCA)		İ.	101					
PIPE ROTBA	DUTER CAPSID PROTEIN VP2	iz	Γ	Ī	403-453	10 483	624-509	Ī		
PVP1 ROTBU	ANA-BINDING PROTEIN VP2		- -	411.316	\$31.957	607-659	13:13:			
	RWA-BINDING PROTEIN VP2			Γ	334-350	Γ	12.5			
	RMA BINDING PROTEIN VT2		1.67	482.516	\$13.867					
PVP3 ROTSI	RMA BINDING PROTEDN VP2	AIN COWDEN		12.40	104-221	113-511	Γ	201-746		
PYPIO ASPET	PMA-BINDING PROTEIN 171			415-637	969-609	660-755				
PVPII FAGIV	PHOSPHOPROTEIN PIO	VER VIRUS (STRAIN E.15) (ASFV)	19.10							
7. P.11 AST 87	EAULY 11 KD PROTEIN		13.75							
2007	PROSPINATE IN THE	AF ALCAN SWENE FENER VIRUS (STRAIN DATIN) (ASFV)								
TANAM 11 4.74	2 - 1 - 2 - 2 - 2 - 2 - 2 - 2 - 2 - 2 -	A CALIFORNICA MAINE SA AN VISCORDES VIBRIES		Ì		1	1			ĺ
PUPJI VACCC	EARLY 35 KD PROTEIN	,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,	T			T	1		Ì	
PLP35 VACCP	INDICADDOLEMANT ENVELOPE PROFESS P13	Ī	L		Ī			1	Ī	
PVP15 VACCV	INCHUNODORIDIANT ENVELOPE PROFECS P15		=			Ī		Ì	Ī	
		VACCINIA VIRUS (STRAIN WR)	===					İ		Ī
PVP) AliSva	TAINIUNODOMINANT ENVELOPE PROTEIN P19	_						ĺ		
PVP1, 81V10	VPI CORE PROTEIN	RAIN VACCI		340.274	104.704				İ	
Pv.P), B1V13	VP) CORE PROTEIN		П	3			Γ			
PVP1 BTVIA	VP) CORE PROTEIN		П	2						
	VP) CORE PROTEIN		П	Π						
PVP1 EICDVA	VPI CORE PROTEIN	(SEROTYPE I) (EID)	Ī		151-692					
	VP) CONE PROTEIN	VIRUS		111.770	111.112	151-103				
Vel tov	PI PROTEIN	SIGELY	Т							
2101	INCOME COME SECURITION OF THE PROPERTY	ALCO DIVINO STRUCK		Ì	1	Т				
10101	INTER COMPTION OF THE		1	22.62	14.16	907-90	10433		1	

	ALLSIONS		2	4114	AREA?	757	J	AREAS	3	
1111			2	14.31	3	431-483	***			
111	TOTAL PROPERTY OF THE PROPERTY	CHUNIAN HERPESY IRUS 4)	÷							
11	2 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1		33	59433						
1	0 PEO 150 PAGE		2							
	CAPSID PROTEIN P40	N THORNEY .	2							
PVP48 VZVD CAPSH	CAPSID PROTEIN P48			114.111						
Γ	CAPSID PROTEIN P40	==								
Ī	STRUCTURAL CLYCOPROTEIN CPAI	A POL VIIEDRUSIS VIAUSI			95					
Ī	CUIER CAPSID PROTEIN VP4		2							
J	GUIER CAPSID PROTEIN VP4					117.101				
Ī	A COME PROTEIN PAR PRECUASOR	ENTIAGEN			175	10.00	137.191			
Ī	A CORE PROTEIN PAA PRECURSOR	(STRAIN WE)				(4.10)				
Ī,	A CORE PROTEIN PAR PRECURSOR	VARIOLA VIRUS								
Ī	MANUE CORF PROTEIN PUB PRECUASOR	FOWLPOX VIRUS								L
	MAINE COST PEDIEIN PAD PRECENSOR	VACCINIA VIRUS (STRAIN COPENHAGEN)	3							
Ī	POPE PROTEIN PAR PRECUBSOR		1.17	23.62						
Ī	CONTRACTOR OF CO		1.17	23:163	144-21					
Ì	TOTAL PROJECT OF THE PROPERTY	INITISEROTYPE 10/150LATE USA)	579-617	619-633						
	V74 CORE PROTEIN		109.445	£09-£43						
	VP4 CORE PROTEIN		109-695	19-69 19-69						
PVF4 BTV3A VP4 C	VP4 CORE PROTEIN		109.693	(PG-FG)						
	ORE PROTEIN	12 200	414.511	531.430						
PYPE RDV DUTE	OUTER CAPSID PROTEIN VP4	A INOS IS INOS INO		444.473	627.679					
	TRUCTURAL PROTEIN PNS:			27.51	111.11	15:53	528-453			
1	OUTER CAPSID PROTEIN VP4	STRAIN BOAL)			1					
	OUTER CAPSID PROTEIN VP4	1	2		200		114 411			
1	CAPTION PROJECT VP4		=		2		*****	136.441		
Ī	TANCO PROJECT VP4		2	*	221:374					
	CALLER TAPED PROJECT VP4		=	18.3						
	24× 23 20 20 20 20 20 20 20 20 20 20 20 20 20	HIGHLAN BOTAVIAUS (SEROTYPE I / STRAIN 10%)	-	2	20.00	43:31	330-048			
VP4 ROTHS	COLUMN CASA CASA CASA CASA CASA CASA CASA CAS	ILIBIAN ROTAWRUS (SEROTYPE 27 STRAIN RV-3)	1.15	216-273	11:31	19:31	527-652			
	COLER CATALOGUES AND AND AND AND AND AND AND AND AND AND	INDIAN ROTAVILIS (SEROTYPE 1/ STRAIN 690)	1.35	13:14	237.274	11:30	484-511	37 460		
Ī	GUICE CATSID FROIEIN VE	HAMAN BOTANTEUS (SEROTYPE 2/STRAIN DS!)	1.15	116-173	137.378	10.51	327-453			
T	A CASID FROIEN VIV	MANIAN ROTAVIRUS (STRAIN X 8)	1:38	233-234	145-379	414-513	321-518			
	QUIER CATALORINA TEL	STRIPE STATE (STRADE KI)	<u></u>	317.118	413-313	\$37.652				
Ì	OUTER CAUSID PROTEIN VT4	HISTANDON VIEW (STRAIN 126)	 =	116-213	317.378	413-517	517-652			
_{	OUTER CAND PROTEIN VY	CONTRACTOR (CEROT VPE 1 STRAIN MID)	1	377.314	413-517	530-645				
	CA CASID PROTEIN VP	CONTRACTOR SECTION OF THE SECTION OF	2	11:31	116.314	404-510	531-443			
	ER CAPSID PROTEIN VP4	CONTA ROLL TINGS (SEE SEE SEE SEE SEE SEE SEE SEE SEE S	=	114.31	11:31	483.517	537-652			
VP4 AOTICA OUTE	OUTER CAPSID PROTEIN VP4	INDIAN ROTAYING (SEROI FFE STRAIN F)		1	113.274					
PVP4 ROTHT OUTE	OUTER CAPSID PROTEIN VP4	MODELLA KOLANIKOS (SENOLITEC): STENIK MAN		114.331	21.11	61510	3844			L
	OUTER CAPSID PROTEIN VP4	HUNIAN ROLAVIKUS (SERVO) 17E V SINAIN SI INCENSIO		111.273	15	603.517	137-453			
	OUTER CAPSID PROTEIN VP4	MUNICA MOLANICA SERVICIA SE SE SERVICIA SE SE SE SE SE SE SE SE SE SE SE SE SE		11.33	25.35	48.517	117-652			
	OUTER CAPSID PROTEIN VP4	MUNICAL MANUS (SEROITE 17 STANIA WA)		114.511	\$38.420					L
Γ	OUTER CAPSID PROTEIN VP4	PORCINE HOTAVIROS (SERVOTTE 3 2 STRAIN 030)			14.33	201.334	289.614			
	OUTER CAPSID PROTEIN VP4	PORCEME ROTAVIRUS (GROUP C/ STRAIN COWDEN)	2				33.05	140.612		
Ī	OLITER CASID PROTEIN VP4	PORCEME ROTAVIRUS (STRALM GOTTI RUED)		77.97			130.430			
Ī	OLITER PAPER PROTEIN VP4	PORCINE ROTAVIRUS (STRAIN YN)	ŝ	3:2	111.111	916.316				
	CARGO CARCO PROTECTION VOL	ALC SUS ROTAVIRUS	=	•	3		76-37			
1	AC AUGUST AND A CONTRACT OF THE CONTRACT OF TH	SIXTIAN LI ROTAVIRUS (STRAÍM SATI-FEN)	:	15.51	528-610					
ĺ	COLER LANGUE BEOTEN 174	SINIAN II ROTAWAUS (STRAIM SATI-SCAI)	5.5	311.214	145.174	464-518	23-446			
ĺ	COLEMN TAN PROPERTY ONCE	WOUND TUNIOR VIRUS (WTV)	11.42	117-195						1
NOT AHSV4	STAGE DESCRIPTION	AJECAN HORSE SICKNESS VIRUS (SEROTYPE 47 STRAIN VACCI	1.51	113.239						
000	OUTER CANSID FROIEIR VE		23.55	41.176						

173000	ALL MOTH	All Viruses (no bacteriophs fes)			105.1	7 7 5 7	ARTA S	AREAG	ARCA?	AREA
TIVE STATE	PROTECT		4	4:		11770		Γ	Γ	
1210	OUTER CAPSID PROTEIN VP3		2	20.2		207.745			Ī	
1010	CALIFER CAPSED PROTEIN VPS		Z	V2-130	2				ŀ	
	CALTER PARTIE PROTEIN VES		2	127-321					Ī	
	OUTER CAPEID PROTEIN VP	Ī	2	13:143	140-223					
VIV.	CHITCH CAPSED PROTEIN VPS	I AFRICA)	2	63.163		-			T	
PVPS EIDVI	OUTER CAPSID PROTEIN VPS	_	₹ -	227.56		101,101	1			
VOR 1674	CHITER CAPSIO PROTEIN VP3	DISEASE VIRUS (SEROTYPE I) (TIED	26.35		12.00					
N PS WTV	OUTER COAT PROTEIN PS		2	21.0	1000					
DVPAI BTV10	CUIER COAT PROTEIN PS		14.70	347-366	X-16					
VOEL MAN		SOLATE USA)	5.33							
PVINI NOVAC	PROBABLE NONSTRUCTURAL 419 KD PROTEIN		76.70							
PV-942 BTV10		DSIS VIRUS (2	91.10						
JONAN PROX	VP6 PROTEIN		=	2						
NOVAC NOVAC	MAJOR ENVELOPE GLYCOPROTEIN PACCURSOR			E T						
PVP61 NPVGM	MAJOR ENVELOPE OLYCOPROTEIN PRETURSOR			1						
P. P. D. TVII	MAJOR ENVELOPE GLYCOPROTEIN	CHAIS (GAL)	27.00							
N.M. BIVIS	VP6 PROTEIN	BLUETONGUE VIAUS (SEROTYPE 11 / ISOLATE USA)								
P. P. 01VI	VP6 PROTEIN									
SIVIS 47.5	VP6 PROTEIN	ī								
PV P6 01V2A	LP6 PROTEIN	N WILL								
P. P. ROV	VP6 PROTEIN	DIVEE 1/ ISOLATE USA)			100.00					
2 12 12	STRUCTURAL PROTEIN PO	RICE OWAL VINUS (POV)		200						L
F. P. WT.V.	STRUCTURAL PROTEIN PA	WOUND TUNIOR VIRUS (WIV)								
PLP14 NPVAC	STAUCTURAL PROTEIN PO	WOUND TUNDS VIRUS (STRAFN NJ) (WTV.)		****						
PAPE KPVCP	P74 PROTECK	AUTOGRAPHA CALIFOLNICA MUCLE AR POLVIICIMUSIS VIRUS								
PUPIS HISVSA	PA PROTEIN	CHOMISTONEURA PUBLICA PULCI AN TILL THE TOTAL	3	16.311	29:00					
PLP IN NOVAC	PROBABLE MENBRANT ANTICEN 75	FAR PON VIOLINGSIS VIRUS	2:3	163.303	079-40	ļ				
	No. C. D. Marcheller	ALTERIORGIST VISITS ASTROPHY BE 10/1504 ATT USAN ISCREDINGED	2							
27.07.1	VY CORE PROJEIN	BELLETONCER CIBLS (SEROTYPE 11 / 1504 ATE USA)	317.102							
	CORE PROTEIN	BILLIA TOKOLIA MALIK MEROTYPE ITVISOLATE USAD	2 2							
P. P. BIVIA	APTOR MOTERS	ALIA)	114-235							
21.11	THE CALL PROJECTS	BLITT TONGUE VIRUS (SEROT YPE 7 ISOLATE SOUTH AFRICA)	114.23							
	TO COME PROJECT	BILITIONGUE VIRUS (SEROTYPE 27 ISOLATE USA)	164-138							
100	Mary Cost and Life	YPE 1) (CIU)	16-50	134-131						
	CONCERNITION ALL PROJECT PASS			<u>=</u>						
	MONSTELL TREAT PROTEIN PKS7	WOUND TUNIOR VIRUS (WTV)	÷	2	2					
PAN KPVOP	CAPSID PROTEIN PRO	AUTUGRAMIA ('ALII ORNICA NUCLEAR MILYIII IIROSIS VIRUS (2		2					
P. P. BTV10	CAPSID PROTEIN PIT	ORGYIA PSEUDOTSUGATA NUL TRAFSIO PULTIEUROSIS VINCA		100						
PVP0 BTV11	NONSTRUCTURAL PROTEIN PR	BLOBIONGUE VIRGO (SERO) THE TOTAL STATE LOSS.		118.318						
PATE B1V()	MONSTRUCTURAL PROTEIN PO	BLUE TOROUGH VIEWS (SERVITED TO 1501.A TE USA)	× 101	87.58						
7.71 BIVE?	NOVETERCTURAL PROTECT P	BILIFTONCIE VIRUS (SEROTYPE 17/150LATE USA)	Z 102	115:219						
PVPI BTVIA	NOVSTRUCTURAL PROTEIN TO	IN (ETONGUE VINUS (SENDITYPE I / ISOLATE AUSTRALIA)	24-102	185-219						
PVPI BIVIS	MONSTRUCTURAL PROTECTION PE	BLUETONOUE VIRUS (SEROTYPE 1/150LATE SOUTH AFRICA)	24-102	18.319						
NIA DE LA CO	l	BLUGTONGUE VIRUS (SEROTYPE 1/150LATE USA)	2 2	2						1
NA STA	STRUCTURAL PROTEIN VP8 PRECURSOR	FOWLPOX VAUS						I		
\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\	NONSTRUCTURAL PROTEIN PNSS	RICE DWARF YIRUS (ADV)		27.50						
P.T. WIW	STRUCTURAL PROTEIN PP	WOUND TUNIOR VIRUS (WTV)	2							ļ
PITC BYDY!		_	7 2							L
PYPHE NOVAC		SAME TYPE TOWN DWAN VIRUS (ISAA I E MAY 1919 (BIDA) 1777								L
SCASS SHOW	19 KD POLYNEDRAL ENVELOPE PROTEIN	AUTOCRAPIIA CALIFORNICA MULLEAA FULTITRUMUSIS TIMUST								

		A	i	1	ALEA?	1			i	Ì
reen	1	VIEW STATES IN THE STATE OF THE STATES OF TH	131.101	304-265						
	THE PROPERTY ENVELOPE PROTEIN	т	Γ					1		
NAME AND DE				İ					7	
NAU HVIAZ	NAME AND DESCRIPTIONS OF THE PROPERTY OF THE P	w i :		İ						
N PU IIVIBI	VAD MOTERA	HUNIAN INBILINDOEFICIENCY VIRUS TYPE I (BILLO ISOLATE) (III	+	Ì						
NAU IIVIBI	VPU PROTEIN			Ì						
NEU IIVIEN	CAU PROTEIN	IN TAKE IN THE PROPERTY VIEWS TYPE I (DRAIN ISOLATE) (1)	\$							
PLPU HV IBA	VPU PROTEIN	THE LAND WASHINGTON TORONS TYPE I (BRU ISOLATE) (III)	=							
NYD IIVICA	VPU PROTEIN	-	9	j						
10/10/10/10/10/10/10/10/10/10/10/10/10/1	VPU PROTEIN	THE PROPERTY CHAINS TYPE I FELL ISOLATE) (HIV-16	9-4							
	L'ALL PROTEIN		=							
2	200.000	INDIAN BUILDING FILLENCY VIACO LITTE AND LITTERS AND L	9.6							
	The state of the s	HIGHEN BESCHOOLS SCIENCY VINUS 1776 (1913 SOCK) CHILL								
12.12	LAD MOINING	INDIAN DURINODEFICIENCY VIAUS TYPE I (IRCSF ISOLATE) (III								
P. P. IIVIMA	CAU PROTEIN		2							
SIVI D		_	4.40							L
Velvi ile	IND PROTEIN	_	4:3							
Halon de	VPU PROTEIN	_	•							
	NATIONAL PROPERTY.		3							
E A	74.00									
2		3								
V.PU SIVCZ	VAC FROISING									
VPX HV2D2	VPU PROTEIN	Ę	Ī							
VALUE BSNIV	VPX PROTEIN		٦							_
101 ROTS1	ALPHA.A PROTEIN		349-217				ļ			L
20103	NONSTRUCTURAL PROTEIN NCVP1		11-1							
PASON BOLGA	CZ6 MOTEIN	JUNEA ROTA	P9 1 69							
0.00	CP6 PROTEIN	ROTAVILUS (CROOF BY STATE OF THE STATE OF TH	31.50	£4.103						
PALCE BOTH	VPEPROTED	ON BESTELLS	Ī							
POTOS POTOS	VP6 PROTEIN		9.43							1
100 POTES	VPSPROTED	MORCING HOLI AVIAND STORES CO. ST. ST. ST. ST. ST. ST. ST. ST. ST. ST	3.36	201-120						
PVCS BOTBU	CLYCOPROTEIN VP3	DOVINE ROLL VIEW COLUMNIA COLU	131.53	199-236						1
101.00	NONSTRUCTURAL PROTEIN MCVP.)	BOVING ROLA VIRUS (STICKING ON)	31:	101-234						
	MONETREE TURAL PROTECH MCV?	PORCINE ROTAVIRUS (SERU) TVE 27 31 ECHICAGO	Ī	199-236						
	MONGTHICTIAL PROFER NOVPS	SOLIAN II ROTAVIRUS (STUADE SALLI)	Ţ	=======================================	160.336					
	MONGTON TOTAL PROTECN NSVAPO	BOVINE ROTAVIRUS (STRAIN UK.)	Ī	15.50 15.50	35.53					
	SONGTHETHAL PROTEIN NOVP	SINGAN II ROTAVILUS (STRAIN SALI)	Ī	312-530						1
	CI VIDEO LEGA VET	BOVINE ROTAVIRUS (SEROTYPE & / STRAIN UST)	Ī	21.38		L				_
10101		BOVING ROTAVIRUS (STRAIN AS)	Ī	944.446			_			
7V509 RO184	CLT COROLLES VI	BOVING ROTAVIRUS (SEROTYPE 67 STRAIN 61A)				ļ				
SOP ROTBA	GLYCUTED TO	BOVING ROTAVIRUS (STRASN A44)								
P. 509 ROTES	CLYCOTOTISM ST	BOVINE ROTAVIAUS (SEROTYPE 10 / STRAIN D211)				-				
PVSOP ROTOR	CLTCORD SIGNATURE	BOVINE ROTAVIRUS (STRAIN KK3)		91					•	
PVSOF ROTEN	GL TCOPROJEIA VI	BOVING ROTAVIRUS (STRAIN NCDV)	Ī			-				
VSOS ROTOT	GLYCOPROTEIN VP	BOVING ROTAVIRUS (SEROTYPE 1 / STRAIN 1449)				-			L	
PVSOP ROTEU	GLYCOPROTEIN VP7	DOVINE ROTAVIRUS (STRAM UK)	2.	26.58					L	L
1.500 ROTC?	GLYCOPROTEIN VPI	CHICKEN BOTAVIRUS A (SEROTYPE 1/ STRAIN CIT)	315-236				 -			
PVSON ROTEL	GL VCOPROTED VP1	ENVINE ROTAVIRUS (STRAIN LOSS)					-			L
PV.509 #01/04	GLYCOPROTEIN VP1	ROTAVIBUS (CROUP B / STRAIN ADRY) (ADULT DIABULEA ROTA	-		į					L
VSOF ROTGI	CLYCOPROTTIN VP7 PRECUASOR	BOTAVIRUS (CROUP B / STRAIN IDIR)	-					-		
PVS09 ROTH	GLYCOPROTEIN VP7 PRECURSOR	MARIAN HOTAVIAUS (SEROTYPE 47 STRAIN RV-4)	7			<u> </u>	1			L
VSOS ROTIES	GLYCOPROTEIN VP 1	INDIAN BOTAVILUS (SEROTYPE O / STRAIN RK9)	143-330			-	-	-		L
NTON BOX 14	GLYCOPROTEDIA VP 1	MANAN ROTAVIRUS ISEROTYPE 27 STRAIN HUS)	363-320			1				
PVSOF ROTIES	CL YCOPROTEIN VP?	THE AND ACTIVATED (SEROTTPE O/STRAIN DIT)	3.43	8 2		1		+	1	-
COLLOS ROLLO	CLYCOPROTEDI VP?	TOTAL STATE (SEROIVE 2/STRAD DSI)	112-110			$\frac{1}{4}$		-	ļ	ļ
POLICE BOTTO	CL VCOPROTEDI VP?	MANAGEMENT CONTRACTOR OF COMPANY (ON 15)	1282-330	L		_				

1	TI CIVITY.	AB Viraser (ne becteriophoget)	Ţ					19114	18517	1 7 3 8 7
67.47	STATE OF THE PROPERTY OF THE P		1410	ABEA.	77.77	1	2018	0	9000	
100 mm	GLYCOPROTEIN VP3	HUNIAN ROTAVIRUS (STRAIN 1.26)		B						
	101 VI 010 010 VI 010 V	į	٦	917.110						
	The second secon	IND STRAIN DI	3-43	201-120						
NO.	CE LOS PROPERTOS CALLED	HINGAN ROTAVIAUS (SEROTYPE 37 STRAIN P)	162-120							
N SO ROISER	CT. COLUMN CT.	MARCH ROTAWALES (SEROTYPE 1/ STRAIN ARV)	282-320							
20103 20103	OF TOWNSIEM AND		203.330							
E LOS	OF TURNISH ST	SEASTAN BOTAVIBUS ISERCTYPE 4/STRAIN ST THONAS 31	×=	3.5	182-320					
NO ROTHY	CT ACCAMONIC AV	INTALA HOTAVILIS (SEROTYPE 4/ BIRALY VATO)	Γ	204-343	313.130					
W 1011/10	C. T. C. S. S. S. S.		Γ	107-330						
2101	GLYCORDIES VF	191	313-320							
(XOI (I)	GLYCOPHOLES V.		283-330							
Z 101 5	CC TCCTROINE VY		Ī	206-343	211.320					
SOF ROTES	GLYCOPROTEIN VP7		2							
1 500 ROTP6	CL VCOPROTEIN VT)		917.110							
509 RO1FB	CLYCOPHOTEIN VP?			200 300	101.100					
71 SOF ROTPK	GLYCOPROTEIN VP?	POSCONE ROTAVIAUS (SEROTYPE 47 STRAIN BLX-144)	T							
1 509 ROIPM	GLYCOPAGIEIN 17?	PORCENE BOTAVIRUS ISTRAIN K)		277						
500 ROIPY	GLYCOPROTEIN VP?	PORCINE ROTAVIRUS (SEROTYPE 47 STRAIN BAIL-1)		201.742	277.72					
V. 500 BOTEM	GLYCOPROFEIN VP?	PORCINE ROTAVIRUS (STRAIN YA!)	=	202:320		\downarrow				
15101 1075	CLYCOPROTEDN VP ?		361-370							
74104	CI VCOPLOIFIN VP3	1	313:330							
20100	NONCTRIPLITA AL CLYCOPROTEIN NOVE	BOVINE ROTAVIRUS (STRAIN NCDV)	73.161							
	Marca Crart Table	BOVINE ROTAVIRUS (GROUP C/ STRAIN SHINTOKU)	17.58							
201010	LONG THE THE AT THE VEGET OF THE VEGET	BOVING ROTAVIRUS (STRADA UK)	191-66							
	MONSTRUCTURE OF CONDUCTOR MONSTRUCTURE	HIDIAN BOTAVRUS (STRAIN A22)	13.167							
2010		HUNIAN ROTAVINUS (STRAIN AS4/CLONE 2)	3)-162							
20101		MAIAN BOTAVIAUS (STRAIN A64 / CLONE 6)	73-167							
TVS10 MOINE	LIBOR CLOSE CAPED PROTECT	HAMIAN ROTAVIAUS (CROUP C/STRAIN BAISTOL)	121-151							
10 10 10 10 10 10 10 10 10 10 10 10 10 1	NOMETRICATION OF STREET NO. 12		1).116							
100 min	NOWSTRUCTURAL GLYCOPROTEIN NOVPS									
10101	NONSTRUCTURAL PROTEIN) (ADULT DIARRUEA ROTA		8.136						
NATION ROTHY	NONSTRUCTURAL PROTEIN		743							
VSI POTIES	MINOR OUTER CAPSID PROTEIN		<u>8</u>							
PVSII ROTKO	MINOR OUTER CAPSID PROTEIN		97.54							
PVSII ROTIED	MINOR OUTER CAPSID PROTEIN					1			1	
PVS11 ROTHW	MINOR OUTER CAPSID PROTEIN	HUMAN ROTAVIRUS (SEROTYPE 1/STRAIN DSI)								
Sil ROTSI	NUNCH OUTER CAPSID PROTEIN	HUMAN ROTAVIRUS (SEROTYPE 1/STRAIN WA)								
VS46 TORVC	handa guter capsid protein	SIMIAN II ROTAVIRUS (STRAIN SATI)								
PVSII KIIRDI	SATELLITE RNA 45 KD PROTEIN									
PVSH ARUNDS	SMALL HYDROPHOBIC PROTEIN					igg				
PVSII MUNIPE	SMALL HYDROPHOBIC PROTEIN	AND (STEAM EUROB								
PVSH MUNDA	SMALL HYDROPHOBIC PROTEIN	MANUS VIKUS (SIRAIN EDITIONOMY)								
PVSII KIUMPB	SMALL HYDROPHOBIC PROTEIN	ALLEGATION OF THE POST OF THE	5							
rvsti blubipe	SMALL HYDROPHONIC PROTEIN	PIUNTA VIRUS (3) INCHA CELTANA)								
VSH MUNUM	SMALL HYDROPHOBIC PROTEIN	ALDER STRUCTURE OF STRUCTURES	3							
VSH MORDIK	SALALL HYDROPHOBIC PROTEIN	MUNUS VIRUS (STRAIN ACTUALISM)							ļ.	
VSH LUMBEL	SMALL HYDROPHOBIC PROTECT	MUNCO VINCENTAL BRICADA IN								
VSH MIDORM	SMALL HYDROPHOBIC PROTEIN	MUNICOLATING COME MANAGE VACCINE	===							
VSH MONDT	SMALL HYDROPHOBY, PROCEIN	INDIANGE CHELSCOME AND TAX AND SAID	7							
איזון איזון איזון איזון איזון	SMALL MYDRUPHOBIL PROTEIN	MARIPS VALUE (STEATH URABE VACCINE AND)	7							
VSII REOVO	SAALL HTDROTTOBL TROITING	REDVILUS (TYPE) / STRADY DEARING)	<u></u>	100	113-139					
VSII REOVI	MORAL PROJECT PRESENTATION	REDYILLS (TYPE 3 / STRAIN DISIONES)	<u>:::</u>							
PVSI1 KEOVI	SIGNATURAL CONTRACTOR									

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171	141 LID 735	All Virusei (no butterloph iget)	AREA! AREA!	A.1 ABEA.2	П	44744	1		
COLNE.	PEDITIN			261					
	CICATA I PROTEIN PRECURSOR		16.14						
ASIS ME OVE	7,000			<u> </u>	-				
VSI) REOM	Significant Control of the Control o			<u> </u>	1				
PVSIS REOVO	SIGNIA I MOTORIA			<u> </u> 	1				
VSIS REDVI	SIGNIA 1-5 FROTEIN		=	1	\dagger	Ī			
V\$12 11EVOU	SICAIA I-S PROTEIN	KEV)	25.15	1	+	T	Ī		L
VST1 1EVACE	STRUCTURAL PROTEIN 2 PRECURSOR		11.331		†				
VST1 IEVAIY	STRUCTURAL PROTEIN 2 PRECURSOR	5	116-152		1	1			
VS11 HEVPA	STRUCTURAL PROTEIN 1 PRECURSOR		118-153				1		
KENSE CION	STRUCTURAL PROTEIN 2 PRECURSOR		186-220						
5.075	STRUCTURAL PROTEIN?	ESOSKIE V	30.151	<u> </u>					
	11 March 114			<u> </u> 	İ				
VII CAPVI	PROJECT STATES		2	<u> </u>	Ì				
TY TO CAPVE	TA PROTEIN		1		t				L
PVIER EDV	TAPROTEIN	B95-4) (HUMAN HEIDESVIRUS 4)	٦	245	†		T		
PVTER IKMVA	PROBABLE DNA PACKAGING PROTEIN		417-451 617-451	=	1				
PVIER HSV6U	PROBABLE DWA PACKAGING PROTEIN	ANDA-1102)	161.502			1			L
PVIER HSVED	PRODABLE DNA PACKAGING PROTEIN			<u> </u>	1				
PVTCA USVII	PROBABLE ONA PACKAGING PROTEIN	(\)		696-744	1				
PY TER HSVSA	PROBABLE DNA PACKAGING PROTEIN	$\overline{}$	136-367		1				L
PVTER VZVD	PRODABLE DNA PACKAGING PROTEIN	COLUMN SOUTE CONTRACTOR DUBLASTIVE	100-411		1				ļ
PVV PIGILA	PROBABLE DNA PACKAGING PROTEIN	ANI (PIV.4A)	5						\downarrow
ACA CENTA	V PROJECT	HUNIAN FAIRING CUENCA SA TINCO	5.53						1
2010	VI PROTECT	SENDAL VIRUS (STRAIN 674)	014						
	HYPOTHETICAL 10 I KD PROTEIN	Starologus VIAUS-LIKE PARTICLE 33*1		-					
200	HYPOTIE TICAL 10 8 KD PROTEIN	SULFOLOBUS VINUS-LIKE PARTICLE 35VI	25.50						
	HYPOTHETICAL II 6 KD PROTEIN	SULFOLOBUS VINUS-LIKE PARTIELE 33VI	3 0						
AVOINT A	NYPOTHETICAL II 9 KD PROTEIN			<u> </u>					
STATE STATE									
100 M	2								
VO(1 111V4	HYPOTHETICAL 13 1 KD PROTEIN IN COAT PROTEIN	FILTRE CALICIVIEUS (STRAIN PURICE)	9.	-	 				
AAISE BIDAS	HYPOTHETICAL 13 9 KD MOTEN IN COAT PROTEIL	PARSIT (GAROLUAGIC DISEASE VINCE INTINES)	9						_
25.0	<u> </u>	PARBIT IEMORDIACIC DISEASE VIACANI INC.	100						
W 10 31 14	HYPOTHETICAL IS I KD PROTEIN	CASSAVA LATENT VIRUS (SIEARS) NEW TANK	10.5		<u> </u>				4
AND MINO		CASSAVA LATENT VINUS (STICAL) MICERIAN)	19.9	Ī					
PY 11K SSVI	HYPOTHETICAL IN SKD PROILING IN NO PROTEIN	DADYA PRODUCED SECTION	2.20	2					1
PVIAK SIVI	HYPOTHETICAL IS NO PROTEIN	SULTOLOGUS VIROS LINE PARTICLE SON	5						
PYILL ADERY	SIVPOTIETICAL 13 T KD PROTEIN	SILI OLOGUS VIKUS-LIAL PARILLE SST.	3.00						ļ
VIAK SSVI	HYPOTHETICAL PROTEIN C.164	HUNIAN ADENOVINOS TITES	<u> =</u>	11:11					1
PY17K SSV1	HYPOTHETICAL ITOKD PROTEIN	SULT OF DRUG STRUGGER CAN PAGE 18 SECTION OF THE SE		18:18					\downarrow
PY11K SSVI	NYPOTIETICAL PLED PROFES	SOLICIOS INC. INC. DANIES EST.	103-136						\downarrow
P. 104 SSVI	HYPOTHETICAL ISO KO PROTEIN	SULF DE CARDE VIBILITY OF PARTICLE SAVI	13.107						1
PYZEK SSVI	HYPOTHETICAL 20 4 RD PROTEIN	SULFOLORON VINOS-LINE PARTIES FOR SALVER SALVE	137.180						1
\$13 SOCH	INPOTIGITICAL 18 5 KD PROTEIN	SULFOLUCIO VINCE LINE FANT NEL 221	35:25	<u> </u> 					1
100	HYPOTHETICAL PROTEIN 2	SOYDEAM CIALOROTIC MOTILLY VINUS	Ī	171.00					4
	HYPOTHETICAL 31 5 KD PROTEIN	SULFOLOGUS VIRUS-LIKE FARTILLE 33'1	١						
NAME AND AND	NINDONETICAL 11 1 KD PROTEIN	SULFOLOBUS VIRUS-LIKE PARTICLE 33V1	131.34	-					1
71 500107	IN POTIBLICAL ST S KD PROTEIN	LAUTOGRAMM CALIFORNIA PONTER TO THE	115.166						4
	IN POTIETICAL PROTEIN I	SOYIEAN CHOROTIC MUTTLE VINUS	=						4
200	HYPOTIE TICAL SOKD PROTEIN	SULFOLOBUS VIRUS-LINE PARTICLE 3311	14.00	<u> </u>					1
	HYPOTHE TICAL PROTEIN?	SOYBEAN CHECKOTIC MOTTLE VINUS		54	346-307	658.700	L		4
2	HYPOTIG TICAL SS 7 KD PROTEIN	SULFOLDBUS VIRUS-LIKE PARTICLE 33VI	Τ	Ī					4
	II VEGING TICAL PROTEIN B	SOYBEAN CREOKOTIC NOTTLE VINUS	L	114.221					
		THE PARTY OF THE P							

		M. Viennes (am heater)			П		П	П	
	A11.VIO118		AREA LABOR	7387	4	738	1	44	1000
177	Visiona payon payon in the payo	TOWLPOX VIRUS IISOLATE ID-A IIINIUNICII)	5.00					1	
ı		DOME POR VISUS HISOLATE HP-418 MUNICHI	-37 61.95					1	
100 VA		TOWN BOX CHELS (150k ATE 10 ATHRIDADE)	15.149						
P. Boy Fourty		CONTRACTOR ATE UP ATEMICINE	44.378						
PINIO FOWPM	IIIYPOIIETICAL BANIII ORI 7 FROTLIN	CONTROL VIEWS (1904 ATE 119.4 MINISTER)	157:331						
PIRIZ POWPM	HYPOTIG YEAL BANGINGEN TO THOUSEN	DOWN BOX VIEW (1501 ATE 19-4) ([ALINEALISE	11.13	α					
PUBLI FOWPM	INPOSTE TICAL BANINGON IS PROTEIN		137.163						
PyRL2 [8V	HYPOTIC HEAL BANKING IN PROPERTY	N FILEPESSIAUS 4)	138.506						
PUDINI MEVS?	VOICE 10 10 10		147.188						
No lower	200	COUNTRY CARITY (CARATHER)	160.204						
PICAL HSV0	SIYPOTIE TICAL 36 FRO FROILIN	CANERY CASE A CR. DISPOSE CATELICACTE AND INC. 11 (MIDLIN)	18.31						
PI GAT HSYNDA	OL YLOPROTEIN		16.31						
PINI VACCV	GITCOTROIC	Ī	11.71						
PYRES VACEV	HYPOTHE FICAL 21 7 KD HINDHI-C PROJEIN	CAPTORIS CARING STREET	34.50	11					
7) KR: 20V	IIYPOTIE TICAL HOST KANGE J' 4 KD CROICIN	BOS. B. HILLSIAN HERPESVIRUS 41	16.51						
PILIS ADE41	INPOTILE TICAL BEAUT PROTEIN	•	39.61						
יוני נפי	5	NOT. BY CHILDIAN IS BUESVIRUS 4)	67.123	 -					
PIORI COMIV	HYPOTHE TICAL BLRF7 PROTEIN	-	24.147	<u> </u> 					
איניסט נפטני	HYPOTHETICAL 13 KD PROTEIN		11:11						
אימעז רפרא	IIVPOTITETICAL IS NO PROTEIN	STATE CONTRACTOR	189:134						
7 OR 1771	IIIYPOTIGETICAL 28 4 KD PROTEIN	STATE OF THE TENAN VIBILS I (STRAIN KRAIN (TIVI)	16.34		_				
PIONI ADEGI	HYPOTHETICAL 4 9 KD PROTEIN	THE MANUFACTURE OF THE PARTY OF	10.00						
PICKA TIVI	HYPOTHE FICAL 11 3 KD PROTEIN	AVIAN ADENOVIACIO ANTANA VIENE I CERAIN REALITIES	100						
PORD TIVE	HYPOTHETICAL & I KD PROTEIN	THE EXICURITY OF THE PARTY OF T	10.110	 -					
riner Tivi	IIVPUTHETICAL IS 4 KD PROTEIN	THE PRIOR OF LEAST VINCE ASSESSED FOR THE STATE OF THE ST		<u> </u>	 - 				
PLUAL, TIVE	HYPOTHETICAL IS 3 KD PROTEIN	HELDSOFTGO SECTION OF SECTION SECTIONS	-						
PLUED TTVI	HYPOTHETICAL 16 & KD PROTEIN	THE LANGE TO STATE OF STREET AND THE ALL STREET	-	<u> </u>					
Pinat IIVI	HYPOTHETICAL 7 3 KD PROTEIN	THE PROPERTY OF THE PROPERTY FAMILY STATES	\$10:112	<u> </u>					
P108W 11VI	MYPOTHETICAL 33 7 RO PROTEIN	THE PROPERTY TEMAN VIEWS OF STRAIN KRAINTIVIN	•	<u> </u>					
P.P.12 B.TOV	HYPOTHETICAL 13 I KD PROTEIN	BITCH TINCED BATH LEADAN VIBUS RIBY	1 1 1 1 1 1	<u> </u> 					
EVP12 BTBVP	HYPOTHETICAL PIZ PROTEIN	TE SHILL IPPINESS (RT				_			
P1 P1 R 10V	MYPOTIGTICAL PIZ PROTEIN		11:101 104-157	2					
P. P. R. B. VO	HYPOTHETICAL PTO PROTEIN	TE PITT (PPINES) IRT	11.101 104-137						
PYP46 RTBV	HYPOTHE TICAL P14 PROTEIN		T	5					
PYP44 ATOV	HYPOTHETICAL PAGENCY	TE PHILIPPINES) (RT	107-231	=					
P) P63 NPVAC	III TO THE LICAL THE TAU IN THE CONTROL OF		12:33						
PINA TRVA		FOBACCO MECROSIS VIRUS (STRAIM A) (TNV)	148						
TO LOS	AVOIDE TICAL 11 A RD PROTEIN IN POLYTIEDRIN S	AUTOGRAPITA CALIFORNICA MUCLEAR POLYHEDROSIS VIRUS (116-153						
Adapt Toxa	HYPOTIETICAL 17 3 KD PROTEIN	DRECTIOUS PANCREATIC MECROSIS VIRUS (SEROTYPE IASPER)	25-46						
PYO! ALEPY	ILYPOTHETICAL 76 KD PROTECN IN TK STECTON	AMSACTA MOOREI ENTOMOPOXVIRUS (AMEPV)	1	T					
DAVE 11 STAND	HYPOTIGICAL PROTEIN IN TK SAEGION	ALISACTA MOGREI EMTONIOPOXVIRUS (AMEPV)	45.70						
DAVE HEVE	HYPOTIG RICAL PROTEIN NO	HERPES SINDLEX VIXUS (TYPE 6/STRAIN GS)	H	1	1				
DAVE HIVE	HYPOTHETICAL PROTEIN IU!	HENDES SINGLEX VIRUS (TYPE 67 STRAIN GS)	1			-			
NAME OF TAXABLE PARTY	INPOTITE TICAL PROTESM IVA	HEIVES SINDLEX VIRUS (TYPE 6/STAAIN GS)	332.286	3		-			
VARI FRV	REPETITIVE PROTEIN ON 3	CHILD INDESCENT VIXUS (CIV) (INSECT INDESCENT VIXUS TYT	?		 	1			
VEL ENV	HYPOTHETICAL BRASI PROTEIN	EPSTED-GALA YAUS (STLAIN BOS-B) (ILLAIAN IER PESYIRUS 4)	Print	+					
VIII EBV	INTOTAL BIRE! PROTEIN	EPSTEIN-BALL VIXUS (STRAIN B95-6) PILAKAN HERPESYIKUS 4)	//	1					
OVEN CALL	1				-				
AVAC VACCC	HYPOTHETICAL 24 6 KD PROTEIN IN UBIQUITIN 37L		13.40	ž		1			
PYVAG VACCE	HYPOTHETICAL IS SKD PROTEIN	VACCINIA VIRUS (STRAIN COPENHAGEN)	1						
PYVAN VACCE	INPOTHETICAL 93 KD PROTEIN	VACCIDITA VIRUS (STRADI COPENHACEN)	1111						
PYVAN VACCO	HYPOTIETICAL 14 1 KD PROTERY	VACCINIA VIRUS (STRAIN COPEMIAGEN)			 				

	AREAS AREAS AREAS SAFAL SAFAL												
	Г	ARIA SAMO											
		AKEA1 14	13.57			11-41	29:90	46.30	-	1301		9:33	
	in the second section is a second section in the second section in the second section is a second section in the second section in the second section is a second section in the second section in the second section is a second section in the second section in the second section is a second section in the second section in the second section is a second section in the second section in the second section is a second section in the second section in the second section is a second section in the second section in the second section is a second section in the second section in the second section is a second section in the second section in the second section is a second section in the second section in the second section is a second section in the second section in the second section is a second section in the second section in the second section is a second section in the second section in the second section is a second section in the second section in the second section is a second section in the second section in the second section is a second section in the second section in the second section is a second section in the second section in the second section is a section in the second section in the section is a section in the section in the section in the section is a section in the section in the section in the section in the section is a section in the section in	The second secon	JRUS	VACCINIA VIRUS (STRAIN COPENIAGEN)	VACCINGA VIEUS (STRAIN COPENDIAGEN)	VACCEDIA VIBIR (STRAIN COPENIAGEN)	ALCINA CITY OF THE WORLD CENT	VACCEDIA VIRUS (STANDA COPERTINALE)	VACCOMA VIRUS (STRAIN WR)	VACCINIA VIRUS (STRAIN WR.)	VACCINGA VIRUS (STRAIN COPENIAGEN)	CAPCTURE VARIATION COPENIAGEN	
		A CONTRACTOR OF THE PROPERTY O	X	V VIII	VOTIGITICAL 19 KD PROTECT	POTMETICAL 1.4 KD PROTEIN	POHISTICAL 92 KD PROTEIN	V NOTICE I SEED MOTERA	TOTAL SECTION	V Caronina a series and a serie	TOTHE INCALL 1 AND THE PROPERTY.	POTICITION, I 4 KD PRUIES.	POTHETICAL SI KD PROTEIN
			שנינוני	FILE SANIE LEB	PYYTH VACCC	PVVCC VACCC	3	TANK BOLL	PYNDB VACEV	או בע אענגא	PYYOR VACCC HI	PYVILA VACCC	

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TABLE VI

107 X 178 X 4 SEARCH MOTIF RESULTS SUMMARY

FOR ALL VIRAL (NON-BACTERIOPHAGE) PROTEINS

	MCCENE	147117814	All Vivanes (no becteriophages)	T	NCA 3	AREAL	381.44	ABEAS	10110	T THE	1864	AKTA C
	HI WASH	PROTEIN		Γ	987.1114		!				Ī	1
	AND LINES	POT 154 KD PRO		Т							Ì	:
The Activities	MAY LINVAL			1				İ				
DETA APPLIES THE APPLIES	THE LINE OF THE PARTY OF THE PA		SEPATITIS DEL TA VIBUS (1501 A 1E AMILILICAM)		-							
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	Y V	CONTRACTOR OF THE PROPERTY OF	TOLLATO BUSHY STUNT VIKUS (STILATN BS-1)	8								
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PCOAT THICKIV	COAT PROTEIN	TOBACCO MILD CREEN MOSAIC VIRUS								1	
PCOAT TMV	COAT PROTEIN	TOBACCO MOSAIC VIXUS (VULGARE)	104-12							1	Ĩ
PCOAT TAVCO	COAT PROTEIN	TOBACCO MOSAIC VIAUS (STRAIN COWPEA)	76-138					٦			
KOAT THUDA	COAT PLOTEIN	TOBACCO MOSAIC VIRUS (STRAIN DAILLEMENSE)	3				Ì	1		+	ا۔
PCOAT THYEL	COAT PROTEIN	TOBACCO MOSAIC VIDUS (STRAIN ER)	104-133					Ì	 	i	ļ
PCOAT TAVO	COAT PROTEIN	TOBACCO MOSALC VIRUS (S) RAIN O and KOKUBU)	<u>=</u>						i	+	-į
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PCDAT TNVA	COAT PROTEIN		60-10							j	
PCOAT TRIVES	COAT PROTEIN	TOBACCO RATTLE VIRUS (STRAINS PSC and PLB),	110-145								
PCOAT TYBVA	COAT PROTEIN		16-31							1	ļ
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PONE? ADEO?	EASTY ESA DNA-BINDING PROTEIN		66-73					ļ		-	ĺ
PONE EBV	MAJOR DHA-DINDING PROTEIN		117-100-	104 - 1066					1		
PDMSI HCMVA	MAJOR DNA-BINDING PROTEIN	AIN AD169)	3						1	+	
PONSH LENSA	MAJOR DNA-BINDING PROTEIN		2	513-534						1	Ī
PONEL MONYS	HAJOR DNA-BOODING PROTEIN	AUTUME CYTOMEGAL OVIRUS (STRAIN SAILTI!)	=					1	+	†	
POVEL POVIC			*						1	1	
PONEL PORVC	-BONDONG PROTEIN	SOUTH CYTOMEGALOWING (STRAIN COLBUIN)		46-176				1		\dagger	Ī
PENEL VACCC		VACCINIA VIRUS (STRAIN COPENHAGEN)	ż	M -				1		\dagger	Ī
PDMI VACCV	DNA LIGASE	VACCINIA VIRUS (STRAIN W.R.)							1	İ	Ī
POYEL VARV	DNA LIGASE		3	22:149	3					1	
PDPOL ADELL	DHA FOLTHEBLASE		7						1	1	Ī
POPOL CREPV	DNA POLYNGRASE	ENTORIOPOXVIRUS	•	207-740				1	1	\dagger	Ī
POPOL CHANS	DNA POLYNGRASE	CHEORETLA VIRUS NY 3A						1	†	\dagger	Ī
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POPOL MPROS	DNA POLYKSILASS		311.133								
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PENY BIVE	ENV POLITICION	PACIFIC SALVA PROPERTY VIEWS (ISOLATE 123)	7	1			1	ļ			<u> </u>
SENO BIVE	ENV POLYPROTEIN	BOVINE INCOME THE PROPERTY OF	104.17								ļ
	SALV PAY VERATERY	BOVING LEUKEMA VIRUS (ALERICAN ISOCALETEN)	1				L	_			_
PENV BLVA	EN PACIFICA	SOUTH STREET VALUE (AUSTRALIAN ISOLATE)				ļ		ļ		L	_
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WAY THE DESIGNATION OF THE PERSON OF THE PER	INV NOLYPEDITED	EQUINE DI ECTINOS AMENIA VINOS (STILLA)	444.913								1
10000	TOTAL BOX VORDITED	EQUINE DO ECTIOUS ANEMIA VIGUS (ISOLATE WYCHING)		777				L			
DA LLAY	ENV POLITICAL PROPERTY.	ITEL INFERROCENDUS VINUS ECE!								L	L
EN FEW	ENV POR YPRUIED	TEST KIN BENEVERIETE NOV VIRUS (150LATE PETAL UNIA)	650-630					-	ļ		L
PENV FINE	ENV POLYPROTEON	SET TO BE A MANAGEMENT OF THE MAIN ATE SAN DIEGO	639-648	730-747							1
PLAN BIVED	ENV POLYPROTECH	PETITAL DESCRIPTION OF THE PROPERTY OF THE PRO	640-616	171.748		_					1
	MATORIAN NOT AND	FELDIE DOGROOEFICENCY VINUS (130CA) E 17C/				L	_				
	THE RESERVE	TET THE FIRE FIRE PROVIDES (CLONE OF E4)				1		ļ		L	L
PEN FLVC	ENV POLYPRUIES	THE TREATMENT WAS IN TRANSPARING ASSOCIATION AND ASSOCIATION OF THE PROPERTY ASSOCIATION OF THE PROPERTY ASSOCIATION OF THE PROPERTY ASSOCIATION OF THE PROPERTY ASSOCIATION OF THE PROPERTY ASSOCIATION OF THE PROPERTY ASSOCIATION OF THE PROPERTY ASSOCIATION OF THE PROPERTY ASSOCIATION OF THE PROPERTY ASSOCIATION OF THE PROPERTY ASSOCIATION OF THE PROPERTY ASSOCIATION OF THE PROPERTY ASSOCIATION OF THE PROPERTY ASSOCIATION OF THE PROPERTY ASSOCIATION OF THE PROPERTY ASSOCIATION OF THE PROPERTY ASSOCIATION OF THE PROPERTY ASSOCIATION OF TH	490-519								-
PEN ILVG	(ENV POLYPROTEIN		\$10-339						$\frac{1}{4}$	-	+
1011	JENN BOX VPEGIEDA	FELDIS LEUKEMAN VIKUS (STRAIN LANDON CO.)	443.616			-			_		
	CONTRACTOR COMPANY	FELDA U UKEKIA VIRUS (STRAIN SALMA)			100 271		-	-	L		_
1000	CAN COLUMNIA	HABALA SPUNIARE TROVING	-			-		-			-
₹ 000 ×	ENY POLYTRUIEIN	THE SAME CANDELL CANDER AND CANDER AND SELECT	265								<u> </u>
NA BEVGA	ENV POLYPROTEDY	FELINE SALCOMA VINOS (31 PAGE)	200			_					1
	ENV BOY VAROTEDA	FELDIE SARCOMA VIRUS (STRAIN CA)							_		
3	Printed September 1	(FEI THE SANCONCA VOLUS (STRAIN SN!)		1		-					_
PENS PENSO	ENV POLITING BUY	THE SALE AND THE PRESENT A VIEWS	176-203			}			-		-
VEN GALV	ENV POLYPROTEON	MIT NI WAS STANDARD TO SELECT THE SECOND STANDARD TO SECOND STANDARD STANDA	342.376					-			+
SEN URITA	ENV POLYPROTEIN	HOMAN I CALL LE CALCA CALCA CALCANIANT A 101	341.134							$\frac{1}{1}$	+
41.00	LENY BOX VOROTEIN	PARKA T-CELL LEUKENDA WAUS 1775 (COURS)	111111		L	L		_			_
	100000000000000000000000000000000000000	HABAAN T-CELL LEUKBADA WAUS TYPE I (ISOCATE KIT-2)						-	-	L	L
PON HILLIN	ENY POLITICAL	HANAN PARIT TRINSMIA WAUS 179E II	336.170				-		-		ļ
25 H 20	ENV POL TPROTEUR	THE STATE OF STREET OF STREET STREET STREET STREET	24-502	6 10-612	200				+	-	ļ
PENV HVIA	ENV POLYMOTED	FUNDATE SECTION OF THE PROPERTY OF THE PARTY	345.594	(9)1-663	395.0						+
I I I I	ENV POLYPROTEDA	HUNCH BOOKOOD KERKT VIRGITIES CONTRIBUTION OF THE	Sep. Sep.	1979	116.0	L					۲
100 PM	GAV BOL VPROTEDA	HANKAN DOADNOOFFICTENCY VIRUS 19TE 1 (UNIT FOLLA)	3	111.364	65.50	6.9.9.9	1187.4115	L			_
	THE RESIDENCE OF THE PARTY OF T	JABAN KANDOR KENCY VIRUS TYPE HIBIANN SOLATE				T			L		_
PENY HAIRM	THE PERSON NAMED IN COLUMN NAM	HINLAN BOADWOOLD ICHENCY VIRUS TYPE I (BRU ISOLATE)	2			110				-	-
PERV HVISK	DAY FOLTFOILE	LINKLYKE KALENDARISICHENCY VIRUS TYPE I ICDC-451 (SOLATE)	197-424	20.00		T			+		
PEW NVICE	ENV POLYPROTEIN	THE LAST THE MANAGEMENT OF THE TAPE THE LISOLATES	233.78	7	54)-541	621.610	-			1	1
PEN INIEL	ENV POLYPROTED [®]	HUNCAN DESCRIPTION OF THE PART OF A TAIL AND THE	36.38	117-119	111-111			_		+	<u> </u>
PAN LIVING	ENV FOL YPROTEDM	PRINCE PORTION PRINCE AND PRINCE	25.12	631-683	191-618	L	_				1
	eve les venotion	HUNLAN BOACHOOD KIENCY WHUS LIVE LINAS INC.		100	Т	52.13	L	-	L	_	
DIV HVID	THE PART OF THE PA	HABLAN BARBADODES ICTENCY VIAUS TYPE I (MID ISOLATE)				Т	-	-	ļ	-	L
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PER WITH		THE PROPERTY OF THE PROPERTY AND THE PROPERTY OF THE PROPERTY	3.4-3.63	077477	783.81	1	$\left \right $	1	ł		l

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PCCENE	1011/1264	All Vieuses (no becteriophages)	Y SY	AREA!	AREA 3	ARIA 4	ARFAS	ARFA	AREAT	AREAL	AREA 9
PENC NO KI	ENV POLYPROTEIN	HUMAN INGRUNODE/ICIENCY VIRUS TYPE I (STRA!N KII-1-GF))	Г	25.78	100	2.4.5			٠	7	
PENV HVILLA	ENV POLYMOTEIN	ILITALA BANDODE PICIENCY VIRUS 1 YPIL 1 (NIAL 1509, ATE)	245.505	12:10	74.136						
PENY HVING	ENV POLYPROTEDI	INDIAN ILDAMOCEFICIENCY VIRUS TYPE I (NIFA ISOLATE)		429-441	789-816						
PENV HVIDA	ENV POLYPROTEIN	HOLAN BOADHODE/ICENCY VAUS 1776 I (AIN 150LATE)		20.20	412.484	391-819					ļ
PEN HVINS	IENV POLYPROTEIN	HUBLAN BOACHODERCIENCY VIRUS TYPE I (NEW YORK-) ISOLATE)	╗						j	1	j
PENY ININD	ENV POLYPROTEIN	HEBITAN BOADNOOFFCIENCY VITUS TYPE I (NOK ISOLATE)	7	2					ĺ	j	
PEAN HVIOY	ENV POLYPROTEIN	HUBIAN BOALDAGEFICERY YOU'S TYPE I (OYI ISOLATE)	34.50	20.70	187.020				1	†	1
PENV HVIIV	ENV POLYFROTEIN	HUMAN DOLLACE ALIENCY VIAUS ITTE I (FYZ) ISOLATE	Ť	1		177, 777,	110 070		1	1	
MINI NG/	DAY POLYTROTEIN	HABLAR BOARCOOF (CERCY VINUS TYPE T JURIAT ISOLATE)	107-007	201-27			200		Ì	1	
S AA AA	ENV POLYFROTEIN	HILDOGAN INDICATOR FLUIDIC TO VIDOS TOPE TO STOLE SOCIALIS	7						İ	\dagger	
SEN HAIR	ENV FOLTFROTEIN	HORACA DEMONSTRATION OF VINCE 1778 1 (812) INCATE	Ī						Ì	İ	
PENV HVIX	LINY FOLYTROIEIN	HUMAN BENCHAUSE RUBALT VINUS 1778 (194 ISOLATE)	Т		Į.			I	-	÷	į
PENV NVIWI	EKY POLYFILDIBIN	HUDGAM INDICATED TO THE TOTAL	T						Ì	1	
PENV HVI IN	ENV POLYMOTED	HUBILA DOMINOCEPINE OF VINUS 1778 1 WALL ISON ATE.	X			1			İ	1	
PENV HVIZ	ENV FOLTFRUIELW	CHARLES IN THE CONTROL OF THE PARTY OF THE P							İ	İ	i
AND TRUING	ENV POLITICISM	THE TANK THE PROPERTY OF THE P	Ť	Tot to	1	61.00		Ī	İ	 	1
PLAN INTE	SENV BOT VEROTEIN	HONAN MANDED FIRE IN POLICY PORT 1.2.14 (C) ATT	T	109:1	614.678	100			-	!	į
PENN NAME	FAV BOLVER TRIP	HABLAN BOADSODESICIENCY VIEUS 1726 1 (2 ALE 12 3) SUI ATE.	7	97.646	- 12				İ	Ī	
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ACAN DAME	MATCH IN VALUE IN	INTERIOR INCOME TO THE PARTY OF THE PARTY AND THE PARTY.	Ļ					İ	İ	İ	:
STAN AND	TOTAL PORT OF THE PARTY OF THE	THE REPORT OF THE PARTY OF THE	Т	37.46	- 10.71	114.14			İ	Ť	İ
	CONTROL OF THE PARTY.	THAT IS NAMED TO BE TO THE PART OF THE PAR	Ī				1973		İ	İ	i
VENT MYZOI	ENV POLITICIONE	TOTAL BEAUTIES THE STATE OF THE	Ī		-				i	-	İ
VENY MYZNZ	ENV FOL TPROTECT	THE MAN DOCUMENT HERE I THE STREET STREET	T		$\overline{}$		£ 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2		i	İ	-
NOW MAZED	ENV POLYFROTEIN	HAMAN DEPARTMENT FOR YINGS 177E 2 (1904 A) E FOU)	╗				İ	-	i	+	7
DV MAIN	ENV FOLTFEOTEIN	SUPPLIED DOUGHOUSE FLIENCY VINUS 177% 2 IISULA 10 973 10 973	Т		9	780 674	j	1 !!!!	-	:	į
20 M	EAV FOL YEAR IN	HUMAN CONTROL ICIENCY VIRUS 1972 2 (ISOLATE SHILIST)	1		1		-	Ì	İ	1	-
VENT BIYES	ENV FOLTPROTEIN	TICHAN MUNICIPALITING VIROS 117E (ISOCATE SI)	+						İ	İ	Ī
TEN MOI	ENV FOL TPROTEIN	MINE CELL PUCUS-TURNING BIORINE LEUKENIA VIAUS		Ī			Ī	Ì	İ	i	
CON MON	ENV POLITICISM	AUNT CELL FULUE-FUREING PIURING LEURENIA VIRUS (1904A LE C.5.)			Ī			1	1	i	
W. T. W.	TOTAL CONTROL OF THE PARTY OF T	CAN MONTH ELECTRIC DISTR	200						İ	İ	
	CONTROL OF CHANGE	CASES TO THE PROPERTY OF THE PA		Ī						1	1
75.V. Z. V. V.	END FOR CHANGE IN	TABLE MONTH LEGISLAND VARIOUS (SOUTH ST)						1		\dagger	
PEN LE VIE	FIRST POR VALCETAIN	TREATMENT OF THE PROPERTY OF STATE OF THE PARTY.						Ť	Ì		Ī
L	ENV POLYPROTEIN	HOWALLY MARRINE LEUKEMIA VIRUS	216.540					Ī		T	1
ı	ENV POLYPROTEIN	KIRSTEN MUNDE LEUNZARA VIRUS	6-6			Ì		Ī		İ	
1	ENV POLYPROTEIN	MOLONEY MUNDE LEUKENIA VIRUS	\$03.543								Ī
PEN SEVED	ENV POLYPROTEDI	AADJATION AURDIE LEUKEAUA VIRUS	497.314								
L	ENV POLYPROTEDI	AADIATION MIXINE LEUKEMIA VIRUS (STRAIN KAPLAN)									
١	DAY POLYPROTEIN	HOUSE SANDALARY TUNOR VIRUS (STRADA BRA)	138-489	615-195						r	
PENV MARTVO	EAV POLYYROTEIN	LECUSE ELLIGIBLE TURIOR YIRUS (STRAIN GR.)		\$62-519							
PENY MONAY	EXV POLYPROTEDI	SDGAM MASON PELZER VIRUS	437.70			Ī				1	
/Dry Power	ENV FOLTFRUIEN	THE MUNICIPAL CONTROL OF THE STATE OF THE ST	Т					1	1	1	
AND BLOWD	ENV POLYTRUIES	OVER LESS TABLE SERVICE TO SELVE CONTRACTOR						1	1	1	
PENY MENY	ENV POLITICAL	CHAN DAMY WITH THE IT	1	100.75	T			1	1	†	
PAN CHAI	CONTRACTOR OF THE PARTY OF THE	COCAM BOALW VIRILE TITLE 1/2 CELAIN I K.1)	T	L	431.100	141.101		Ì		T	Ī
17/10/10/10	THE COURT OF STREET	CENTAL MANABORITORIES VICTORIA (ARTICIONAL ARTIC	Ţ,	T.	Т	10.00	16.5	Ì	Ì	T	I
SENT SINK	CAN PARTIE AND THE PA	CONTRACTOR OF THE CONTRACTOR O	Ť		Т		11.14	Ì	1	\dagger	
PEN STVAI	ENV POLYPROTEIN	SDAAN BAARNODESICENCY VINUS (ISOLATE AGA / CLONE GR. 1)	1	111-111	Т	614.701		T	T	T	Ī
PEN LIVA?	PAV POLYPLOTEDI	SPACEN BARDNODE FICENCY VIRUS (TYO-) ISOLATE)	T	248-216	Т	431.431			l	T	Ī
	ENV POL VPROTEON	CHAIN ANZ PE BOADNODE FICTENCY VIRUS	-	11.11	Т	10.76	137.164		\dagger	+	Ī
PAN SING	EXV NO. VPROTEIN	SPACEN BOADNODERCIENCY VIRUS (ISOLATE CB))	т		Т	784.816				t	Ī
PEN SIMI	DAY FOLYPROTEIN	SEGAN BEANNEDERCENCY VIRUS (ASSIST-8) ISOLATE)	т	930-609	631.318			Ī	Ī		Ì
PEN SIMA	ENV POLYPROTEIN	STREAM BEACHORPICEDICY VINUS (NOUS) ISOLATE)	114-113	277.266						l	Γ
PEW SIMM	ENV POLYPROTEIN	SIMMAN BRANDHODEFICIENCY VIRUS (KAW 150LATE)	193.404							l	

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			Г	34-310	103-111		İ	<u> </u>	1	:	
		S (STRAIN COPENIIAGEN)	Ī	_	302-332			İ	Ì	Ī	
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		EAIN DUMAS)				H		1	1	1	
	OTEN OTEN STANDARD MOTEN TARGET METEN				-			1	1		
	OTEN STOLENO MOTEN STREET OF THE STREET OF	THE REPORT OF THE PARTY OF THE				t					
	SECULING MOTEN		T	140 000		-			1		
	SECULING MOTEN		7		1		T				
	SFORUTING PROTEIN		٦	7	1		T				
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П	SFORKUNG MOTEIN			2		†	T				
	五色		136-169			t	†	T			
	É	VIRUS	116-147			1	İ				
Ī			69:59			1	Ì	1			
١	ŀ	Γ	1810-291			1	Ì	1			
T			144-131			Ì	1				
١	200 ST CONT.	ſ	621-646				1	Ì			
١			П	417		†	1				
POAG POAG		GIBBON APE LEUKEADA VIRUS	811:16			1	1				
٦	ALA CAROLEIA	HUBLAN BOACHOEVELLE VIRUS 1 TO 1 TO 1 TO 1 TO 1	111-10			1	1	Ī			
1		INDIAN BOADOOF CIENCT VINOS 17 F. L.	11:113			1	1	T			
- 1		HARLAN BOARBOOK! ICENCY VIRUS 17FE! (MR 130-5)	1			Ì	Ì	1			
_	GAG POL TPRUICES	SABLAN BOARNODE ICIENCY WRUS TYPE JUSTICE BUT			Н	Ì	1	Ì			
- 1		TOTAL BOARDOET REACY VALUE 1778 2 (1300-A) 15 (1300-A)	11:11					1			
٦	l	HERAN BEAUCOCK CENCY VINUS TYPE 2 (1900 A) C					1				
	GAO POLITICO ELE	HIGHEN BOXINGOED ICENCY VIRUS TYPE 3 (130LATE 31)	186.397								
	THE TREATMENT OF THE OWNER WAS THE	HIGH TER BITIACISTED AL A.PARTICLE	9	101-101	918-168						
FGAG BHIA METRO	LETT COVERED A THE CASE FOR YPEOTE	TINOUST INTRACISTICAL A PARTICLE	9								
	6	LANISE DITACISTANAL A.PARTICLE	100	1				1			
	TED OWO TOTAL	LICELLY LANDIALY TUNOR VIRUS (STRAIN BRA)			 						1
		LADICE LIANDLATY TISHOR VIRUS (STRAIN CIN)		10.10		T					1
		LOUGE MAJORALY TEMOR VIRUS (STRAFFI GR.)	5								
0		FINALAN MASCIN-PIZER VINUS (NOMV)		134.463							
		SACOMATONYCES CENEVISIAE VIRUS L-A	19		<u> </u>						\downarrow
	5	ENAM BOOMNOOF ICENCY VIRUS (ISOLATE AGAI) CLUNE UN!)			-						1
П	GAG FOLYPROTEDS	THE THE BOATHODE FEETENCY VILUS (KIW ISOLATE)		1							
	CAC POLYPROTEIN	PRATAIN TRADESICIENCY VILUS (STA 150LATE)		1	İ						1
PGAD SIVAIS GAD FO	GAÖ FOLYPROTEDI	TINAN BARBERGENCY VIRUS (\$236SLATE)		1	İ						_
Γ	GAD POLYPROTEDI	STATISTICS OF STATE OF VIRUS (PBIACE) ISOLATE)			+	T					
Ĭ	GAD POLYPROTEIN	THE ACT OF STREET		1					L		
,	GAG FOLYPROTEDI	FEMALUAL PROVIDES SEV.		17.							
ľ	GAO POLYPROTEDI	EXTENSE LEGISLES VILLES TYPE I (STRAIN ABAP)			1				_		
	PROBABLE RELICASE	THE SECURITY SANUEL IS TRADA 11)		15	1						
		UNEITED A FOSTER VINUS (STRAIN DUNAS)			1						
Ī	PROBABILE IGENERAL	SE BOYDE COLONAVOLUS (STRAIN PLS)		1						1	1
	ENACHUTURE ESTRACE MECHES	SEPTEMBER BOYDE CORONAVALIS (STEADY LY:138)		-							1
	HENADOL UTDONES I BANK THE TANK	THE PROPERTY OF THE PARTY OF TH									

CENE	100017554	All Virenes (se betterfephages)	Т	*****		7 7 4 9 7	ABVAC	ANTAG	A REA ?	AREA	AREA 9
TILE HAME		VIRUS		4	т		Г	Т			
DAA CVBO	NECURSOR	BOVING CORONAVIRUS (STRAIN QUEDEC)			T						
PIEMA CVIOC	HIEMAGOLUTININ-ESTERASE PRECURSOR	HUBIAN COROMAVIAUS (STRAIN OCC))	788-741								
MELLY TAKE	HISTARCOLLY INDIN PLACURSOR	INSTITEMEN A VIRUS (STRAIN WAICHUOMS)	367-653							ŀ	
24.4	HEMACOL IN MAN PRECISE TOR	INCLUENZA A VIRUS (STRAIM ADANCKOKIM)	24-51	10.1							! L
CHIEF THE	INSTANCED IN NOW PRECINGOR	INSTITUTAL A VIRUS (STRAIN ABUDGERUGARAIOKKAIDOVIAT)	381-451								i
111	Transfer in Son	MIGHTENZA A VIAUS (STAXIN ACANGLANDACOLIANS)	9.36								
	SELVANCE INFORM BERGINGON	DOLLENZA A VIBUS (STRAP) ACHICKENALABANAIM)	181-181								1
	THE PARTY OF THE PARTY DESCRIPTIONS	INSTITUTED A VIRUS 1818AIN ACTUCKENCERMANYAVIOL	31-34	111-441	494.528	ĺ				1	
1	CONTRACTOR OF THE CONTRACTOR O	THE CHAPTER A CORPORATE AND HER BANGEMENT CONTAINED	200								
EMA MOK	HEMAGGE UTWIN PREL URSUM	THE COURSE A COURT OF STATE AND A STATE CONTRACT OF STATE	1	į	:	:	:				
MIEMA IACKO	HEMACOLUTINIH PRECURSOR	INTERICA A VIAUS ISTRAIR ACTION REPORTED TO THE PROPERTY OF TH		177.71	Ī						
EMA IACKY	HEAVACALUTININ PRECUASOR	INCLENZA A VIRUS (STRAIN ACTICA ENVICTORIALIA)									
HEAT LABAN	HELLAGGE THE BON PRECURSOR	INSTITEMENT A VIRUS (STRAIN ANDICKIAL BERTAZIVIA)	381-450								
177	THE CLASSIC THE NAME OF PERSONS	THE LEWIS A VIRUS 1STRAIN AND KINAL BERTANO 161	(57-57)	190.543		اً					
	TOTAL STREET STREET	WALLENZA A VIBITS OF BAIN AMERICAL BERT AND VA	147.653								:
ENGA MOAT	INCHARCALUININ PILL URSON		1	411.434							_
PIENA LABA	HELLAGGE UT THIN PRECURSOR	INFLUENZA A VIRUS (STRAIN ACIAC EVALIDER (ACIACA)			: :	!	į		:	: : :	:
SHELL APPER	IIS MACCA (TIDEN PRECINSOR	INFLUENZA A VINUS (STRAIN AMACKACZECHOSLUVAKIA)6)	31.631	İ							
1000	CELLA COLLINATION BARON IN COL	INFI LENZA A VIXUS (STEAM ADMICK/EMCLANDVIVS)	31.55	402-411	26-33						
200	TOTAL STREET	PARTIE DE A VIBILIE SETBAIN APRIL PRAINCE AINCVITE	10-11								
HENA MOHI	INMAGGLUTININ PRECURSOR	INTEGRAL A VIACE LE PORT PORT PORT PORT PORT PORT PORT PORT	1								<u> </u>
PHEMA LADAR	HELLAGGLUTINGN PRICURSOR	INFLUENCA A VIRUS (STRAIN ACCIONAR NATIONARIA)									
RLA LABA	HARLACCITY ININ PARCUMSON	INFLUENZA A VIXUS (STRAIN ADUCKAIOKKAIDOVI MO)	1	İ							
111111111111111111111111111111111111111	SPECIAL COST THE NATION BENCHMENTED	INFLUENZA A VIBUS (STRAIN A/DUCK/NOKK AIDO/1/12)	711-437			į	ı		:		_
	TOTAL STATE OF THE PARTY OF THE	THE HENY A VINING REPORTED AND PROPERTY PAINTINGS			:						
HIEMA IADRIS	HEMAKALUININ FRELURSON		117.111								
ENA CABIN	HEMAGGLUTININ PRECUMSOR	INPLUENCA A VINUS (STEVEN AUGUSTUMENTO)									
HELLA LABAT	HELLABOLUTION PRECUISOR	INFLUENZA A VIEUS (STRAIN ADUCKANOKKAIOO/10/15)	169-146								
HUA TANK	THE LA COLL LIM SOME PROPERTIES	BULLENZA A VIRUS (STRAIN ADOCKARELAND/11)A1)	415-445								
STREET TANK	DELLA PART INTERNATION OF INCOME.	THE LIBRICA A VIBLIS ISTRAIN AND UCKNEACH IIS SAW16)	31.56								
1	THE STATE OF THE S	SARTIFELY A MIRTIE STRAND AND STRANDHIS NO 20/20/201	387483								_
MCMA MORO	HENCOLLUI MIN TRECORSON	THE PROPERTY OF THE PARTY AND	11:31								L
HENA MON	PENAGRAUTEM PRELUASOR	THE PERSON AND ADDRESS OF THE PERSON OF THE	1								
EMA MONY	HEMACGLUTDON PRECURSOR	DOLUENZA A VIRUS (STRAIN ACIULINEM TUNO (A 18)									L
HEMA IADM	HEMAGGLUTING PRECURSOR	DOLUENZA A VIEUS (STRAIN ADUCEMPEW ZEALAND) (776)									
HEMA MOU!	HEMAGGLUTED PRECURSOR	INTELENZA A VIRUS (STRAIN ADUCECURRAINE/IND)									ļ
HEMA LADUS	I EMACOLUTING PRECUTSOR	DIFLUENZA A VIRUS (STRAIN AOUX KATKANACIAS)	200								
MEM MEM	HEMADOLUTION PRECIMSOR	INTLUENZA A VIRUS (STRAIN AENGLANDATUST)	2								
ELIA LABOT	HEMAGG UT DON PRECURSOR	DOLUMEA A VISUS (STEATM ACHOLANDOSIM)	40.67	3				1			
PICHA LAFPR	HEMAGGLUTPIN PRECURSOR	BUILDENZA A VINUS (STRAIN AFOWL PLAGUE VIRUS ROSTOCK))	177-221	11442							
PHISTAL LACER	HEMAGGLUTTON PLECURSOR	DOLUDIZA A VILUS (STRAIN ACREY TEAL/AUSTRALIA/2019)	341-451								
HISTORY VACOR	HELLANDS DROWN PARCINGOR	DOFE UENZA A VIXUS (STRAIN A/GUELANARYLAND/100/17)	505-533								
ALTERNA ACTUA	NEWACCH LITTERN PARCHASON	BOLLENZA A VIRUS (STRAIN AGULLASTRAICHANDIA)	504-531								
PEACE LAUX	LISTA AND THE PARTIE TO BE	DOLLENZA A VIRUS ISTRAIN AROUND/LALGIERS/12)	366-452								
THE TAIL AND A	THE LAKEST THE PARTY IN COR.	DOLUMENZA A VINUS (STRAIN AMARIDAVIAL)	75-62								
	THE LANGE OF THE PARTY OF THE	DOLLIESCA A VINUS (STRAD) AFOUNDECAMBRIDGE/(61)	3.52	154-221	187-111						
NEW TANK	LIE LA CATE TREMA PARCINESON	NOTEBOOA A VINUS (STRAIN A EQUINE CAMBRIDGE (77))	75-22	14.23	18-13				L		
STELLY LABOR	HELLACOL STRANS PRECIENCE	INFLIDICA A VIALIS (STRAIN AROUNE)C DETROIT/////	39-36	127-161	453-884						
THE PARTY OF THE P	Deut Act Install ber Citi ton	DOT UNITAL A VIBIUS (STEAM A COUNTED BURGITIMA)	35-52	165-231	311-437						
Valvi Valvi	CHALLACO THAMAI BRECIMENT	RAFILIPAZA A VISUS ISTRADA A/EOUNG/FONTAINEBLEAU/16)	144.432								L
2011	THE DAY OF THE WAY SEED IN SOME	DAR JENDA A VIRLIS (STRAIN AFOUNE/RENTICK YAMS)	164-432								L
	TOTAL DESCRIPTION OF THE PARTY	TARTEMAN A COMPANY AND ARCHITECTURE SATISFIES TO	186-452					L			L
THE PARTY	THE STATE OF THE PARTY OF THE P	PAST INDIA A VINITE STRAND AND UNDA EXCHOLOGICAL	7.5	1 1 1 1 1 1	£ 173						L
THE REAL PROPERTY.	THE CASE OF THE PARTY BUILDINGS	INSTITUTE A VILLE STRAIN AFOLINGA ONDOMISIONI	×.	194-23	18457						
TIENA MALO	Ŧ	INCI (INV. A VIII)S (STEAD) AS OUNTEADAND(A))	186-451								
NEW MAR	i	PARTITION A UNITED AND INCOME AND INCOME.	11645								
TOTAL MADE	Ŧ	INCLUDATE A VICTORIAN AND INCLUDATION MARKETING	7	184-121	311-457						
MEKA MOON	HEMACKEUT INTO THE CAROLE	TAKET HEIGHT A CHRIST ATTENDANCE INTERPRETACT PROTECTION	36.56	127	18.637						
HEND WOLL	MEMACALO DATA PRECUESOR	INTELLIBRATION A VINITE OF A PACKET THE ACTION OF THE PROPERTY OF THE ACTION OF THE AC	116-453						L		
MENA MORO	TOTAL PROPERTY OF THE COLUMN TOTAL PROPERTY O	DATIESTA A VISITATION AFORMACIANTIACONAS	Î								L
WITH THE	THE PART OF THE PA	INSTITUTED A VIRIUS (STRAIN ACOUNTERAD PAULDIUM)	3.5	- F	15731			L			L
	TOTAL DESCRIPTION	THE LEGISTA A VIBLIS 1878 AND INCOMMENSAUTZER AND 13702	97.5¢	14.23	1711			L			L
PIEMA LAKSW	REMANDIANT PREADMENT	INCOCACA N TOTAL CONTRACTOR CONTR									

PCT/US95/16733

PCCINE	167117854	All Viranes (no bacterfophages)		口	1230	र रजार	<u>य</u> रहार	24	1			
FILE RAME	PROTEIN	CONTRACT A VIALUS (ST	10		1	1	T					
IAHTE	ICEMACOLLINDIN PACCURSON	RETTENZA A VIEUS (ST			İ	+	İ					
IAINO	HEMACOLUTINO PRECUISOR	INTELLIGINAL A VIRUS (ST	5UAY/IM3)		i			Ĺ	۲			1
PIEMA MIRR	INTERNACION PRECUESOS	DOLLENCY A VIRUS (STRAIN AUGALANDOWS)		Т	1 150	\dagger	T	T				Ì
3	THE MANUEL OF THE PARTY OF THE	INSTITUTE AZA A VIKUS (ST		T	117.00	+						
PIEMA LAKIE	MEMADOL DI INDIA PRECUMBOR	THE LIENZA A VINUS (ST		Ī,				T				
- 1	IEXAOGLUTING PALCINESON	NATIFICATA A VIXUS (ST	MATTERZA A VINUS (STEATH ANIAL LARDIAST RAKHANDAMA)		Ì	-	T					-
	DENADOLUTORN PECUASOR	THE PROPERTY A CHILINESS	RADI AAIALLALDASTRAKHAM763/113)		İ	1	İ	İ				
PHEMA (AMA)	HENCOCK LITTINGS PRECURSOR	TOTAL STREET	CHARLES A A VISITE SET BAIN ANIAL LANDINE W YORKINSTOTE	اء	-		İ	Ì	İ			
	HEMACOLUTININ PRECURSOR	IN CHANGE AND ASSESSMENT ASSESSMENT OF THE PARTY OF THE P	BAIN AAGENPHISTORY				1		t			
ł	HELLACOLLI ININ PRECUESOR	INPLUENZA A VIAUS IS	The second secon	199	111-131		1	†				
	INTERNACE IN BUILD PARCUASOR	DOLLENZA A VOLUS (3)	MILLENZA A VILLE (STILAIM APPLIANTING 14)	15:52	111-111		-		1	Ī		
	SELL FROM THE BOWN PRICEUTS OF	DOLUMBA A VINUS (ST	DGLUENCA A VILLE (STRAIN AND ACTUAL COME)	Ī	163-441			j	1			
3	THE TANK THE BEST IN CO.	INSTUENZA A VIRUS (ST	RAIN AMINE/SWEDEWIN							:		
MEDIA TAKIN	CANADA INTO THE PARTY OF	NET TRIVE A VIRUS (STRAIN ANTWOVA)	EAIN ANTWOVES)			<u> </u>		- ::!	:	•		
MEMA LANTS	PENACEURIUM PRECUESOR	THE LEWY A VIETE 151	MATTERS A VIETS (STEAM APILL) WITALL'ALAIM (12004)			1	Ť	İ	Ī			
HENA IAPIL	HENAGOLUTININ PRECUESOR		BANK ABIRETORICOUNT	**			İ	Ì	Ť			
SUPPLIES TANKE	TIENAGGLUTING PRECURSOR	INPLUENCA A VIACA IS	SE CHI A MINISTER	15-92		-	1	1				
1	WELLA CHAIN TOWN PRECUASOR	NECUENZA A VIAUS (S	POLICIAZA A VINUS (STANIO AND MANAGEMENT TO A STANIO TO A SERVICIO TO A	167-191		_		j				
X X	STATE OF STA	INFLUENZA A VIRUS (SI	PAIN ARUDOT 1000310 ACM.	11771								
	200 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	INSTURMENT A VIX.US (S)	PAPI ASEALMIASSACIUSEI I STUREL		1 1 1 1	(04.50)						
FICHA IASES	IEMOGLUTINIS PRECINGO	INTELLIBRIZA A VIRUS (S	ARTIFIED A VIRUS (STRAIN ASHEARWATER/AUSTRALIA/12)		Ť	+		ĺ				
HEAL MSH	SELACOLUTION PIELUSON	27 MINO 1 4 CASH 1 6 F. S.	MAN THE WAY A CHELLE LETTEN AND TAKE INCA ICTORIANS (SOURS)			1	Ī					_
HEMA LASTA	HEMACOLUI DEN PRECURSOR	IN LUENTA A SINGLE	THE PART AND ANY AND PARTY.	25.56		+	j	İ	Ī			L
THE LATE AND A	HEMACOLITINON PRECIMINA	DATUERA A VIRUS (3	CALL TO LEGISLAND AND LAND L	\$15.448					1			
	THE PARTY OF THE PARTY OF THE COLUMN TWO IS NOT THE COLUMN TWO IS	INTUENZA A VIRUS (S	NOTUENZA A VIRUS (STRAIN ATURKE TIMELANDI)			-						
A LATE	ICHACA UI MA CALCANO	STATISTICS A VIEWS (\$	PARTIERY A VIEUS (STRAIN ATURKE VAKINNESOTATION)									
PIESTA LATICAL	SEMACOLUTININ PLECUASOR	TELEVISION A STATE OF THE PERSON	TEAM ATURKE YOMTARIO 1111/44)	Т		1		Ī			L	
A LATKO	HEMACOLUTINON PILECUASUR	Station 1 Charles	PEALS AFTERE YOUT ARIONITIES?	•	Т		Ī	T				L
THE LAW AND THE	HENDOGETHENDS PRECURSOR	THE LUENCA A VINUE IS	THE PROPERTY OF THE PROPERTY O			787-101	1					
ŧ	HELLACKE LITINGS PRECURSOR	DAT LIENZA A VIAUS IS	DALLENZA A VIRUS IN THE ALLENDE CALIFORNIALS	419-400	\$00-536			Ì	1			ļ
	LIETA AND THE CURSON	INTLUENZA A VUIUS (S	TRAIN ALLONS THE SCHOOL STATES									
	THE PROPERTY OF THE PARTY OF TH	INSTITUTION A VIRUS (S	TRAIN ATERNALIST MALINO W. 1.3	Γ	111.455							1
1	CALLACA THE NOT DESCUESOR	INSTITUTE A VIAUS (S	PALDENZA A VIALIS (STRAIN ANDORWIOTITE)	Τ	416-218							1
	THE PARTY OF THE PARTY IN COLUMN TO SERVICE	INCLUIDED A VINUS (STRAIN AUSSANOTI)	TRAIN AUSSIANOTTI		17.11				!			1
	ICENTACE INC. THE CHANGE	PARTITION A VIRIUS (S	PARTITIONA A VIBIUS (STEAD) AVICTORUAYIMS)								L	
-	DESTRUCTION MECHANISM	SATISTIAN A VIEW OF	ANTIBODA A VINIS INTIA DA ANTISON SAUTIVIII			1					L	L
HELY LAWIL	MENDER CHEMINAL PRECURSOR	A 51 40 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	CONTRACTOR OF CASE AND APPLIANT ENGINEERS	X £		†						L
ALESA TANA	HENCHOLDINGS PRECURSOR	DO LUBACA A VICTOR	THE AND AVENDED CORADOV(77)	19-09	317.453							L
MANA IAZO	HESTAGE UTDEN MECUASOR	DALUESCA A VIII O	DALUBAZA A VIRUN (NI NI	107161								ļ
MAN AND	HASTA BATTITISM PRECURSOR	DOLLENZA A VINUS (S	TOTAL AND THE PARTY PARTY IN THE PARTY IN TH	117161								1
	THE CLASS OF THE SAME SEED OF STREET	PATUENTY Y NOVES (\$	THAIN ASWINDS HOW HOW THE THE		3							1
200	TO SECURE THE PROPERTY OF SECURE	DOLLOWA A VALUE (S	DOLLENZA A VIELS (STRAIN ASWINGANDIANA) 726/14)		3							
27	POTON PROPERTY.	INCHES A VIRUS OF	SALIENZA A VILLE ISTRADI ASVINEARV JERSEVI (716)								L	<u> </u>
15 to 1000	MENTOC LITTON PICE LINES OF	STATE OF THE PARTY AND ADDRESS OF	THE PASSA & CHARLES OF ANIA AS WINDARKELLINGS	317-433			Ī				L	L
HELL WALL	IGHTANGE UPDEN PRECUESOR	TOTAL STREET	CONTRACTOR CONTRACTOR AND MARKET CONTRACTOR	400-431	1346	1	Ī					L
PASTAL BASING	HELLINGOLUTION PRECUISOR	CALCACATA A CAST OF A CAST	TO A PARTHOUSE)	386-121	419-473						ļ	ļ
CHILLY AND IN	HELLANDE UTBON PARCHASOR	INTLUENCA B VICTOR	23 - 12 1 - 12 - 12 - 12 - 12 - 12 - 12	394-429	113-461						1	1
ALTERNATION OF THE PERSON	HELLICE TYPEN MECHASOR	DALUENZA B VIXUS	DELUENCA DE VICTO DE L'ACT	191-411	113-113							ļ
A112	LIFETA CALLIFORNIA PRECUESOR	THE FUENCY BYTHE	I LAIM BROWN ROSE	100-430	4117							1
	THE STANDARD PRINCIPLE OF	INGLUENCA B YOU'S (STRADY BALEDAG)	TRADE MEES (0)	017 911	436.435							4
100 V	THE PARTY OF THE PARTY OF THE COR.	DOLLING A B VOIUS	DOLLIEDATA B VINUS (STRAIN BALARYLANDOVS)		717							
HOA MAN	THE PERSON NAMED IN COLUMN TWO IS NOT THE PERSON NAMED IN COLUMN TRANSPORT NAMED IN COLUMN TWO IS NOT THE PERSON NAMED IN COLUMN TRANSPORT NAMED IN COLUMN TWO IS NOT THE PERSON NAMED IN COLUMN TRANSPORT NAMED IN COLUMN TWO IS NAMED IN COLUMN TWO IS NAMED IN COLUMN TWO IS NAMED IN COLUMN TWO IS NAMED IN COLUMN TWO IS NAMED IN COLUMN TWO IS NAMED IN COLUMN TWO IS NAMED IN COLUMN TWO IS NAMED IN COLUMN TWO IS NAMED IN COLUMN TWO IS NAMED IN COLUMN T	DOLUEDZA B VIXUS (DELLEGIA BURUS (STRAIN BACKONISMOS)							L		
AEM MAN	HEMACALUI STATE THE STATE OF TH	INSTITUTE A B VOLUS	HOLLEGEA B VILLS (STIALN BOLEGONSHO)			Ī				Ĺ	L	۲
N Post	MENAGGLUTING PRELUKSON	I DE LIESTA B VIRUS	STEATH INSTRUMENTATION								L	\sqcup
TY DOS!	HEMADOLU DON PRECUENCE	INSTITUTE A SALUS	STRAIN INUSSIVICONS)			1					L	L
PHENA DOUG	MENANCE UT DON PRECUESOR	DATE LENGTH B VIRUS	DATIENCE WILLY (STEAM EVICTORIANA)	101-114						L	L	L
A BOW	IEMADGE UTDON TELLUASIV	TANK TRUTA B VIETRA	THE PERSON IN COURT OF THE ACT OF THE PARTY OF THE PERSON IN COURT O	7	Ì						L	Ļ
HESA DON'Y	HENVOOLUTION PRECUSSOR	THE PARTY OF THE P	THE PARTY OF THE P	495-571								ļ
PHENA PROCA	HENLAGGE UT DOM PRECURSOR	TO PUT OF THE PART	POLICE CALCULATION (STRAIN CONT. AND/1920))	413-359						1	1	ļ
	SELLABOLUTORS PALCUASOR	DATUENCA C AMOS	STAND OF SERVICE CONTRACTOR	403.339						1	1	╀
	ISTANCOLUTION PRECUISOR	DAT USAZA C VIRUS	DELUMBAR CYRUS (STRAIN COREAT LALES THE STREET	462-336							1	+
	THE PART OF THE COR.	IBOULDOZA C VICUS	STRAIN CHYCOOLAI)					L	_			
	Charles and the same of the sa		10.00							1		

П	107517864	All Virnoss (no bacteriophages)	Τ	ARFA 2	AREA 3	AREA	AREAS	ARLAS	AREA?	AREAL	AREA
THENNE	Phoyette	With									
	HEMAGGLUTOWN PRECURSOR	DOLLERZA C VIEUS (STRAIM UR TOTOMIAL)									
HENY SICK	HEMAGGLUTOWN PRECURSOR	INFLUENZA C VIRUS (STILAIN CALISSISSIPPORO)									Ī
HEM NOW	HEMACCLUTION PRECURSOR	INSTITEMENT CYRES (STRAIN CHARMIS)								ŀ	l
Γ	SEMANGE LITINGS PRECURSOR	BALLENZA C VIRUS (STRAIN CAIGNEUNICHONI)	ŝ	ĺ							Ī
Ţ	HE MACOULTINOS PERCINAGO	DISTURNIZA E VIRUS (STRAIN CPICARLING/11591)	40.53	ĺ							1
T	CHELLA PART I THE WAY DE SPILIE SOLE	DALLENZA E VIRUS (STRAIN CPICHELINGASMIS)	413.559	1							Ī
N. P.	HEMACOLITIONS PRECINCOL	BULLENZA C VILUS (STEAP) CTAYLOW(17)1/47)	483-559								
н	HELLA COCK LITTERIAL BERGING COR	NELUENZA C VIBUS (STRAIN CYAMAGATA/1601)	411-539								
ı	THE PROPERTY OF THE PROPERTY OF THE PARTY OF	LEW PARTIE MERASE WARDS (STRAIN AUSTRALIA-VICTORUA)))	16-99								
ı	PEMAKALUI IMIN MEURAMININ NSB	THE PARTY OF THE P	19.43								
ı	HENACCE UT DON-NEURANDASE	ALICA CASTLE LASEANE VINCOLO INVESTOR DE ANTONIO	77.0								
	PENACKAL UTBADA NEUTAMINI DA SE	NEW CASTLE INSTANTATION (SIGNIN DIG 12)				L					
PIESTA NOVI	HEMACOLUTININ-NEUKAMINIDASK	NEWCASTLE DISEASE VIAUS (STRAIN BI-HITCHNEIUA)									
ATMA ABVI	INMACOR LITERDI-NEURAMINIDASE	NEWCASTLE DASEASE VIAUS (STRAIM ITALIENMS)	10.5	ĺ						-	:
TANK TO SE	AFTA CATA I TIDATA AFTA AMENIDA SE	NEWCASTLE DISEASE VIDUS (STRAIN MIYADERAS))	64.91								
	THE A COLUMN WITH WATER A MINISTER	NEWCAST SPISEASS VILUS ISTRAIN OUR ENSLANDAM	16-99								
Т	SHELLE COLL THE INVESTIGATION A CIT.	NEWPASTI RINGEASS VIEUS ISTRAIN TEXAS O B /40)	16.91								
,	HERMAND INGRANGUA AND A SECOND ASSESSMENT OF THE PERSON OF	CHANCA CON BY REALTH VIRING ACTION IN STRUCKS	1			L				I	
I	IEDIALOU INTERNEDIALOUS SE	MINAPORT MARKETS VIETA	20.00	1		L					
J	JEMACOLLI ININ-MEDILAMINIMASE	THE CONTRACT INCOME. TO SELECT AND TO A SELECT OF SELECTION OF SELECTI	X.16	166.193			L		L		
,	JONANGOLUTIMIN-MEURAMINIDA SE	NUMBER OF STREET STREET	į								
HELL PIDS	HEMAGGLUTININ-NEURAMINIDASE	BOVING PALAUP LUENCA 3 VIAUS									
PHEMA PUSH	JEMACCLUT DATH WEUTANDUDASE	HUMAN PALAING LUERZA) VIRUS (SERAIN REH 47002)				1					
HELL PURA	HEMACOL UT DYDK-NEURALDWIDASB	HUMAN PARADGLUENZA 3 VIRUS (STRAIN AUSTINISATA)									
PIESZ PURT	HEMACCALUTIND - WEUTAMINDASE	HUMAN PARADOLUZNZA 3 VIRUS (STRAIN TEXMOTO)	2.7					1			
MENT HIRI	HEMACAL HEINN-NEURAMINIDASS	HUMAN PARANGLUENZA 3 VIRUS (STRATN TEXPIOSAZ)	33.70								
THE PERSON	HEMACKS ITTEMPORT MANDENERS	HILLAN PALAINGLUENZA 3 VIRUS (STRAIN TEX/12677/11)	17-61								
Ţ	HEAT COLUMN NET TO A MAINTE A CANADA	IN BLAND BARDET URNZA 3 VIRUS (STRAIN WASHWAITH)	13-61	L							
I	TEXT COLUMN TO THE ACTION AND A COLUMN TO THE COLUMN TO TH	IN MALE BARANNI ITEMPA S VIRENS (STRAD) WAS (VISINI)	17-11			L					
T	MENTAL CONTINUES BERTHER CONTINUES OF THE CONTINUES OF TH	EACTOON POLYMEUS	166.314	336.383							
THE PARTY	MENTAL MAINT MAINTAIN A LIBRIDA CO	SENDAT VIBIR (STRAD) Z / HOST MUTANTS)	79.106			L					
T	DELLA PORT PRINCIPAL SPET DE L'ARRIGNA CE	SENDAL VILLE (STRAD) FUSHING)	78.10								
TOWN SECTION	TENCHOLOGICAL TENCHOLOGICA TENCHOLOGICAL TENCHOLOGICAL TENCHOLOGICAL TENCHOLOGICAL TENCHOLOGICAL TENCHOLOGICAL TENCHOLOGICAL TENCHOLOGICAL TENCHOLOGICAL TENCHOLOGICAL TENCHOLOGICAL TENCHOLOGICAL TENCHOLOGICAL TENCHOLOGICA	CHARAI WRIS (STUAN HABRIS)	20.00								İ
	THE STATE OF THE PARTY OF THE ALPHANISA CO.	SENTAL VIELE ASTRAIN HVD	79:104			L					
	CENTRAL DE L'ANNE DE L'ANNE ANTICONNE	CENTRAL CHIEF ASTRAIN 21	20.50								
NA NEWOX	SEPANDED INC. 15 IN THE SECOND	ENAL VIOLET	13:33	134.421							
1	ICHAGGLUT INDIAN LINAMININA SE	CARPENIA CHAIRE (CTILATA COPENIA CENT	100	175.202	216-243	L					
- 1	REMAINED INTO PRECURSOR	U.A.P. WILLIAM VIEW AND MAN. TO	109-146	13.70	100		L	L	L		
HENCE VACE	HENALOGUE MAN PRELIMENT	OAPTHA CHEM STRAIN TAN TAN	10.14	111-702	116-243				L		
٠,	INDIANULUI DUM PRECUASOR	VAPPERATE VIEW ASTRAIN	106-146	195.202	100				L		
.1	HEMILIANI WAS THE WAS TO SEE	VARIOU A CORTIC	111.141	13:51	11.246	L	L	L			
ALLAN VAA	TEMPORED I DAM TREADMENT	IN BLAN A DOMONDE TYPE S	180					L			
PIECE AND	THE YOUR ARROWS THE PROTECTION	INDIAN ADENOVICUS TYPE S	100			L					
SIEVE ANENS	STATE OF CHAPTER	RUMAN ADENOVIOUS 177855 1 and 7	97-127								
HEY There	NOSTON PROTECTION	HUMAN ADENOVOUS TYPE 2	146-173	339-316	433-460						
MINEY APERI	HEXAM PROTEIN	HEBLAN ADENOVICUS TYPE S	348-375								
LAN ANELS	SAYON PROTEIN	HIMAN ADENOVIRUS TYPE 40	396-133								
PART ANDRE	HOSTON PROFEDS	BOVING ADENOVICUS TYPE 1	305-131								
William China	ITAMOREHAGE DIGUICONO 18 KD PROTECT	COWPOX VIBUS	21-55								
A LOWER		COWPOX VIRUS	462-419								
TOTAL AUTO	LATE PROTEIN 1194L	AFAICAN SWINE PEVER VINUS (STRAIN BATIV)	(124)								
ALTER ALTER	LATE PROTEIN EDICE	AFARCAN SWENE FEVER VILUS (STRAIN BASIV)	112-143								
PIRAC CANON	INCLUSION BODY MATRIX PROTEDI	CALABIOWER MOSAIC VIRUS (STRAIN DA)	17-44								
THE PARTY	ONCH LISTON BODY MATTLE PROTECT	CAULIFLOWER MOSALC VINUS (STRAIN DAS)	13-44								
THE CLAY	DICE JUSTON BOOM MATRIX PROTEIN	CAULIFLOWER MOSAIC VIRUS (STRAIN PVIAT)	383-410								
PIGLO CERV	INCLUSION BODY MATRIX MOTEDI	CALINATION ETCHED RING VIXUS	3								
DAM DAM	INCLUSION BODY MATTUX PROTEDY	FIGWORT MOSALC VIXUS (STRAIN DXS)	922				1				
YOU SOCKY	DICTURION BODY MATRIX PROTEIN	SOVERAN CHECKERTIC MOTTLE YIRUS	1					1			
PICIT HCMVA	PROB PROCA PRANSPORT PRO ULSS	HUNGH EYTOMEGALOVIRUS (STILATA AD149)									
TILLE TRATES						1					

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HE RAME	PROTEIN	CONTROL CARAINI STRAIN 15	1	2	Ī	Ì			į		
PICIT HSVIA	2	ADV SALITIES	- - - - - - - - - - - - - - - - - - -	Ì	Ī		- :	!	:		•
ICII MONYS	PROB PROC & TRANSPORT PRO			Ì		Ī					
EES HSVII			9	Ī	Ī	Ī					
PLEAL HISVII				Ì	Ī						
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TEES HOWA		THE LAND SYNCHOLD BUTTER (STRAIN ADIEN)	76.162		Ì	Ī			1	!	:
PRIS HOWA			7			-			:		
FILLS HOWA		PKCIFIXI	81-38		1		:: ;	1	1	•	
PETER PSYCA	TEINTES		111.152								-
100 STATE	TEINICA		131.163						١		
	PROFER		٢	140.10)					j		
	SALES TALKET TO A CANCET PROTEIN IPS		Ť						'		
7575 MISV		OPOXVIRUS			Ī						L
		PARENTAL STREET OF THE STREET	7	Ì		!	-	:			
	THYMEDE KOASI		340-386					:	í	•	
WHILE SEVICE			134.36							!	i
J	PUSCUMBER WINASE	CHELLIS VIRUS ISTRACT THURSE COST									
TAIL BEIN	No. of Concession, Name of Street, Str	Ī			Ī						
KAN KEWI	CAME TO PROJECT STATES	CAPPINA VILLE ATTEND COPEMIAGEN)		Ī	Ī		1				
PELLI VACCE	3		19:10								
HOLD VACCV	8	NAC ALCONOMINATION OF THE PROPERTY OF THE PROP	141.131								
WEST VACOR			147:174								
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1											
PERF VARV	POSSELLE PROJECT AND AND AND AND AND AND AND AND AND AND			Ī							
PKAOS AVISU	ACS TYROSDIE KDIASE TRANSF PRUIEIN	CLEASURE CONTRACTOR OF THE CON	12-49								
PKRYK AVOU			(64:33)								1
Valva a series	TYPEDEDA REMASE TRANSF PROTEIN YES		114.411								
Water State	I ATE INSKED PROPER	HULLA ADENOVIRUS TYPE 3	114.411								1
	TAN ING KIS SHOTTEN		1								
	I AVE INA P.D PROTEDA		111				L				
OVER A BUT	TANK IN PROPERTY										
200	TO STATE AND AND BUILDING THE PARTY OF THE P										
אנו ושלו	LATERT POLICE TROUBLE	FECTERAL VISUS (STRAIN CAO)	2							ļ	ļ
PUOI EBVC	LATENT SELECTION OF THE PROPERTY OF	ENTITION AND (STRAIN RAIL)	2								_
FUGI CBVI	LATENT MEMBRANG PROJECT										
7.00 EDV	CON TEMPORAL PROTEDY			189-316	467-524						1
PARTE DWGA	LOUIS CAPOND DESTAGE LANGE SUBURI	SACORE FUNCTION AND PROPERTY OF THE	Г	116-160	(\$9-0(9						
ANAN WANT	LEIKA CAPPED DEPAR, LAKOR SUBURI	VACCINIA VILLIA (SI INCIA CUTENTIA CATA	Г	31:118	159-019						
0.00	LINNA PAPPING DIE YNG. LAKOE KURUN	VACCINIA VIRUS (STILAIN WR)	Τ	201.313	436-653						
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THE PERSON	MUCLEOCAPSID PROTEIN	HUNTAVIAUS LA CAUSSE		L							1
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PICA COVO	MUCLEOCAPSID PROTEIN	CANINE DISTEMPER VIRUS (STRAIN OND/R\$TEPOORT)	2			1	Ì	1	<u> </u>	<u> </u> 	Ī
THESE CHAY	MUCLEOCAPSID PROTEIN	CHANDIPURA VIRUS (STRAIN 1651514)						1	<u> </u>	1	1
PHCAD CWCAL	MUCLEOCAPSID PROTEIN	CANING ENTERIC CORONAVIAUS (STRAIN KI)1)	<u> </u>							<u> </u>	ļ
PHCAP CYPTU	AUCLEOCAPSIO PROTEIN	PORCINE TRANSMISSIOUE GASTROEMTERITIS CORONAVIRUS (STRAIN PURD		Ī			İ	\dagger	1	\dagger]
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3	NUCLEOCAPSID PROTEIN	FELING DO ECTIONS THE CONTIN VINUS (STRAIN 19-11-6)	5				\dagger			<u> </u> 	1
34.2	MUCLEOCAPSID PROTEIN	KAZAKA VIKUS (ISOLATE K.180)	1			1		t		<u> </u> 	1
PHCAP KREVE	MUCLEOCAPSID PROTEIN	INDEAN RESPIRATORY SYNCYTIAL VIRUS (SUBGROUP B / STICKIN 18537)	١	B :	- I			1		1	Ī
PHCAP HASVA	MUCLEOCAPSID PROTEIN	HUMAN BESPÜRATORY SYNCYTIAL VIRUS (STRAIN A2)	1		1		1	1		+	Ī
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PICA LASS	MUCLEOCAPSID PROTEIN	LASSA VIDLIS (STRADA JOSEAN)		1.504			j		<u> </u> 	<u> </u>	
PHCAP LYCVA	MUCLEOCAPSID PROTEIN	EYAPHOCYTIC CHORDOMENINGITIS VIAUS (STRAIN ARKISTRONG)	16-03				j			4	1
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PHCAP PITHW	NUCLEOCAPSID PROTEIN	HUMAN PARADIREURAZA I VIKUS (STRATIN WASHINGTON 1937)	П	44.431	j		1				Ī
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PRCA PW	NUCLEOCASED PROTEIN	PHEUMOMIA VIRUS OF RUCE	93-430								
PHCAP KABVA	HUCL EOCAPSIS PROTEIN	SAMBLES VIRUS (STRADY AVOI)	133-163								
PHCLE EABW	NUCLED CAPS SE PROTEIN	ACRES VALUS (STRADO PV)	13)-163								Ī
HCF LAIVE	NEXT EGGAPSID PROTEIN	RABIES WAUS (STRAIN SAD BIG)	133-163								
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Ī	MELSEN PRINCIPLE	DENOIS VINUS TYPE 2 (STRAFF 1995) FUNDA 31			-	1115.3143	1 1104-1111	=		İ
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HOLD HEVIN	CENDRE FOL YPROTEIN	FIEFATITIS C WAUS (ISOLATE TAIWAN)	=	MS-1072	_		j		_ <u>:</u>	
MAN O HOAV	CENTRAL POLYMOTEIN	HEPATHIB A VIAUS (SPEALW 24A)	113.101	21. IM	11111111111	22.11		-		
PHOLO JOAN	CENOAR POLYPROTEIN	HEPATITIS A VIBUS ISTRAIN (3C)	101.237	102 - 1048	1117.114	1454-1411		·		
200	PERSONAL INC. CALC. PRINCIPLE	Life PATITULE VIOLET CATO AIM 1881	T	100	1111.111.00	100		-	<u> </u>	<u> </u> -
		CASE ACCOUNT A COMPLETE ACCOUNT OF CASE		İ	-				<u> </u>	<u> </u>
	WENCHER FULL TRUSTER	MECALIFIES A VINUS (STANIS)							1	
PPOLO HEAVO	CONCRET POLYPROTEIN	PEPATITIS A YIKUS (STICIN GATE)	┪	į						
MAYON O'DOM	CONCRET POLYPROTEIN	HEPATITIS A VIRUS (STRAIN IDL. 175)	٦	1071-104E	103-114					4
PROLID IO AM.	CONCRET FOLYPROTEIN	HEDATHIS A VIXUS (SPICAIN LA)		1021-104	101-114					
PHOTO HOAVI	GENERAL FOLVERDY	HEFATITIS A VIRUS (STRAIN MES)	1	101-101	1603.149					L
PPOLO SPANI	CENTRAL POLYPROTEIN	(SDUDNIEDATITIS A VIEUS (STEATH AGN. 17)	107.34	1023-1053	1113.1143			_		
TAYER DIDE	Charles Intervention	GENTAN REPAREIS A VIEUS (STRAIN CY. 145)	1					-	<u> </u>	<u> </u>
TIAM VINE	Constant les transfers	LOBALAN BUDANATUR 14	ī	585-585	612.679	7.190				L
THE PARTY		LA SALA BATTALON DE LA SALA	1	1444.4003						
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POLG IALY	COLUMN INC. 1771.01 P.L.	MANAGE ENCENTAINS VIRUS (SINAIM SALVI)	T		7797-9447			+	+	+
MOCO MAN	CONTROL FOR THEOREM	JAVANESA EMEETHALI IIS VIRUS (SI KADI JAGAAS782)			() A ()	Ì		1		
HOLD MEY	CENTRAL POLYPROTEDY	JAPANESE ENCEPHALITIS VIRUS (STRAIN MAKATANIA)	Τ						1	\downarrow
POLO KINIDA	CENTRAL POLYPROTEIN	KUNUDI VIELUS (STRADIN PODANIC)	긔					1	1	4
HOLD LAWY	CIDIONG POLYPROTEDY	LANGAT VING (STILLIN 1721)	٦	1634-1661						
PROLIGIOUS	CADADIAN POLYPROTEIN	LANGAT VIRUS (STRAIN YELANTSEV)	463							-
AIT DOWN	CENTRAL POLYPEOTERS	Locabed B.L. Vacus	431-463							4
PHOLO LIVES	CENONAL POLYPROTEIN	LOUPING BJ. VIRUS (STRAIN SB 536)								-
PPOLIS MOTA	CENONG POLYPROTEIN	MOSQUITO CELL FUSING AGENT		1054-3043	1301-1330					_
AND POL	CONCRET POLYPROTEDI	MALE DWARF MOSAIC YOUS	10-39						_	
PROCE MYEV	CENCHAE FOL YPROTEIN	INCREASY VALLEY ENCEMBALITIS VIAUS	312-256						·	
POLD OLIV	GENOME POLYPROTEIN	ORNITHOGALUM MOSAIC YINUS	Г	16-91	Г					L
PROLID PEATO	CENDAG POLYPROTEIN	PEPPER MOTTLE VIRUS (CALIFORNIA ISOLATE)	377-404	704-738	131.434	400-927	1021-1911	14181-8413	1767-1814 2433-3464	3
POLG POLIV	CLASSAE NOLYPROTEIN	POLIOVICUS TYPE I (STRAIN MAJIONEY)	Q	1681-1881				-		
Prote Politi	CONDICTION TO SECURITION	POCJOVECUS TYPE I (STRAIN SABIN)	189-269	1011.191	1903-1933					
PROLID FOLIS	CENCINE FOL VPROTEIN	INDUSOVALUS TYPE 3 (STRAIN LANSING)	Ē	1801-1931				-		L
WE BOX IN	CONCRETE POL VPROTEDI	POLIDVALUS TYPE 2 (318 A.N. W. 2)	_	169:104						
PROLED POLIS	GENOMIE POLYMOTEIN	POLIOVIAUS TYPE 3 (STRAM 33127)		0(6)-004						L
HOLD POLIL	CENCHE POLYTROTEIN	POLIGYBLIS TYPE 3 (STRAINS PIA EGNI)! AND PIA EGN 1241 [B)	1060-1098	900-1930						L
MOLD PAY	GENOME FOL YPEOTED!	PLUM POX POTYVIBLIS (STRAIN D)	_	1446-1525	3468-1668					
PROLO HVEA	CONONCE POLYTROTEIN	HUM FOX FOTYVIAUS (STAAIN EL AMAR)	1144-1187							Н
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1	CENORE POLYMOTERN CENORE POLYM	VRING FLOW DOX POTYVILUS (STAJIN AANCOVC) FLOM DOX POTYVILUS (STAJIN P. FAUTANT IIA) FLOM DOX TAND TO VILUS (STAJIN P. FAUTANT IIA) FLOM TO REAGNOT VIRUS (STAJIN W) FALANTA REAGNOT VIRUS (STAJIN W) FALANTA REAGNOT VIRUS (STAJIN DPD)) FALANTO VIRUS Y (STAJIN STAJIN)	100 11 11 11 11 11 11 11 11 11 11 11 11	100.132	110.17						
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	NAME TO THEOREM SEE TO THEORE	POTATO VILUS T (SI LALA PROPURATION)	Г	93:460	201-735	36.5	177.11		:		
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	THE STATE OF THE S	PARISHIP VEH DW PLECK VIRUS (ISOLATE P.121)	ãÌ	1107.271						Ī	
	AND THE STATE OF T	TREATMENT OF THE POST OF THE P	10-33							T	
	DATE OF THE PARTY	PACKET CHARLES AND AND CONTINUE COMMANDER THE PACKET OF TH	1034-1060								
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ſ	OLG FOL THEOTEN COLG FOL THEOTEN COLG FOL THEOTEN COLG FOL THEOTEN COLG FOL THEOTEN COLG FOL THEOTEN	THE REST WHEN BUT SOLD IN CONTINUE WALLS (STRAIN DA)	100	100-223							
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Ī	OME POLYTROTEIN	WATERLOW MOSAIC VIRUS II		1111							
1	ONE POST CONTRACTOR	WEST NOT BY MADE	X								
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١	ONE COLTENIES	COTT AND RECORD CARTIN ACTE AND PASTEUR 17D-2041	5	1						Ī	
L	ONCE POCYPROTEIN		19.49								
Γ	GENOME POLYPROTEIN	CUCCHINI TELLUM MOSALE VINOS	1043-1101	100.103							
	CENONE POLYMOTEIN	POLICYICAL I (STRAIN BLANCHET)	1405. 1467								
Γ	HOMSTRUCTURAL FOLYPROTEIN	VENEZUELAN EQUINE ENCEPHALITIS VINOS (31 PAIN 1 PRINCIPAL SOCIETA									
Γ	NON-STRUCTURAL FOLYPROTEIN	FELDIN CALICIVITIES (STILATED CFUSE FIV)	710								
Γ	LETELICELIEAL POLYPROTEIN	I SLINE CALICIVALIS (STRAIN PS)	77.	140.136							
L	L'STRIKETURAL POLYPROTEIN	INDAMINE VINUS (STRAIN BURNA)									
	LOS CONTINUED BOLVEROTEIN	HEPATIFIS E VILLS (STRAIN MEXICO)									
I	THE PARTY IN VIEW THE	(IEDATITIS I VALUS (SPILADA MYAMPIAA)	27.70				1				
Ť	CALL STATE OF THE	HEPATITISE VICIOS (STILVIN PAKISTAN)	200	Ê							
1	March 1 March	Lamost Music Walls	455-913								
1	ACMS RULE URAL PART PART PART	PANYANG LAVING VIII IS 18 TRADIS COLUD	2453-2440	_					Ī		
5	STRUCTURAL POLITICAL	THE ARBIT LIFELS OF BUSEASE VIRUS	313-367		_	_					
1	MONSTAIN LONG TOUR PROPERTY.	GARE BLUE OVELLE AND AND MAD	1037-1014	3.5	3411-2445						
	NOWSTRUCTURAL FOLLTRUILLIN	ACOS PARTIES TO SELECTION OF THE PARTIES	146-133	1047-1114			i				
Г	NONSTRUCTURAL POLYPROTEDY	HOSS ILVEA VINCE (See 18)	3040-1087	1_							
M	NITRIDCTURAL POLYPROTED	TUBELLA TRUS (STORES)	11134-11111			L					
Γ	NONSTRUCTURAL POLYPROTEDI	SDALIG FOREST VOLO	936-970			L	L				
	NOMETRUCTURAL POLYPROTEDI	STATES VILLE (SAME) THE CONCLUS AT TAKEN EVEN TO THE CONCLUSION OF	4.31								
	NONSTRUCTURAL POLYPROTEIN	WESTERN EGGING ENCENNALITY VINOS	110			L					
T	STRUCTURAL POLYPROTEIN	A VIAN DIFECTIOUS BUILSAL DISEASE VIEUS (STRAIN 30 VV)	Т						L		L
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T	AND WATER AT BOLVPROTED	AVIAN DEFECTIOUS BUILDED DISEASE VIRUS (STRAIN CU-!)	7			\downarrow		ļ			
T	STORY BY THE STANSON	AWAN BOTECHOUS BUTCAL DISEASE VIRUS (STRAIN E)	20.00								
1	STRUCTURE TO THE CASE OF THE	TANAM MERCHENIA BLEAKL DISEASE VIRUS (STRAIN POC-91)	112-210								
PDV4	NUCTURAL POLYTROLEIN	A STANDAR CONTROL BUILDING MARKET VIRUS (STRAIN STC)	151-151								
٦	STRUCTURAL POLYFROIDS	PARAMETER STRAIN GILL UP	136-361								
0	STRUCTURAL POLYTROIEUR	TEXAST BRUGE CHAIR (CELLAIN MELOS):	639-619								
	STRUCTURAL POLYPROTEIN	EXECUTE CHIEF CHIEF THE ABILITY	916-911								
	STRUCTURAL POLYPROTEIN	CONTRACTOR OF THE CONTRACTOR OF STRAIN EDSOYN 12-5)	1133-1165								
8	STRUCTURAL POLITICISM	TAKWASIA UMINI SETADAK KR CA AND HOLLY!	[1138-1163						\downarrow		
	STRUCTURAL POLYTROLEUM	LANCESCO LINCOLD DIVISION SALVES	1M-924								
À	RUCTURAL POLYPROTEIN	TATALOGIC POPAGE CARTE CARTE ACTION NATIO	704-749	115.141		Ц					

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		CANALA MANAGEMENT OF VIRIA 1/98 1/8111(COLATE)	313.344	614-860							
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1		ENGAN MACALIPERS VIRIS	Т	630-00						L	
		UAAAA	1	431-305	173.900				-		
Ī		ROUS SAUCOMA VIRUS (STRAIN PILAGUE C)	797-634						_		
Ī		LICE TIPICAL BACKLIFORM VIRUS	7	29.93	14-10	202-229	(10-01)	Η	1022-1049		
ļ		ALCE TUNGRO BACILLIFORM VIRUS (ISOLATE PIULIPPINES)	3	39.01	116.20)	202-226	410-11	14 F () ?	1022-1049		
Ī	702		***						·	Н	
			36	541-574	169-619						
		SINGAN BANDWOOFFICIENCY VIRUS (AGNOM ISOLATE)	13:33								Ī
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PPOL SIVAL POL POLYPROTEDI			672-515					1	1	\dagger	Ī
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PPOL SINCZ POLYPROTEIN		1	ı					1]

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		SINIAN ISORANODESICIENCY VIRUS (NOTHER 23 1300-711)	550				_	_	1		١
		THAT HALL BEING PICIENCY VIRUS (KOW ISOLATE)			1			\mid			
		SETTED RAN PAPER SECTION VIRUS (F130-SAGIA ISOLATE)		Ì	1	Ť		 		Ī	Ï
		STATE OF A RICHARD FRANCE VIEW VIEW (PRINCE) (SOLATE)	494-516		1	1	T			Ī	
		ACCOUNT TO SECURITY OF SECURIT				1	1	t		Ī	١
Ш		SOURCE MONKET NOTING THE COLUMN	264-395	14419		j	1		1	Ī	
l	ELT VALATIC BOL YPROTEIN	SOMETH CHECKED I LE VINUS	Ť	149-01				<u> </u>	j		
		SIMILAN ALTROVIAUS SAV-1	ī	917.610					-		١
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		MOUSE MANDARY TUMOR VIRUS (STRAIN BRA)	,								
Ī	VACIETY TAKE	CARRELANDADA PERIOR VIAUS (STRAIN CHI)			1						
HEN BUILDE		TOTAL TATE TO BE THE CHAIN AFTER MICE.	2.4			:		•			
l	PROTEIN PRITE	MOUSE MANORALY TUNIOR VIAUS (2) PARIN ON)					_				
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ŀ		AUTOMOVIE CONTRACTOR DE CONTRACTOR CONTRACTO	16-41	201-128					-		ŧ
1	A VISORON	ACACTIS SECETION MULEAN FOLITICIONOSIS TIMIS	1					Ì	Ì		
٠	1	BOKOVX MOM MUCLEAR POLYHEOROSIS VIRUS									
1	O. Metalin	RITHING CIBBER CLANIA NOCLEAN FOLYICEDROSIS VIRIIS			1			İ	İ		
Print Saves	POLYNEDADA	CONTRACTOR OF THE BANK OF THE BANK STREET STREET	*					Ì	ĺ		
1	VOI STIERDA	MITTANIA COMEN MANAGEMENT OF BASE AND VIEWBOOK VIEW IN 1815	17-71					1	1	I	
١	SA VIENE	LYMANTELA DISPAR MULTRAVSIO POLICIAN TOLICIAN									
ı	Ext Company	MANESTRA BRASSICAE MUCLEAR POLYMEDROSIS YIRUS			Ī						į
	OL TIMEDIA	AS ENT BOST THAT SOUT A BOUT TICAPSID FOL YILL DROSIS VIRUS								Ī	
ı	OL Mether	VALUE OF THE PARTY	713	_				İ	Ì		į
Ł	PAY MISTALDA	ORGYIA PSEUDOTSUCATA SIRVE CAPTURE	ļ							į	İ
200	Section 1	PANOLIS PLANGEA MALTIPLE NOCLEOKAPSIO POLITICALMUSIS SINCE									
- 1	TOTAL PROPERTY.	CHASTAPPETA ESPECIA MARCLEAR POLYICEDROSIS VIAUS (STRAIN US)	•								
_	OL WEDNIN	ACCESSOR A DESIGNATION OF A POLITICAL PART OF COLOSIS VIRUS	7					t	Ī	Ī	
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Γ	LEV PROTIEM	Spular particular in the second secon	100	Ĺ						1	
T		VISKA LENTIVEUS (STEATH 1919)	Ę	1	99.300						1
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	LINCOLL COMOSTAL ACCOUNTS		724-731						Ī		
	DOME OF THE PARTY PARTY AND THE	THE PERSON OF THE PARKET OF THE	- F						1		
SHI UNIT	THORKE BEHOSHI REDUCT LAKOR CHA	VACCORA VICUS (STILLAR CONTRACT)	141.401								
1	WHAT SAME BELLEVE LANCE CHA	VACCEMEN VI	197 193								
	AN 1 25/6 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	IVALIONA VARUS									
VALV	LINGS COUNTY IN TAKE I WAS I	TO SECRET A PARTER VIBILS (STEAD) DUDIAS)	115-146						Ī		
PERI VIVO	REDIRECTORNOSMI REDICTI CARGE CINA	TANK THE TANK THE PARK I LET BE A PARK	10:04								
1KVAL	PERSONAL PROPOSONI REDUCT SWALL CHA	LOVOR POUTS VIALUE 177E 1 12 PAINT 27	7	217-540							
L	THAT HOLL A EDGE TRANS TPEC ! ACTOR	VACCINIA VINUS (31 RAIN W.R.)	16.14	1	55.55						
	AUX AN AREAC TRANS INCC FACTOR	VAUGLA YRUS	771.01	217.102	111111	1967					
T	10 to 10 to	VAREBUS (SPILAN COPENIAGEN)			T		110171101				
PEPOL VACE	DAY OF THE BUT BOY IN PA	TOAPPENTA VIRUS (STRAD) WR)	1		T						
ı	DOM-COUNTY OF THE CO.	Cabre & Child	137-254								
	ONA DORCHED HOW FOLL IN NO	N. T. C.	\$ *	14-155					1		
1	DALE DALECTED LIVE FOL. 138 FD	CAPIDOS VINOS (31 INVIN NO.1)		605:117							
	THE PARTY AND THE POLITICE	COWPOX VIRUS		3							
	Contract Contract Con 119 Kin	VACEBRA VOLUS (STRAIN WR)			Ī						
1	THE PARTY IS NOT THE PARTY IN T	12. Kind A Willie	-	C1 - XO							
PALPOS VALV	DAY, DOLECTED MAY POL 133 KD		(34-6)								
SALES PANK	TOWA EXPLICITED TOWA POL 35 KD	CAPIDOXYIEUS (SERAIT N.P.1)	1	92.30							
TAKE VARIA	THAT THE LEG DAY FOL 19 KD	VALCORA VIRUS (STILATE W.K.)									
	TALL MANAGER BUA BOL 19 KD	VALIGIA VIIUS	2								L
ANA ADEL	THE PERSON AND AND ASSESSED.	I AL YSTAD VILLE		_							
MINON LIEV	ANA COLLECTION DAY FOR THE PARK	Text more Ant Petiting Visited	184-913	1639-167							
PLYOL EAV		ALCO TENDED A CHRONIC AND	1115-402								
ı	ANA DESCRED PAR POL SUR PI	UNITED TO THE PARTY OF THE AND	115-146								
l	BAY BOLECTED LIVA FOL SUB PT	DOLLOWICA A VICTOR IN THE ANALYSIS AND A PROPERTY A	3								
l	TANA SHIRECIED DAY POLICIO PI	DIFLUENCE A VILUS (STILAIN AND LITTURA AND			-	L	L				
ı	ALC: NAME PARK BULL BOL SLIE PT	INTELLIGICA A VINUS (STRADA AFOWL PLACOUR VIAUSARUS I ULLAZA)			1		ļ				L
THE WIT	THE PARTY OF THE P	TATELL BARTA & VIRIUS (STRAIN ANGULLAKAR YLAND/704/77)	2								

PCGTKE	1107217244	IAN Viruse (no becieraphages)	Г			ľ	_		• • • • • • • • • • • • • • • • • • • •		
П	PROTEIN		7	7	7000	3	2		_		1
PREST WALD	RMA-DIRECTED RMA POL SUB P2	DOLLENZA A VIRUS (STRAIN ACOUNCE, CONDOWN (1971)			İ		-	i	<u>:</u> 	<u>:</u> 	:
١.	RNA-DIRECTED RNA FOL SUB P?	INCLUDING A VIAUS (STIRKIN ALCOUNT) EMAILS SELLY SELLY			1	:	1	<u>:</u>	:	:	:
PREZI MEGE	ENA-DIRECTED RIVA POL SUB PI	THE LUMBER A MALL OF THE TAX AND PARTY OF THE PARTY OF TH	7			Ī	Ī	İ	İ	<u> </u>	İ
	KINA DARECTED KNA POC 308 71		9-146								<u>.</u>
	BUA DISEPTED BAA TO SUB FE	DETERMENT OF THE PRINCIPLY AND THE VOICE OF THE PRINCIPLY	19:14						_		
1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	THE PERSON AND THE PARTY OF THE	INSTITEMENTAL VIBUS (STEATH ANTHONE)	10.146								-
PART IAPO	BNA BIRECTED BNA POL SUB PI	DELLENZA A VRUS (STRAIN APINTAL/ALDERTALIWY)	19-14					_		:	i
PLET LANE	ANA-DIRECTED BAA POL SUB PR	INFLUENZA A VIRUS (STRAIN APUERTO RICORI)4)	19-146					1	-	i	-
PLEM LABOR	ANA-DOLECTED BINA POL SUB P.	INSTURNZA A VIRUS (STRAIN ARUDUY TURNSTONEMEN ILRS: YAMA)	19.14								
PARPS 14154	SAA-DOLLCTED BNA POL SUB P2	INGLUENZA A VIRUS (STRAIN ASINGAPORE) 151)	119-146							1	
JULY LATELY	RMA-DELECTED LIVA POL SUB PS	INFLUENCA A VIBLIS (STRAIN ATURKEY AND WESO TAN) 1/10)	119-144					1		1	
PREP IAMY	ANA DOLECTED LAW POL SUS PI	DIFLUENZA A VIRUS (STRAIN AVICTORUANAS)	19-146	111.334			Ì		-	1	1
PREPS LAWE	ANA DORECTED BUA FOL SUB PI	INGLUDICA A VIRUS (STRAIN ANYLLSON-SMITHUT)	115.146								
HALF LAND	ANA DERECTED RAY FOL SUD PT	INFLUENZA A VIRUS (STRAIN ASWING/MONK) KINKURITH)	10:14							j	
PREPY (A21)	ANA-DURECTED RNA POL SUB P?	INFLUENZA A VIRLIS (STRAIN ASWINGAIONG KONGVIZMIZ)	116-146							1	
11/2/1	INA-MIRCTED RAY FOL. SUB P.	DOLLOWER A VIRUS (STRAIN ASWINGAOWAIS)	119.146								
1	MAY DORECTED RAY POL SUB PS	INFLUENZA A VIBLIS (STRAIN AS WINE/TENNESSE ELIENT)	119.146								
L	ENA DIRECTED BUX NO. SUR P.	DELUENZA B VIRUS (STRAIN B/ANN ARBOR/ING (COLD-ADAP) (ED))	133-184								
ı	ANA-DIRECTED RIVA POL SUB P2	INFLUENTA B VIRUS (STRAIN BANN ARBONING WILD-TYPE)	164-194				į	:	:		
١	ENA DIRECTED BUA POL SUB PT	INFLUENZA B VIRUS (STRAIN DISINGA PORGZIZUM)	157.194								!
L	RNA DIRECTED BNA POL SUB P.	INSTITUTED A VIRUS (STRAIN AUDOCERIGAR/100K KAIIXO/1771)	111.547	İ							
	DELA PRINCIPER DELA PER CITA PI	DOST DENZA A MINUS (4) RAIN ACHILE/1/43)	311.336								
1	WALL PASSESSED IN THE P	TANKET DESIGNATION OF THE PARTY OF THE PROPERTY OF THE PA		20.00					-		
1	TANGET IN THE TANGET IN THE PER	THE THINS A CONTRACT AND ASSENDENT SINGLESS CONTRACT SINGLESS CONT	413.514								
	GUL MORPHED BULL BOL GIR 51	THE LIBYTA B VIZING (STRAIN BLANN ARBOILING ICOLD ABAPTED))	<u>€</u>	50.50							
J.	BAY DIRECTED BAY BY UND BY	INSTITUTED BY WILLS (STEAM BY ANN ARBODING WILD: TYPE)	3	473.500							
ı	NAT SHEET PER DAY NOT RUE P.)	INTLUENZA C VILUS (STRAIN CHERLINIAS)	508-536								
1	BAA BOLECTED BAA FOL SUB PJ	INTERESTAC VIALUS (STRAIN CIUSO)	104-336								Ī
1	ANA-DIRECTED DAY POL SUB PJ	THOCOTO VIEUS	961.671	351-318							1
	ANA-BIRECTED NAA POLYNGHASE	HUMAN CORONAVIRUS (STRAIN 129E)	316.363 300	Ž	1011-2001	11:12	1		1	1	
PERDA CYLLIN	MA DIRECTED BUY POLYMERASE	MURINE CORONAVIRUS AUIV (STRAIN JIBA)	5			Ì			+	1	Ī
PALM MEV	ENA-DOLECTED RNA POLYABILASE	BERNE VAUS		357-314	7	1	1		1	1	Ī
PLEYS CYLES	ANA-BOLLCTED RNA POLYNGRASE	MUDING CORONAVIRUS ADIV (STAAN ASP)	113-113			1	Ī	1	†	\dagger	Ī
PREAD COALTH	NAM DOLECTED RAY POLYNERASS	MANUAL COLOMA VALUE NOVO (STRATIO JOST)	10.00	11.16	311.413	T	1	T	t	t	Ì
PILL COM	ANA-DOLECTED RNA PUL TMERASE	TOTAL BANEFACK BENEFICIES COME AND ASSESSED TO	110.147	2304.2331	35.77.574	T		Ť	İ	t	
SAN SAN SAN SAN SAN SAN SAN SAN SAN SAN	SAC-DUCK I SO BAN FOLLY BANKS	AVIAN BEECHOUS BRONCHITS VIRUS (STRAIN ROSS))	65.200	į		Ī		Ī			
PER PTVIO	ENA SIMPLIFIC BHA POLYAGRASE	BELDETONGUE VIXUS (SENOTYPE 107/SOLATE USA)	1013-1059								
PARK HIDOW	INA POLYMERASE	BUNY ANWELL VIEUS	80-114	117.330	1803-1861	1192-1916					
PLLM CDVO	RNA POLYNELLASE BETA SUBUNIT	CANDE DISTEMBER VILUS (STRAIN ONDERSTEROORS)	14-51			╗	╗			1	Ī
PRINT, HANTY		HANTAAN YDUS (STIAIN 14-118)	404.4)	e :- 39	264.591	7	903:046				
PARME HOUSVA	RNA POLYMERASE BETA SUBUNIT	HUMAN RESPONTORY SYNCYTIAL VIRUS (STRAIN A3)	101-101	10-311			1007-1014			7.00	7 TOP 7 TOP 6
PARM HABYH		MANBURO VIRUS (STIAZIV MUSOKE)		2				2	\dagger	†	Ī
MIN WIN		MAKBURO VIRUS (STUAN POPP)				1	Ī	T	Ť	Ì	T
PRIKE MEASE	INNA POLYMERASE BETA SUBURTI	MEASULES VILLUS (STRAIN EDMONSTON)	Т		7.1		1	1	t	T	
PRINT MANAN	RNA POLYKERASE BETA SUBURIT	MUNOS VIDUS (STRAIN MOYAMAIA VACCINE)	7		70	1	1	1	1	†	Ī
PREM. HOVE	ANA POLYMERASE BETA SUBURIT	NEWCASTLE DISEASE WILLS (STIAM) BEAUDETTE CAS)	¥ 7	100	27	16.51	1	T	\dagger	t	Ī
PLAN PLANT	RNA POLYMERASE BETA SUBUNIT	HENAN PALADOLUENZA I VILUS (STILATA TOMINIOA)	47.77				21.00	1000	+		Ī
	ANA POLYACILASE BETA SUBURIT	HUMAN PANAMELLENAN STRUCK STRUCK STRUCK STRUCKS				-		-	1648.3031	t	
PAR PUSO	RAA-DOLECTED IURA POLYMERANE	PUMALA VEROS (SERAIM INCLANA DE)		1	1110	T	T	-		t	Ī
W. IN	THA POLYMENASE BEIN SUBURI	TABLE VINCE CONTRACTOR IN CONTRACTOR			1616.3006	Ī	Ī	T		T	Ī
PREP. EASYS	ENA POLTMEASE BEIN SUBORII	EVALUES VALUE (STEAM STATE OF THE PRIMARY VALUE	135.103			Ī		1		t	
100	ENA-DOLLIED MAN POLYMORANS	ADD VALLEY PEVER VIRUS (STRAIN ZIL 548 KHZ)	1334-1563	1633.1647				T		T	
PARTY COOK	ENA POLYNERALI BETA SUBLINIT	SENDAL VALUE (STRAIN 2 / HOST MUTANTS)	259-479	1043-1116	1735-1194 2145-2180	2145-2150	П				
PLY SED	RUA FOLYKERASE BETA SUBURY	SENDAJ VÆUS (STIAIN ENDERS)	917-609	901-036	1549-1536 1865-2000	1665-2000				1	

HILL RANG HILL RANG HILL ROOM HILL ROOM			- Y	ARGAI	AREAL	j					
TTT	DEC TITLE		1	13	1315-1756	3145-2160					١
Ш	BALL AND VACUEASE BETA SUBURIT		٢		31.35	250.00			1	1	
П	AUX PRINCIPLE BALL MOLVIORIASE		Ŀ	E	1680-1710	3130-2143	_			١	
Т	THE BOY WATER AND STATEMENT	-w1)		91116	36.	1911-3000	2010-3103				
	TO BE VANDALIS		۴	1000	31.611	1195.1239	1330-1357	1415-1442	1671-1698	23.18	
T	THE MISSESSEE BAY POLYNORASE	TOWATO SPOTTED WILT VIRUS (BIAZILIAN ISOLATE CENTITION VI	15	134.311	371.336						
Ī	MATINE STATES		-	10	101						۲
Ī	THE PAST OF PERSONS	UCKUNIZAJ VIAUS	Ė	1							
T	ANA POLIT PROMOSE	FIFTS VIRUS (SEROTYPE NEW JERSEY / STRAIN HAZELING									
PERM. VIVER	INA POLYMENAM BEIN SUBMIT										
	NA POLYNGRASE BETA SUBURUI		7	-							
Г	DVA POLYMERASE BETA SUBURAT		338-364	564-191							
VI LY YEAR	ENA TRIBECTED BYA POLYMERASE		154-311								
T	BITT A TIME BUILD JOHN BANA POL					L				ĺ	
T	TAY AND BUT AND BUY BOX							L			_
	MIATIVE EMA-ON EAST CO.	BASIS BY VELL FOR DIVALE VIRUS (ISOLATE PAV)	117:14								
	HUTATIVE BNA-DOLBNA FOL		312.79								L
MOVE OFFI	PUTATIVE BUA-DIR BNA POL	Г	111.18	÷.0	141.44						
Ţ	SHEATHAR BHA, DISEANA POL	Ī	717.650	1646-1067							
	AND THE REAL PART AND	23 31 1501 15 2111	1	917.69							
	The same of the sa	7	Т			ļ		L	L		
PALENO BEDYS	PUTATIVE ANALUS BOX 100	TRALIAN 002-73	┪				ļ				L
PRUPO INDVA	PUTATIVE ENA-CHE ENA PUE.	THE CHAMME SALES BEAT WE CROSES VIRUS (SEROTYPE JASPER)	71).150								L
JANA O	PUTATIVE RNA-DOLIDIA FOL		3.50	į							
AVAIL PRINT	PUTATIVE BIXA-DOS BNA POL	1000	114.66	1633-1079							
	BUT BOI SOUR ACE	KAIR ARAIS INCINO	98.7	716.714	1011.1099		L				
V	THE PERSON NAMED IN COLUMN NAM										
O PPANS	PUTATIVE DIA-DUCKA PAGE	DEALTH HAPE I STEAD DEARING									L
ALLO LEOVO			=								ļ
SEED BIDN	ANA DIRECTED RNA POLYMERASE	REOVINOS (1778 1/ 2) KANA LANCY	68.49	218.203	701.51						1
1	TO THE BAY BOLD STREET VP	BOVING ROTAVINUS (STRAIN NO)	Ī	311.341	20.10	1975-1002		_			
	THE PARTY OF STREET OF	BOVING ROTAVISUS (STRAIN UK)	T		1	107		L	L		
PERSO ROTEU	MANAGER AND THE BUSINESS CO.	MORPHIE BOTAVIEUS (CROUP C/STRAIN COWDEN)				1001	1				L
Pillo Rothc	THE DIE THE POL SOCIAL ST	PARTICIPATION OF THE PARTY NEED	65-73	2		Т					L
O LOTH	RAY DO DAY FOR SUBURIL VI	CONTRACT IN DATE AND AND BAILS	65.45	2	3						L
MING LOTE!		SUPPLY TO BOTH THE BOTH AND THE A	147.188								ļ
PRING SCALA	ILVA DOLECTED BUSA POLYNEBASE	SACOMARDMILES LEVE VIEW - VINCE	163.204	141-111	1105.1134	1976-200	-				1
C.77. 04. 9	BUX MILYMERALE	I ACALIBE YOUS	336-357		1347.1434	-					1
2	SHALTING BNA DAL BAN POL	TOBACCO MED CREEK MOSAR, VIKUS (1MY 3 INVIT)	111								
	THAT THE WAY WE A COM AT THE SUSPENSION TO A THE STATE OF	BOVING RESPONSIONY SYNCYTIAL VIRUS (STRAIN ASSIMA)				-		L			
¥ 1		CANONE DISTEMBER VIRUS (STRAIN ONDERSTEPOORT)	200				ļ	_			
NEW COVE	ACCOUNTS TO A TABLE STREET	TAKELAN TESPONATORY SWEVYIAL WILUS	1			\downarrow	-				L
VER 1815		TENTAL SECTION APPLIES THAT AND THAT VIRIOS (SUBGROUP B / STRAIN 1853?)	96-141								L
PRILITY HOLSVI	ENA POLYMORASE ALPHA SUBURI	TOWNS THE PERSON OF SAME VIEW (STRAD) A1)	17:14								1
A 1013VA		HUMAN HEAT ON THE STATE OF THE STATE OF THE ALVERTANCE ALL STRAIN LONG!	199-141		- -						1
PER PACY	INA POLYNGIASE ALPHA SUBUNIT	MALAN RESPONDED TO THE TOWN OF	115.130		L						4
STATE AND AND AND AND AND AND AND AND AND AND	NAM POLYAZEASE ALPHA SUBURIT	MEASURE VINUS (STILADE ELINOTES) CHI	70.5								4
		GEASTES VISUS (STIADN D-1-CA)	11211				L	L			_
		MALKET ES VINUS (STRADA YANKOATA-I)			1	-		L		L	
		HERCAN PALADINE (ENZA I VIRUS (STRAIN C)S)			7177	-					
PRATT FILTE	AND THE REAL PROPERTY OF THE PA	THESTAN PARADITIENZA I VIRUS (STRAIN COS)				1		ļ		L	L
P MINC		TOWASTER SANSET THEN ZA T VIRUS (STRAD) CI. 5/73)	11-94			+					L
		TOWNS AND A PARTITION A 1 WRITE (\$12AIN CI-1403)	14-111	÷.			1				ļ
PERP PINE		CONTROL TANDESCO A CONTROL	167-194	33:32							1
PERSONAL PROPERTY.		PRINCIPLE OF THE PRINCIPLE OF THE PROPERTY OF	1	223-236							1
1	ENA POLYMENASE ALPHA SUBUNIT	HUMAN PALADMIUMAA 3 VINUS (30 MAN)	3	200	305.314	Ĺ					ļ
ATT MAN	ENA POLYNOMASIE ALPHA SUBUMIT	BOVING PALADELUINZA 3 VILUS	7	266.395	L						4
THE PARTY	THE PAR WAREANS ALMAS SUBURGE	HABITA PARADGLUDICA J VIXUS (STRAIN NA VIEW)	17.7		L	 -	L				4
	THE REAL WARRACH ALPHA SUBURUT	HUDGAN PANAMPLUENZA 4A YURUS (STICAM TUSHIBA)				-	L	L			
		EXAMES VIRUS (STEAM PV)			1		1		L	L	
TEN TANK		SEDIMAL VIRUS (STILADS 2.7 HOST MOTANTS)				-	-		L	L	L
903	THE POST OF THE PARTY OF THE PRINCIPLE	EDIDAL VILLE (STEAD) 494)			\downarrow	\downarrow	1	-		L	L
200	THE PURI THE ACT OF THE POST OF THE PARTY.	SENSEAL VINUS (STEAD) PUSIONS)	200		1	-	+		-	L	Ļ
200	RNA POLYMENASE ALTER SUPCIN	CENEZIT CHETA APPLIANCE	130-357	2		-		+			1
000 1111	LINE HOLYMERASE ALIPHA SUBCINI	DELEGACION VINCON CONTRACTOR CONT	1336-151	27 10		_					4

POCINE	1810 13804	All Vange (as betterlephages)		H				П	П	П	Π
PILEHAME		VIRIUS	TYTY	7	3	A SECTION	<u> </u>	र रहार	ARCA CARCA	7	1
PLUP SW		SDZIAN VIKUS S (STIAIN W))	Š	2			+	\dagger		+	Ī
PLODE VACEV	PROTEIN	VACCINIA VIRUS (STRAIN WR)						\dagger		+	Ī
PEDDE VARV	I BISMUTASE LIKE PROTEIN	VARIOLA VIRUS		171	137	1		+	1		Ī
PEHIR AMENY	, DOG	AMSACTA MODILE ENTOWORDINGS						+		T	1.
PWII LWXVI.				-	ļ					1	Ī
PWB WACY	SERVE PROTEDANS DOMINOR :				ļ			-			
PHY CHAP	CVIAIL	PARAMECICAL BUILTANIA CILLONELLA VIAUS I	3								
PIALL VACEV	_	VACCULA VIAUS	95-133					1	-		٦
PTAGE FOWPY	2	FOWLYOX VIALUS	151					+		+	Ī
PTAGE VACEV		VACCINEA VIRUS	2					+	+	$\frac{1}{1}$	Ī
PTAGE VARV	TRAMS ACTIVATOR PROTEIN CKI	WANDLA VILLE	2	_				+	1	+	T
PPALA_BPOV	LANGE Y ANTIGEN	BUDGELUSTAR FLEDGLING DISEASE VIRUS	2	\downarrow				+	1	<u> </u> 	Ī
PTALA POVBO	LANGE FANTIGEN	BOVING POLYOMA VIRUS		-	!	:			<u>:</u>	·	-
PTALA POVILA	LAKOL T ANTIOEN	HAASTEA POLYOMAVIRUS	7				1	\dagger	1	+	Ī
FIXEA PORTY	LANGE Y ANTICEN	LYACHOTROPIC POLYOMAVIAUS			ļ		1	+	1	+	Ī
FTALA POWU	LARGE T ANTIGEN	MOUSE FOLYOMA VIRUS (STRADY 3)		\downarrow	1			t		+	1
TALA POWA		PROUBLING TO THE STATE OF THE S		ļ						-	ĺ
יואר איני		MOUSE FALLOMA VIALES (STRAIN LAAM POINT) SMALL FLANGOS)		100.00	13.446			t		-	Π
PTATE NOVAC	TILANS-ACT TILANS NEW FROTEIN	AUTOLOGIST HINE TA THE TOTAL CONTINUES CONTINUES		7	1				-	-	Ī
FIAIR NEWBA	3 3	CARCAL BERTHATER MATERIAL TO THE PRINCIPLE VIEWS VIEWS	13.1	т				l		L	Γ
PIAIR MYCO	5	CONTRACTOR VALUE (CTRAIN BOLD)	11:59	1215-1342	2 1744.1991	1136-1903		 		L	
/1100 PV	LAKUS IEUUPENI PROJEM	AND	1351-1281		•			-		L	Ī
VIEW MANA		THE SECTION AND THE CASE OF CA	164.64	Т						L	
TITO HOAT	LANCE LECCHENISTICS DESCRIPTION	THE BERT BLANCE WATER AT VIEW AT A STRACT WATER	100	۳	1	962.993	1098-1181	1661-1641	1161-1611		
STATE OF STA		COLORED PROVIDER TYPE : (STEATH ADAP)	225.254	Ì	13651333		Т	т	-	L	
1.	ROTEIN	HELDES WALLES SADALING (STRAIN 11)	334-407	Т	-	146.891	949.626	496.1617 14	1469-1469 2102-213	1133	
L		VALUELLA 20STER VIRUS (STRAIN DUNIAS)	11131-1130	10 1119.160	1			Н		-	1
1		HUNLAN AIDENOVIAUS TYPE ?	118-411							_	-
PIN AVIS	NKA	AVIAN MUSCULDAPONEUROTIC FIBROSARCONIA VIRUS AS42	302-336	П							-
ı		SHOPE FILEONIA VIRUS (STRAIN KASZA)	78-43 24-43	111.17				1	-	-	Ī
ŀ		VACCINIA VIAUS	(7-1)						1	$\frac{1}{1}$	1
ı		VARIOLA VIRUS	3					+		+	Ī
		APRICAN SWINE FEVER YIRUS (ISOLATE MALAWI LIL 201)		+			1	\dagger	1	$\frac{1}{1}$	Ī
PTYRY HSVAR	THY WOYLATE SWITHASE	ACENCY AND A TILLES		1				+		+	Ī
PTYLY HSVSA	THYMEDYLATE SYNTHASE	HELDESVILLE SADARU (STRAIN 11)		97.11	20,400			t	$\frac{1}{1}$	+	Ī
A 100 PM	VIX.ON PROTEIN 1812	CONTRACTOR AND CONTRACTOR OF THE CONTRACTOR AND CON		1				+		╀	ì
PULLOR HISVIE	CALCAL PROJECT OF STREET	EALTH DETRETORING TYPE I COTTAIN ABLES	199					-		ŀ	Ī
THE PERMANENT	VILLOS CADAR OF PROTEIN	PERPESYALIS SADIOU (STANIN 11)	Ĩ	302-358	107-191			-	_	L	Ī
PLEA HONA	INTOTACTOR MA	KIRAN CYTONGOALOVINUS (STRAIN AD164)	į								
PULIT EBY	HYPOTHETICAL PROTEIN BBLF!	EPSTEIN-MARK WRUS (STRAIN 1945-1)	3		1					$\frac{1}{1}$	Ī
PULIT HICKYA	INPOTHETICAL PROTEIN ULIS	HUNAN CYTOLEGALOVIRUS (STRAIN ADIA)		1						+	1
PULIT HSVEB		EQUING MEANESVIRUS TITE I (STAIN ABAP)								+	Ī
7.E.14 VZV5	HYPOTHETICAL GENE 44 PROTEIN	VARICELLA 2017ER YOU'S (STRAIN DUNIAS)		\downarrow	\downarrow				1	+	Ī
PULIS HONVA	KYPOTHETICAL PROTEDY UL16	HEMAN CYTOMEGALOVINUS (STRAIN ADISS)	2	1				\dagger	1	+	Ī
PULSE HONVA	HYPOTH PRO UL20 PRECURSOR	HUMAN CYTOMEGAL OVINUS (STRAIN AD169)		\downarrow			1	\dagger	<u> </u>	<u> </u>	Ī
2	COME 40 PROTEIN	EQUING MEMPENYIUS TITE TO THANK ABAPT	100.00	-	1			\dagger		+	T
24.0	CONE 33 PROTEIN	VALCELLA COLLER VINO (21000 COMAS)		304.31	142.189			t	<u> </u>	 	T
MAZS HSVSA	VOCON GENE 19 PROTEIN	TENTER PROPERTY OF IN STRAIN AND AND	1	Т				\dagger		┞	Ī
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THE PERSON	WALCH ENVELORS OF TOP HOLES IN	HOLDER SAMPLEX VISUS (TYPE 17 STRAIN 12)	16-143		1		İ		 		Ī
HI WOOK	CONS. 67 PEOTEIN	HOLFESTONIS SADOU (STRAIN II)	104-115							L	
TI VAND	VOLORI GENE 24 PROTEDI	VANCELLA ZOSTEA VIRUS (STRAIN BIRAIS)	113:03								П
MEI HOWA	INTERFECT PROTEIN ULSS	KINAAH CYTOMEDALOVIKUS (STRADI ADIBS)	115-543							H	

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HYPOTHERICAL PROTEIN (4.5) HEALM CTIONEGALOWIGH (STACH ADIES) 11-10		_	1	1	\mid		L
HYPOTHERPOLL PROTEIN 113 IRAAN CYTOGEOLOVILIS (STAIN AD10) 15-13		4		1	-	ļ	
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15 ED PLOTES			1	1		ļ	ļ
LITTIFFICIES		-	1	+	-		1
14 CD FEGTERS TOLACCO BATTLE VIREDATES VALUE 14 CD FEGTERS 10 CD CD CD CD CD CD CD CD CD CD CD CD CD				1	+	1	ļ
HELECALE ALTICOLATAN CALD CONTEAN PACTOR 19-115 11-12			1	4		1	ļ
16 XO PLOTEIN 100A DEATH WILES STATEMY TO) 21-34 1.A PROTEIN 10.00-D DEATH WOTH A VALUE 1.A PROTEIN COWPEL VALUE 1.A PROTEIN COWPEL VALUE 1.A PROTEIN COUNTY VALUE 1.A PROTEIN				4		4	1
A PROFESS A PROAD READ BANK OF THE WAYS 23-36	Г			-	4	1	1
I.A PROTEIN COUNTY SECURE TO A PARLY STALLY FANDS I.A PROTEIN COUNTY SECURE TO SECURE	136-463	616-268		_		1	4
IA PROTEIN GOWER CHARGE WALK FILLY FILLY I. S. CHARGE MARKE VALUE (FILLY F	Τ					-	4
I A PROTEIN CUCIABILI MORACE VALUE (STRAM PY) II. STORIED CUCIABILI MORACE VALUE (STRAM P) II. STORIED CUCIABILI MORACE VALUE (STRAM P) II. STORIED CUCIABILI MORACE VALUE (STRAM P)		-		Н			4
IA PROTEIN CUCHERIS MASSÁC VRUS (STAJN Q)		-		Ц	Ц		+
A ROJECH A ROJECH CUCLEMENT MOSKNE (STRAIN Q)	+	+	-	Ļ	Ц		4
	,	-	-	L			4
I IA PROJECT	135.68	113.14		L			
TOWAY OADERAY VALUE	1	Т	-	-	Ľ	Ц	
I A PROTEIN		+	-	-	L		_
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19.5 KD PROTED	-						

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PCGENE	10721789		_	ī	ARKAS						
П	PROTEIN	MINUS			Т	т	_		Г-		
πc	29 KD PROTEIN	TOBACCO MATTLE VIRUS (31 MAIN COM)	10.10	-	:	!	:		_		
A binv	2A MOTEIN	DECAD BEAM MOTTLE VIAITS	į	:	:		;		: :	:	
YYZ CONV	2A PROTEIN	COWPEA CILCACOTIC VINUS			Ī				-	-	
PVZA_CHWFIN	ZA PROTEIN	CUCUMBER MOSARC VIKUS (STRAIN PART)	L	13.11			T			l	١.
VZA PSVI	2A PAOTEIN	PEAKUT STUNT VIXUS (STRAIN I)	Т				T			İ]
VZA TAV	2A PROTEIN	TOWATO ASPERMY VIRUS						l	l	-	٠
PV30K_HC34VE	TO KEN MAJOR EARLY PROTEIN	HUMAN CYTOMEGALOWRUS (STRAIN EISEMIARUT)	51 01.					 	-		1
OK TRVIC	29.1 KD PROTEIN	TOBACCO KATTLE VIRUS (STRAIN 10 NI)	3	İ	!			:	:	•	:
WILL ADEA!	33 KD MIOSMIOPROTEIN	HIUMAN ADENOVIRUS TYPE 41	20.0				Ì	İ	1		
l	K362 PROTEIN	AFRICAN SWINE FEVER VIRUS (STRAIN BATIV)	201.67	-			T				
L	Priss PROTEIN	AFINCAN SWINE FEVER VIRUS (STRAIN BATIV)	e c	8			1	\dagger	$\frac{1}{1}$	t	l
۱	1A PROTECH	BROME MOSAIC VIRUS					1	1	$\frac{1}{1}$	\dagger	١
VIA GAVEN	1A PROTEIN	CUCLAREA MOSAIC WAUS (STRAIN FIVE)	223-252					İ		İ	
700	14 PACTEON	CUCUMBER MOSAIC VIRUS (STRAIN M)	217.252	Ī		İ		1		+	!
	A MACHEN	CUCUMBER MOSANC VIRUS (STRAIN O)	222-253		ĺ			1		†	
2000	TO THE OWNER OF THE OWNER OWNER OF THE OWNER	CICUMBER MOSAUC VIRUS (STRAIN Y)	133-253						1	1	١
NA CONTRACTOR	JA TROISEN	AVIAN INSECTIOUS BRONCHITIS VIRUS (STRAIN HEALTH)	25-57								
NA OV	JA PROIES	ACHAN INSECTIOUS BRONCHITIS VIRUS (STRAIN C'ALIVA)	29.56							1	İ
WIA BYS	JA PROTEIN	A CALL STREET OF A BROWNING CIRCLE AND A CALL DE THE	6.3								
WID GEW	Ja Paolitin	DANS EV VEIT NW DWARE VIRILE (1602 ATE PAV)	119.146							j	į
WOK BYDY	SOKO PROTEDI	SALES I SELON DATA VINOS INCOMENSOR A PER EL 13	113.147	150-07							
PVSIK BWIVE	SI KD PROTEIN	DEST MENTEN SCHOOL STANDARD AND STANDAR	113.147	424.451							
IK INTYG	SI KD PROTEIN	DEEL WESTERN TOLLOW STATES TO THE STATES TO	124.111	11.432							
PVSKK PLAVI	SA KID PROTEIN	POTATOLEA/ROLL VIRUS (STRAIN 1)	17.76	1				İ	-		
VAKE PLAW	SA KD PROTEIN	POTATO LEATAGLE VIRUS (STRAIN WADENISMIN)							-	Ĺ	
PVSEK BSEAV	SI KD PROTEIN	BALLEY STUTE MOSAK VIRUS									
PVICK HUNI	66 7 KD PROTEIN	POTATO LEATROLL VIRUS (STRAIN 1)								İ	ĺ
WAK PLIW	66 9 KD PROTEIN	POTATOLEAROLL VIRUS (STRAIN WAGENINGEN)	3							t	l
OK ANVL	NO KED PRESTEIN	ALFALFA MOSAIC VIRUS (STRAIN 425 / ISOLATE LEIDEN)			914	384.414		T		İ	
OS VACCC	PROTEIN A4	VACCINIA VIRUS (STRAIN COPENHAGEN)		A10.514	113.109	***			-		
VACCV	PROTEIN A6	VACCINIA VIKUS (STRAIN W.K.)	100	10.377	283.10	314.355			-		
LOS VARV	PROTEIN AA	WALCHUS AND PARENT CRUS	136.306								
LOS VACOC	PROTEDY AS	VACCING VIXOS (BI INCIN COTCONICO)	136.206								
KOR VALLY	PROTEIN AS	VALUE A VICES	50.93								
CO VALV	PROTEDIA9	VANCEL VARIET CONTRACTOR OF THE PROPERTY AND	216.283						-		
PVAII VACCC	PROTEDIA!	VACCING VICTORIAN CONTROLLY	220-284								
AII VARV	PROTEDY ALL	VALUE A LINE	440.467								
TIL VALV	SE KD ABORTIVE LATE PROTEIN	YALULA YEAUS	16.9	30.35							
CO VACCC	PROTECN A20	VALLIFIA VIAN (STANK COTERINALLY)	198	15.55						r	
CO VARV	PROTEIN AZO	A ACCIONATION OF THE A PARTICULAR OF THE ACCIONATION OF THE ACCIONATIO	48.72						-	r	
E VACCC	PROTEIN A12	(VACCINIA VIXIS (STRAIN CUPENHAUEN)	10.75							T	
VALL VARV	PROTEIN A22	VAUGLA VITUS	144						-		l
W VACC	PROTEIN A23	(VACCINIA VILUS (STIXAIN COPENHAGEN)	77 10						ŀ	T	ĺ
VALU VARV	PROTEIN A33	VARIOLA VIRUS								T	
WASH WACEV	PROTEIN A28	VACCINIA VIRUS (STRAIN WR)	67.77				Ţ			T	
PUATE VARV	PROTEIN A28	WANGLA VICUS	67-72						1	Ť	
VACOV	PROTEDY A30	VACCINIA VINUS (STRAIN WR)	<u>~</u>						1	1	ı
A VANTE	PROTFIN A31	VACCORIA VIDUS (STRAIN COPENHAGEN)	<u>=</u>						+	1	۱
VALVA ITANA	PROTEGNASI	VARIOLA VIRUS	22						1	1	
2000	PECITEIN A14	VACCIDALA VIRUS (STRAIN COPENHAGEN)	12.							1	
2000	PROTEIN A14	VACCOSTA VIRUS (STRAD) WR)	<u> </u>							1	
VALV VALV	PROTEDIA ASA	VARIOLA VIRUS	<u>=</u>						+	T	١
VACCV	PROTEIN ASS PRECUISOR	VACCINIA VIRUS (STRAIN WR)	120-132						1	T	١
VANA VANA	PROFEIN ASS PRECURSOR	VANICLA VOLUS	127.154			\rfloor				1	
TOTAL DATE	PROTEDI AJS	VACCINIA VIDUS (STRAIN COPENHAGEN)	=======================================							1	
VACEV	PLOTEDIA ASI	VACCINIA VIDUS (STRAIN WR)	3						1	1	١
WALL VALV	PLOTEDY A38	VARIOLA VIRUS	\$ -							1	
						-					

	10,11,111		4	ABEAI	1	1					l
LE HAME		VIR. 1		021-161					1	Î	
VACCV	479	VACCINIA VIRUS (STRAIN WA)	145.172								١
2070 1770		VACCINIA VIRUS (STRAIN COPENIIAGIUM)	-								
700		VACCINIA VIRUS (STRAIN WR)								ŀ	
		VALIGLA VIRUS									<u>:</u> ا
AC) VARV		VACCINIA VIBUS (STRAIN COPENHAGEN)									
WW. VALLE		VACCENTA VINUS (STRAIN WR)									۰
AVO. AVC.		VALIBLA VILUS	20.7								
ı		VACCINIA VIRUS (STRAIN COPEMIAGEN)						1	-	!	:
ı	PROJEIN AND	VAPORILA VIRUS (STRAIN WR)	61.91					1			ĺ
MAM VACCY		VALUE A COLUM	16-19							Ī	
VAM VANV		A AKING A WAS A MARKINIA COM	35-63	126-156	435-462						
FVAIS VACCE	PROTEIN ASS	VACCINIA VIKUS (STRUM CONTOUND)	21.55	136-156	435-462						l
WALL WACTV		VACEDITA VIRUS (STRADY WR)	9.56								
		SEET COLLY TOP VIRUS	4,644								
V		PARKAVA LATENT VIRUS (STRAIN WEST KENYAN M4)	74-100								
PVALS CLVK		CATALON I ATOMY VIRING STRAIN NIGERIAN)	79-106								
TVAL) CLYN			101-12								
VAL BLCV	ALJ PROTEIN	NOTES TO SELECT AND WAS PARTY.	19:129								
PVALL PAICY		TOWATO YELLOW LEAS COLL VINGS	27.50	93.129			L				
127		CALL DOWER MOSAIC VINUS (STRAIM CM-1841)	5								
		CALLIDIOWER MOSAIC VIRUS (STRAIN O'H)		1							
A CANA		CALIFICAVER MOSALC VIRUS (STRAIN BBC)	277.10	21:0							
VAT CUNE		FATH INTOWAL MOSALC VIRUS (STRAIN NYBISS)	22.70	47.							
PVAT CANNY	APRID TRANSMISSION FRO BLY	PAINTED OWER MOSAIC VIRUS (STRAIN PV 147)	22-70	67-170							l
TVAT CAKM	Ī		23-70	93-130							
AT CAMPS	AMED TRANSMISSION PROTEIN	TOTAL BUTTO BUTTO LINE IN COMMENT OF PRINCIPLE AND UP SAGE	36-70								
AT CONV		CAULTICOMES POSSES VINOS (3) TOTAL	102-138	L							
VAT CERV	APHID TRANSPICISION PROTEIN	CAUATION STORED LING VINUS	13:55	051-501	_	L					
VAT PAND		FIGWORT MOSAC VINUS (3 PANIM DAS)	104-135								
Union VACEV		VACCINIA VIRUS (STRAIN WA)	151	112.21	286-313	124.35					
AN IN		(VACCENTA VIRUS (STILAIN COPENHAUSIN)	151	1	244-313	124.361					
7.00		VACEBRA VIXUS (STILAIN WR)	100		206-313	134-361					
ŧ	PROTEDI SA	VARIOLA VIEUS	24.364								
	M ACCREMENT NOST LANCE PRO PREC	VACCORIA VIRUS (STILADY LC INNO)	725						_		
	M AND REPORT HOST RANGE PRO PREC	VACCINIA VIAUS (STILAIN COPENHAGEN)									L
1	H A PATH, STZR / HOST RANGE PRO PARC	VACCEMIA VIRUS (STRAIN LISTER)								L	
	WASHINGTON HOST BANGE PRO PREC	VACCINIA VIRUS (STRAIN WR)						-			L
1	SANTERS BY BEET MICH.	VACCORIA VIRUS (STRAIN WR)	7000								L
A NOTAL	To constitute the Early Page	VACCINIA VINUS (STRAIN COPENHAGEN)	î			\downarrow					L
AND VACE	PARTIES DE PARTIE DE CASE	VACCINIA VILUS (STRAIN WR)	(e-3)	1	-						L
A 440	PROTEIN BETTER STATE	VACCINGA VOLUS (STILAIN COPENHAGEN)	ž.		\downarrow	\downarrow		-			L
PVB11 VACCE	PROTEIN SIL	VACCESSA VILLE STRADY WR.	13-31								ļ
PVBII VACCV	PROTEIN BIT	County Valle	(13-140								1
PVB16_COWPX	IL I BIND PRO PRECURSOR	CANADA UNITE CENTANI COPENHACEM	258-285								╽
7817 VACCC	PROTEIN BIT	COLOMBIA CONTRACTOR AND MAIN	512-152	_							1
WBIT VACEV	HOTEN 817	VACUAL VICTORIAN AND COMPANIA CENT	27.11	L	L						1
PVBIS VACOC	PROTEON BILL	VACUADA VIACO (STANDA COTESTICATES)	\$15.710	L	L						\downarrow
PVB18 VACEV	PROTEIN BIS	VACCINIA VIKUS (31 MAI)	11.37	L					L		
VALUE VALUE	PROTEST BIS	VALIGITA VIRUS		-	-	-					L
100	BENEAUT ANTIONN & PRECURSOR	VACCINIA VIILUS (STIVAIN COPENHAGEN)	7 7 7 1	1	1		\downarrow				L
TANK SIEAL	STATE ANTHONY & PRECITEOR	VACCINIA YOUS (STRAIN DADLEN !)	2.0	1	-	\downarrow		-			L
1	STATE AND AND AND AND AND AND AND AND AND AND	VACCINIA VILLE (STRAIN WR)	200		1	1	-				L
VAUV VACV	STATE AND AND AND AND AND AND AND AND AND AND	VAUNALA VIRUIS	180-310	-		1	\downarrow				ļ
VALLY VALV	SULL ALE ANTINES ET SECTION	VALEGIMA VIRUS (STRADA COPENHAGEN)	41-22	_				1			ļ
VIEW VACAL	PROJECT BASE	VACCIDIA VIRUS (STRAIN WR)	2-2	7		1		+			ļ
WEST VACO	MOTERA	BEAN ON NO MOSAIC VIRUS	120-147	£		\downarrow			1		╽
PVBL! DOMY	BL! PROTEIN	CARLOL I AYENT VILLIS (STIATIN WEST KENYAN DAR)	114-145							1	1
PUBLI CLVK	BLI PROTEIN	PARTON I ATTACK VALUE (STRAIN NICERIAN)	111-145								1
אונו על	BLI MOTER	TAY TO VETT OW LOCATE VILLS (ISOLATE VENEZUELA)	130-149								1
WIT WWW	BL! PROTED	VARMA VIEUR (STEAD) COPENNAGEN)	405-432			_			\downarrow		\downarrow

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POCENE	167117814	All Virges (no bactimophs/fts)			Т	ABEAA ABEA&		Y TOTAL	AREA 7	A REAL	<u>ک</u>
FILE NAME	PROTEIN	MAUS	10.00	4	7				Т	7	
PVCM SFVKA	PROTEIN CA	SHOPE PERCONA VIRUS (STRADY RASZA)	,,,,,,					T			
SVCSI VACCE	PLOTENCE	VACCINIA VILUS (STIALIN COPENHAGEN)	12.28					T	T	T	l
WCD VACCV	Horibica	VACCERIA VIRUE (STRAIN WIL)	?						Ì	ŀ	
PWSS VARV	PEOTENCE	WANGLA VAUS	*					T	İ	Ī	ł
PYCS LIVE	HAPOTHETICAL PROTEIN CS	SHOPE FIBROWA VIRUS (STRAIN KASZA)	185-125	132-179				T	T	Ī	1
PVCM VACCE	PLOTEINCS	VACCINIA VIRUS (STRAIN COPENHAGEN)	ŝ						T	1	٠
PWGS/VACEV	PROTEDICS	VACCINGA VIRUS (STRAIN WIT)	38-65					Ì	T	Ī	1
PACES VALV	PROTEINCS	STORY YOUR	30.00					-	Ī		İ
PUPPED ULTER	(A) Particular	VACCINEA VIRUS (STRAIN WR)	30-111								
OT COMPANY	100 ACC 140 A-1	VALVALA VIXUS	111-01								
	real and	DAPPEN CHIE STEAM COPENIA CRIA	42:69	13-116		151.279	289-325	\$75-605			
NOW AND	PROTEIN	TO STATE OF THE PARTY OF THE PA	65.66	82.116	Γ	251.279	289-323	\$75-605			
PYCON VACCY	PROTEINCO	VACCEMIA VINCE (STRAIN WA)	14.184		I						
PVC18 VACCC	PROTEIN CIO	VACCIMIA VIKES (STIMEN CUPEANACE)									
PYCIO VACCV	PROTEIN CIO	VACCINIA VIRUS (STRAIN WR)	9		:	•	:		;	;	•
PUTIO VARO	INECTRIN CIO		136-163								
A VICTOR SHOWN	DE STEIN FLY	SHOPE FIREDOMA VIRUS (STRAIN KASZA)	3.30	39-66	137.102	200-240					
	100 CT 10 CT	IVARPORA VIRUS (STRAIN COPENHACEN)	1111-152								
TACITY AND T	PROJECT STATE	GARANTE CIBIT ACTORNIA CIBIL	40.74			L					
PYCIE VACE	PRUIDIN CIPBON	CANADA BARINATA UMBIR JENE AND VACATA	(4.0)				L				
PVCI9 SEVKA	PROTEIN CI9	SHOTE PLANCES (SINCE AND	2								į
PVC28_VACCC	PROTEIN CHORAS	(VACCINIA VIKUS (STRAIN COPENTIACIEM)	10.0						ĺ		
PVCTS VAILV	PROTEIN CIVILLE HOMOLOG	VANCEA VIRUS	276.578								
OF A STAUS	MAINE CAPRID MENTERN	EPSTEIN-EALK VALUS (STRAIN 895.8)	147-174								
THE PARTY OF	MALCO PARENT BROWEN	HERPES SOCH BY VINUS (TYPE 6 / STRAIN LIGANDA-1102)	136-170	285-382							
	PANA CO SECURITION AND AND AND AND AND AND AND AND AND AN	Designation of the party of the art 111	169-799								
PVCAP HSVSA	MAJOR CAPSID PROTEIN	ACCUSATION OF THE PROPERTY AND THE PARTY OF	111.164	100.748							
PVC03 NPVAC	DNA-BINDING PROTEIN	AUTUGRAPIA CALIFORNIA MOCLEAN POLITECIMOSIS VINUS									
PVCOM ADEXX	MINOR CORE PROTEIN	HUMAN ADENOVIRUS TYPE 1									
SOCIAL ADEOS	MONOR CORE PROTEIN	HUMAN ADEMOVIALIS TYPE 5	12.14								
PUTTOR BOWE	192 6 KD PROTEIN	FOWLPOX VIRUS (STRAIN PP.1)	6-33	194-23	321-348						
TANK CANA	PECTENT DE	VACCINIA VILUS (STRAIN COPENHACEN)	240-267	333-360							
200	an Andrew P.	VACCING VISITS (STRAIN WR)	240-267								
	THOUSE PARTY	LAKKWA A WARTH	240-267	L							
1	redient to	CANCELLA COREST CATE AND POPENHACIENS	123-150		L	L					
PVD09 VACCC	PROTEIN UP	TACCAST VINCE (STORY COLUMN CO	131.146								
PVD09 VACCV	PROTEIN D9	VALUINA VIKUS (STRAIN WA)	999								
PVD09 VAILV	PROTEIN D9	VALUE A VIXUS									
PVD10_SPVKA	PROTEIN DIO	SHOPE FIREDMA VIAUS (STRAIN RASZA)									
PVOST CERV	DKA-BODDIO PROTEIN	CARKATION BTCHED KING VIRUS	60.33			1					
PVECE VARV	PROTEIN ES	VALIDITA YIDUS	727.72								
PVFOX VACCE	MOTERN EA	VACCINIA VIRIUS (STILADA COPENHAGEN)	8-18	375							
DAY OF THE	PRINTERN PA	VACCORIA VIRUS (STRADI WR.)	89-116	437-464							
200	Santana EA	VALIDITA VITUS	911-60	367.394	433-464						
11/10/11/19/14	IN PROTEIN	HEMAN PAPEL CALANDOS TYPE IB	60-87								
1 (2) (2)	NOALCOW IN	HUMAN PAPILLOMANDRUS TYPE 2A	21-48								
1000	List be over 1	KIBAAN PAPELIDALAVIRUS TYPE 53	160-207								
1000	K. DO ATEN	HIMAN PAPEL CHAVEUS TYPE 39	103-130		_						
177.00	No. Control	MARAN PAPEL DALAVRUS TYPE 41	15-89	L	L	L					
	In the party of	LATALANDA PART I PALANTRUS TVPE 42	33.59			L					L
100	EI PROIEM	CARACACTER AND PARAMETER TAND AS	146-173								
PVE! MV47	EI PROTEIN	COMPANY TRANSPORT TO THE TANK AS	17 15				L				
PVEL HPVS?	EI PROTEIN	NUMAN PATILLINA TANDS 1116 37									
PVEZS NOVAC	EARLY 25.9 KD PROTEIN	AUTOGRAPHA CALL CANTA RUCLCAN FOL I RELACOSO VIACO					ļ				
PVE1 CLIVIK	PROSABLE EZ PROTEIN	COTTONIAL RABBIT (SHUPS) PAPILLOMA VIRUS (STRAIN RAMSAS)			1	-	\downarrow				
PVEJ HOVOS	PROSABLE E2 PROTEIN	HUKAN PAPILIDAAVIRUS TYPE 3				\downarrow	\downarrow				
PVE2 HOVIS	E2 PROTEIN	HUMAN PAPALICMANTRUS TYPE 13	137-184	1							
NAME AND A	E2 PROTEIN	HUMAN PAPELLOMAVIRUS TYPE 14	61-105	315.342							
PVR2 HPV18	E2 PROTEIN	HUMAN PAPELLOMAVIRUS TYPE 10	313-340		╛		_			Ì	
AIVES LIBVIA	E2 PROTECN	HUMAN PAPILLOMAVIRUS TYPE IA	159-186		_						
Tenan tana	E3 PROTEIN	HADALIN PAPALICALA VIRUS TYPE 2A	139-193								
	ES DE CATALO	LANCAL DAPP COMANTRIES TYPE 13	304-331	L		L			_		_
SVET HAVE						-					1

\prod									-	_	
I		VIRIS	241-851	327-354	-	1		1	+	T	١
		KURAN PAPILLOMAVIRUS TYPE 33	Г	131.157		_			1	Ì	l
1		HIDIAN PAPELIONAVIRUS TYPE 39	Ī	Т	276-303				1	1	$\ $
٦		HINAAN PAPAL DAKAVIRUS TYPE 47	Ţ.	Т		T					ł
		THE VALUE AND MANAVIRUS TYPE SI			-				<u> </u>		
		THE TANK DADE I DIVAVIETS TYPE ST	2		†	1		\mid			
		CHANA DEATH AND VIEWS TIMES ST	1		1			-			•
	MOTEN IS	AND	- - - -			1					
		STATES OF THE PART PLANTING	╗			1			+		
Ī	E E2 PROTEIN	EUROPEAN BLANTAN LAND TO A CUBING TYPE I	267.294	327-361		Ì	1	1		Ī	
T		YOUR CHIRCANEE PATHEORY INCOME	202-220			1		+	+	Ī	
T	R EA PROTEIN	HUMAN PAPILLOMAVINUS LYPE >	11.108					1			ļ
		HUNLAN PAPILLOMAVIRUS TYPE !!	10.00						1	1	١
		HISTAN PAPELONAVIEUS TYPE 16							1		١
		HINAN PAPELLOMAVIRUS TYPE 15	200								
WEA HOWIS	HOBABLE BA PROTEIN	DOMINAL TO BE ALLA LIGHT TYPE TI	75-102						t		
Γ		CHAN FALLMAN VINCE VINCE	63.93		_ 	İ		-	-	:	;
		HUMAN PARLICHAVIRUS I VEB 41	303.229						1		١
1		ABLAN PAMLLOMAVIRUS TYPE 30									
STACH TOACH		THE STATE OF PARTIES OF TABLE 11	30.00		j						
Γ		REAR PALLUMENT TO THE	30-60		-	:		_	•		
		KIDAAN PAPILLOMAVINUS LYPE 913	0/01		_				1		1
EIA HOVES		THINDAN PAPILLOMAVIRUS 1 YM: 60:			!						١
PVESA NEVEC		AN PAPEL PAPEL PARAVIRUS TYPE 35	200							i	
1 10 Kg 2		DOMAN TAY WAS CARTIE WAS AB	<u>=</u>					1	İ	-	!
		HUMAN PATLICAMATICUS I TESS	15-62			Ì					١
2		PYGMY CHIMPANZEE PAPILLONIAVIRUS ITTE	34.103								
WEJ POVI		WANTAN PAPEL COMAVIRUS TYPE 10									į
PVES HOVIE		TATELOUS BASELL PAZAVIELIS TYPE 31			1						
1000		AUTHORIS AND MAIN WORK IN	11-102								L
ACPA UNIVAS	KI MOTEIN	HUMAN PATELLING THE STATE OF TH	119-146								
		HUMAN PAPILLIMAVINUS I TE	75.102	L							1
		RUNDAN PAPILLOMA VIRUS TYPE 43	8			Ĺ					
PVEA HOVE		KUNKA PAPELONAVIRUS TYPE SI	,							Ì	
14 HDV31		HALLAN PAPELLONAVIAUS TYPE ME180			-		L				
WE FOND	La Profession	ATTENDED MILE CALIFORNICA MUCLEAR POLYMEDROSIS VIRUS									
WEN HOVAC	Ī	THE PROPERTY OF CHANGE OF STRUE					_				
140 DA	VIEW DOGANCING ACTOR	PARTY CHEATH DISTANCE (1941)									
VEN DAMI	5	PERMIT A SERVICE VALUE	200								L
VAL VAR			313.34								L
VANA CANADA	205	THOCOTO VILLE	91-110	185-212							
		VACCINIA VIDUS (STRAIN COPERTAGER)	91.110	185-212							1
AVE VALLE		VACCOMA VIRUS (STRAIN WR)	57.5	 -							
TO VACEV	23.81	DACCEMIA VIRUS (STRAIN L. IVP.)								_	
Met VACO		THE PARTY CASE AND AND AND	25.60		1						L
AULUS ANNE	14 KD MAJOR MENDRANCE PRO PRECURSO	VACCIMIA VILLO (3) Main 1117	3								
	Married BA	VAUGA VIRUS	1274-321	L							
MICS VALV		TVAECENTA VIRUS (STRAIN COPENHAGEN)	100								
WILL VACCE	PROTECTION	VACCINIA VIRUS (STRAIN L.IVP)	2							L	
WELL VACO	PROTEDNEIL	Total A Orbite	126-942		Т						L
WILL VALV	PLOTEN FIL	TANCOL TO THE SAME OF THE PROPERTY AND T	<u>5</u>	13:140							L
100	PROTEDY F12	VACUNA VIUS (31 Mary Controller)	10-31	113-140	154-511						1
	PACTOR III	VACCINIA VIRUS (STIVAIN L-1V7)	100	202-236	554.511			-			1
3		VALIGIA VIRUS		21 531	-						
VF12 VARV	MOTERATIO	VAZY-INTA VIRUS (STIKAN COPENHAGEN)							L	L	_
VF16 VACCE	PROTEDN F16	LANGER CONTRACTOR (NO. 1979)	15-61	132:12	1			1			L
SVE IN DAGS	PROTEIN F16	VACCINIA VINOS (31 NOS) (11)	15-62	145-179							1
200	DE OTTER FILE	VALUELA VILLE	146-17	L							1
1	THE CATE IN STREET	FOWLYOX VIRUS	28.16	-	-						1
2	THE PARTY PROTEIN	OUT VIRUS (STRADA NZZ)	77.63	-		L					
MICE CHANGE	A PART OF THE PART	VACCINIA VIRUS (STRAIN COPENHAGEN)	3	-	-	L		_			_
WHUS VACOC	I I I D PUSIUM PROFESS	VACCINITA VIRUS (STIAIN WIL)			-			 -		L	_
WIUS VACEV	KD FUSION PROTEIN	UA CTINITA VINIS (STRAIN COPENIA VINIS	125-251	Т		1	-				L
PYCO! VACCC	PROTEIN GI	CANANA MINISTRAIN WAS	164-19	╗		1	-				-
VALLE VALLE V	MOTERICI	AACUNIA TANGE	225-252	301-335							1
0 10	PROTEIN G	VAUGA VIXUS	96-133	F				1			1
	AS A STATE OF THE PROPERTY.	VACCOCA VOLUS (STRADA W.K.)	1	L		Ļ	_	_		_	
						1				l	l

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		All Virgini (se bacitive pragri)			⇁	Т	7	Т	Т	Γ	
PILEHAMIE	PROTEIN	VIRC	1	7		7	र्	7020	T days	1	
PVOOJ KSVEB	GENE 1 PROTEIN	EQUINE IERTESVIRUS TYPE I (STRAIN AIMY)	****	!	:		:	:	:	:	:
PVOD ISVEK	CENE 1 PROTEIN	EQUINE HELPENAND TITE I (STAKIN ALTHOUGH A)	26.36	14.11	334.310	114.110				Ī	
PVCO: VACE	PROTEINGS	VACUALA VACA (31 AAAA COTCAAACEA)	1 1	34-16	Т	355.319				F	
PVCS VARV	CONTRACTOR CONTRACTOR DECI	ICTATUMES VIRUS I	71-98		Т						١
MOSA VACOR	PROTEIN	VACCINIA VIKUS (STRAIN COPENIAGEN)	306-338								1
PYOON VACEY	PROTEINFI	VACCINIA VIRUS (STRAM MR)	171.301							-	
PVC09 VARV	PROTEIN FI	VARIOUA VIRUS	303-338								
FVG11 EVIL	DENE 13 PROTEIN	SPIROPLASMA VIRUS SPV1-RIAZ B	S)-								
PVOLY REWI	HYPOTHETICAL GENE IS PROTEIN	ICTALUNUS HEAVES VIRUS 1	177.204								
PWGII NBWI	HYPOTHETICAL DENK 18 PROTEIN	ICTALUMUS HEAD-BIS WINUS 1	174-208								
FVOI SPVIA	CASID PROTEIN	SPIROPLASMA VIRUS SPVI-KIAZ B	260-211							- 	İ
PWGI SPW4	CAPSID PROTEIN	SPIROPLASIAA YIRUS 4	287.314	313-410						Ì	İ
PVG13 KBVII	HYPOTHETICAL CENE 23 PROTEIN	ICTALUNIS HELPESVIRUS 1	311-400	\$81-622	668.705	76.52 26.53					
PVQ24 HSVII	INTERNATION CENTERS 24 PROTEIN	ICTALUNID HEAPESYIRUS I	31-58								
PVG28 HSVII	HYPOTHETICAL GENE 24 PROTEIN	ICTALISMS HEAPESVIAUS I	233-290	407-528							
PVGIR ALGEV	HYPOTHETICAL OZR PROTEIN	AMSACTA MOOREI ENTOMOPOXVIRUS	33-64	=							
PVG1 SPVIE	GENE 2 PROTEIN	SPIROPLASMA VIRUS SPV1-REAZ B	215.326								
NO CAN	GENE 2 PROTEIN	SPIROPLASMA VIRUS 4	(41-99)	175-205	262-310						
PVGM HIVE	HYPOTIGHTCAL GENE 24 PROTEDY	ICTALUND MERPESYIRUS I	65-123								
PVG13 RAVE	HYPOTHETICAL DENE 37 PROTEIN	ICTALUND HERPESYAUS I	443-469								
PUCKE DECK	LAVENTARTICAL CROSS SO PROTEIN	ICTALURIO HERPESVIRUS I	651-671	100							
NO.	INVESTIGATION OF PROTEIN	AMEALT'S MOOREI ENTOMOROXVIRUS	3.29								
1000 1000	Carre v Period	SPIROPLASMA VIRLIS SPVI-REAZ D	15.49								
1000 FOVE	CONT. 1 PROTEIN	SPIROPLASMA VIRUS 4	18.52	17.148							
	TOCOCOCOCOCA A DESCRIPTION	LICE PRECORTS EASILIES (STRAIN 11)	138-165								
	ATTOTACE BUT IN IN ALL DANGERS	Heral Dain Leanner Views	142.168	1000	893.934	973.1307					
THE PARTY OF	LIVERATURE AL MANUEL AR DECISION	HERPESVRIS EALLINGSPACK II)	360.3FE		T						
Description of the second	CAR DECITED	AMSACTA MODRE! ENTOMOPOXYRUS	431								
	CONTRACTOR A PROTECTION	SPIROPLADIA VIRUS SPVI-MAZ B	118-146								
PVORT HEVEL	HYPOTH GENE SI KEMBANE PROTEIN	ICTALUND HEAPESYMUS 1	36-61	17.114							
PAGES HEVEA	HYPOTHETICAL GENE 52 PROTEIN	HERPESVIKUS SABARN (STRAIN !!)	47.74								
PVQM HSVII	HYPOTHETICAL GENE SO PROTEIN	ICTALURID MRAPESVIRUS 1	582-609								
PVGS SPVIR	OENE S PROTEIN	SPIROPLASMA VINUS SPVI-RIAZ B	200								
PVGS SPV4	CENE S MOTEIN	SPIROPLASMA VIRUS 4	2								
PVG63 HSVII	HYPOTHETICAL GENE 63 PROTEIN	KTALUMD VENUESVIKUS I	2000		\int						
PVO64 HSVII	MYPOTHETICAL GENE 64 PROTEIN	ICTALUMED PREPARATION I	477.30								
PVCK5 HEVII	MYPOTHETICAL GENE 45 PROTEIN	ICTALUMD PERPESVIKUS I	1213-173								
	HYPOTHETICAL GENE IS PROTEIN	ICIALUM MACES WOO	9741 1741								
Mar (SOA)	HYPOTHETICAL CENE 67 PROTEIN	ACTALONIC MENTION IN THE PROPERTY IN THE PROPE	261.288	L							
1000	DAMPETICAL COME TO PROTEIN	ICTALIATIO SERPESYTRUS (447.481								
DOWN THE	HAYOTETICAL GENE 23 PLOTEIN	ICTALUND HEAVESVIAUS!	388-423								
PACTA LANGE	HYPOTHETICAL CADAS 76 PAOTEDA	ICTALUNIO HERDESVINUS I	200-227	L							
Will Cove	GENET PROTEDI	SPINOPLASMA VIXUS 4	<u> </u>								
PVC#1 DIVB	FIPEOTED	A VIAN INFECTIOUS BLONCHITIS VIRUS	1230-1260	2401-2435							
PVCB 5 CVB5	E2 CLYCOPACIEN PRECURSOR	BOVINE CORONAVIDUS (STRAIN F15)	399-426	642-676	1022-1064						
PVG 2 CVIII	E2 CLYCOPHOTED PRECURSOR	BOYDE COLONAVILUS (STIAIN L9)	199-426		1022-1084	1276-1305					
VIEW S CARLY	E2 GLYCOPROTEDN PRECURSOR	BOYDAL CORONAVILUS (STRAIN LY-131)	199-426	642-676	1022-1084						
MRV + PVR	ES CH. YCOPHOTHEN PRECURSOR	BOVING COLONA VIDUS (STRAIN AEBUS)	399-436	642-676	1023-1084		1				
OEV.	E3 CLYCOPROTEDY PARCUMSOR	(BOVDER CORONAVIRUS (STRAIN QUEBEC)	199-426	F43-676	1023-1064						
2	F2 CL VCOPEDITED MECURSOR	BOYDE CORONAVAUS (STRAIN VACCINE)	254-256	643-676	1022-1064	11274-1305					
Was CME	ES OLYCOPROTEIN PRECURSOR	HUMAN CORONAVAUS (STIVAIN 179E)	710-797	\$09-475	Н						
PVGLS CYMA	E2 OLYCOPROTEIN PRECURSOR	MUNDER CORONAVIAUS NOIV (STRAIN WILD TYPE 4)	M3-6M	1030-1092	~						
PVCL3 CYMAS	Г	INCHERYE COSCONA VIRUS MOTV (STRAIN A 59)	76-63	20163	978-1040						
PVGL3 CVNUC	B1 CLYCOPROTEDN PRECUMBOR	MUNDAL COLONAVINUS MORY (STILAIN HORY / VALUANT CL-2)	1	1030-1092			\int				
FVOL.2 CYMUN		MUNDNE COKONAVIKUS MHY (STRAIN JION)	X2:X2	2						1	

	1107417414		ARCAL	AREA?	AKEA 1	ARGA!	AKIA	1			
ALL VALUE	PROTEIN	IVINUS	Г)	2	1353-1389					1
VO. 2 CVP1	E2 GLYCOPROTEIN PRECURSOR	PORCING TRANSMISSIBLE GASTROOM I EN 113 CONONA SIBLIS (STRAIN NILL 169	Γ	11 (61-50)	069-1145	6161-6561					
	IN GLYCOMOTED PRECURSOR	PORCOGE PRANSMISSIBLE GASTROCATELLIS CONCRAVIRUS (STRAIN PIEZAT).	Γ	t		1351-1387					
PVOL3 EVEN	ES OF YCOPADTEIN PRECURSOR	PORCONS TRANSMISSIBLE GASTRORM ENTRE CONDUCTURES STRAIN PIRED 69	Γ	t	1063-1143	131-138					į
WOLD CYPE	E2 OLYCOPROTEIN PRECURSOR	POLCINE TRANSMISSIBLE GASTROEM PATTIS CONCINCULAR TRANSMISSIBLE GASTROEM PATTIS TO THE TOTAL TO THE TOTAL TRANSMISSIBLE GASTROEM PATTIS TO THE TOTAL TRANS	Т	T	1129-1165						<i>خ</i>
VACES CAPES	E2 GLYCOPROTEIN PRECURSOR	PORCINE LESFIRATORY CONCENTRAL STATES AND THE SECOND STATES AND TH	Г	Г	1139-1165						1
VOILS CVPEN	EL OLYCOPROTEIN PRECURSOR	PORCOVE RESPIRATORY CORDINAVIROS (3 I MAIN MAIN)	Ţ	T	1361-43 1135-1387	1353-1361					-
WOLS EVERT		POSCONE TLANSMESSIBLE CASH FOR THE CONTRACTOR OF THE CASH AND THE CASH	ā		Γ				-	-	
VOL S LOV	PROBABLE MEMBERANE OLYCOPROTEIN	EPSTECH BALL VOICE (STRAIN BRYST)	L	11793	301.136	1072-1148	136-1702				
Valla Papy	ES OL VCOPROTEIN PRECURSOR		ī		1121-1211]					
VOIL BOX	11:3 OLYCOPROTEIN PRECUASOR		Т	T	801.50		Ĺ				
	ES AL VENDROTPIN PRECURSOR	DETILE	Т	Ť	1001			_		-	L
	THE CHANGE OF STANDER COME.		Т	†	1004 1000					L	L
The state of	EL CLICATION PROPERTY	(3)	┑	7	20.00			\downarrow	-		L
VOLUENK	ES CLYCOPIOIEM PIECUESA		101-135	175-902	98-1080					-	-
VOL.2 BYM	ES GLYCOPROTEIN PRECURSOR		95-122	631-658						4	1
WOLL EN	GLYCOPIOTEIN CPI 10 PRECUISOR		18:81	197-424	440-467	131-13					-
AVE BUTTON	CH WOOFLOTEIN S PRECURSOR		Г	107.424	435-462	1132-179	L			_	_
	CONTRACTOR DESCRIPTION	HIDLAN CYTOMEGAL OVIRUS (STRAIN TOWNE)	Т	Т						L	
WILL HOW	CALCALLY AND SELECT PROPERTY OF THE PARTY OF		× ×	1	١		ļ	-	-	-	L
184	OLYCOPROJETA I PRESENCE								1	-	ļ
VOLUMENTS	CLYCOPACTEIN B-1 PRECUESOR	154)		934-961				1	1	1	1
VOLUMENTIAL	GLYCOPKOTED/ B PRECUISOR		416-513 6	616-643		_				4	-
WANT DEVEL	THE VOTESTIEN IN PRECUNSOR	EQUING HEAPESVIRUS TYPE 4	Т	170 710			L	L	-		
1000	OF VANDEDTEIN B PRECURSOR		τ	2	ļ			L	L	L	
1	CONTRACTOR DESCRIPTION		Т				-	-	-		L
VOL HSVED	G. Turkol tin B Presenta		_	933-960			ļ	-	-	-	-
PVOLE HEVEL	OLYCOPROTEIN & PRELUKSUR	STATE OF THE PARTY		352-379				-	1		+
D MAN	OLYCOPROTEIN B PRECURSOR			441-475						+	╁
WOLL LOW	GLYCOPROTEIN B PRECURSOR		460.310			L					1
VOLC HISVII	DLYCOPROTEIN C MECURSOR		464.510							-	-
WAY EVIL	GLYCOPROTED C PRECURSOR		124.151			L	L			-	
THE PERSON NAMED IN	CH VCOPEDTEIN C PRECURSOR	EQUING HERPESYINUS TYPE 1	161.10	Ī			L	L	L		Ц
00.65	GLYCOPIOTED GPV		304.177				_	L			Н
10 to 10 to	CL VCOMOTED OFV	AIN PACIFIC				L	-	L		_	
1	AT VANSHOTTEN E PRECURSOR		1	14.303	314.345	442,489	486.53	ļ	-	L	L
ŀ	FIRETON OF VOOREDIEDS PRECURSOR	I	T	Т	17,716	77	Т	-			L
	THE PERCHASION	T	1	τ			113.00	-	-	-	-
-1	CONTRACTOR OF COLUMN PROPERTY OF	٦	╗	ž				1	+	+	ļ
J١	POSICIO CE L'OCTRO LEGIT PRESCRIPTION DE COMP	CANTINE DISTEMPER VIXUS (STRAIN ONDERSTEPOORT)		7			-	1	+	1	
1	FUSION OLYCOPROTEIN FACTOR	USBLAND BETEN ATOR V SYNCYTIAL VIRUS (SUBGROUP B / STRAIN 1833?)		7	2		1	1	+	+	+
1	PUSION OF YCOPHOTELY PARLUASON	CHRAZA BERREATORY CONCYTIAL VIRUS (STRAIN A2)			200	-	_	-	1	1	+
	FUSION OF YOUNGIEN PRECUISACE	THE STATE OF PRINCIPALITY OF STREET OF STREET OF STREET	18-65	154-203	116-243	444.	481-313	-	-	$\frac{1}{1}$	\downarrow
	FUSION CLYCOPROTED PRECURSOR	HUMAN BESTER (CASE STACE) AND CASE (CTD ATM 155.2)	33-65	154-202	113,243	443-471	488-518			-	$\frac{1}{1}$
	INSIGN OF YCOPROTEDY PRECURSOR	HUMAN KENDA LOKE SINCE LOCATION AND UALLES	226-262							_	4
	PUSION OF YCOPKOTEIN PRECURSOR	MEASURE VILLE VILLE CONTROL OF THE C	231.265			L	L	L			4
	PUSION OF YCOPROTEDY PRECUESOR	MEASURE VILLS (STRAIN DESCA)	228.262			L	L	L		Ш	
WILL LAKEN	PUSION CLYCOPROTEIN PRECURSOR	MEASURS VOUS (STIAIN YAMANA IA-I)	т	47.416		L	-	-			
	FINE THE YOUNG THE PRECURSOR	MAINON VIELDS (STIAM) SEL-!)	T	147.414			L	L	-	_	-
٠ŀ۶	STRICK OF VENERALISM PRECUSSOR	MAININGS VIRUS (STRAIN MYAHANA VACCINE)	Τ			1	-	ŀ	-	-	H
	ETRION OF VONEROTEIN PLACUASOR	MONDES WINCOS (STRAIGH RW)	Т			ļ	1	-			-
	THE PART OF COMPANY OF PARCITAGE	MONEY VELUS (STILLIN SEL.)	Т			1	+	1		-	╀
3	TOWN OF VOORSTITUTE PRECINITION	T	7			1	ļ	1	╀		ļ
1	THE PERCHASING THE PERCHASING THE SORT	T	7	200		\downarrow	1	+	+	ŀ	+
- 1	CONTRACTOR CONTRACTOR	Ť	7	ê			-	1	1	+	+
NO.	COLOR OF COOKS OF STREET	۳	ī			1	\downarrow	1	-	+	+
Š S	PUBLICATION OF THE PROPERTY AND ADDRESS OF THE PUBLICATION OF THE PUBL	T	П	ŝ			1	1	\downarrow	+	╀
ğ	PUBLIC TO THE COURT OF THE COUR	Т	7	92:219	202	4	1	+	+	1	╀
VOL.	PUSICIA DE POSSO DE PRESTA DE PRESTA DE PRESTA DE POSSO D	T	Т			\downarrow	+	+	+	+	ł
	RETRIEVE OF VOORBOTEIN PRECURSOR	Т	Т	7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7		\downarrow	ļ	ļ	+	-	ŀ
2	STATES OF SECOND SECONDS	NAWCASTLE DISEASE VIIUS (STICAIN TEXAS)		460-314			1	1			╀
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PCCENE	107217214	VI ARRIO (at Bettingling)			1	A 484 6 484 4	1 7 3 6 7	ADVA	LVARY	7.07	_
TILENAME	PROTEIN	YARUS	Ť	T	4	4					
PVOLT NOVU	FUSION OLYCOMOTEIN PRECUISOR	NEWCASTLE DISEASE VIRUS (STRAIN ULSTERA)		.1.	1 1 1 1 1 1	-	•		•	:	;
VOLT MOOV	FUSION OF YCOMOTEIN PRECURSOR	MICCASE DISTEMPER VIXUS	Ţ	Т				T			
VOLV MINC	FUSION GLYCOPROTEIN PRECURSOR	HUMAN PARAMETERS I TAKEN (3) PAIN (3)	Ť	Т	376.366	163,115					
	FUSION GLYCOPIOTEIN PRECUISOR	COTO ANI CHESSO.	Ī	Т	Т	410.528					Ŀ
MGC FIERO	PUSION GLYCOPHOTEIN PRECUESOR	N.	T	Т	Ţ	40.528					
TACK TIME	FUSION OF TOTAL OF EACH PROCESSOR		Ι.,	Т	Т					Ŀ	•
PAGE PURE	FINANCE VIOLENTIN PRECINSOR	MINISTER PARAMETURIZA 3 VIRUS (STRAIN NIII 47815)		Т	457-493						
ANN A PANA	RITHON OF VONEBOTEIN PRECIESOR	RINDERPEST VIAUS (STRAIN KABBTE O)	224.265	\$ T T T							
PVG F INDI	FIRESON OF VONDBOTTEN PRECUESOR		224-265	458-506							
POPULA EDINA	PLATON OF VOCUMENTERN PRECIDENCE	SENDAL VOLUS (STRAIN 2 / HOST MUTANTS)	122-149	_	100-00						
PAGE STATES	PLISTON OF VOOPSOTTEIN PRECISEOR	SENDAL VIRUS (STRADA PUSKIDA)	122.149		480-507						
HUNES A PONA	FIRST OF YOUR OTEN PARCIASOR	SENDAL VIRUS (STRADA HARRIS)	122.149	Г	480-507						
TUNE TONG	STRUCK CLYCOPROTEIN PRECLIESOR	SENDAL VINUS (STILAD) INV)	133-149	Г	480-507						
ALIQUA ALIQUA	FIRST OF VICTOR OF THE PRESENT OF THE	SENDAL VIRUS (STRAIN 2)	1	Т	480-507						
2000	TOTAL CHARGE BEING	SIMIAN VIRLE AL	14-185	Г	459.496						
LACE SAGE	FUSION OF TOPROTEIN PRECONSOR	FERTILE WAS IN COMMANDE	Т	T							
SAC TOAL	PUSION OF TOWNS IEEE PRESUMENT	THE PEC BUNGATE A PREFIT OF VIEW	Т	Т	23.484						
PVGU TRTV	FUSION OF TOUR MINISTER PREACURAGE	I CHARLE INCIDENCE AND THE PROPERTY OF THE PRO	431.447	Т			,			L	L
PVGLO BETV	SPICE CL. YCOPROTEDY PILECUISOR	BOATAS EPIREMEAND TO THE THINGS	161 60		T						
PVCLO BASVC	MAJOR SURFACE GLYCOPIUS EIN U	10.7			T						
PVGLO JOSVI	MAJOR SULFACE CELYCOPHOTEIN G	T	1	1							
PVCLO JOSVA	MAJOR BURFACE GLYCOPROTEIN G	-	8	1							
PVOLO HOSVS	MAJOR SURFACE OF YCOPROTEIN G	HUMAN RESPUNTION STACTTIAL VINUS (STRAIN REDSING)		1	T						
PYCHO DIDY!	MAJOR SURFACE GLYCOPROTEIN G	HUMAN RESPIRATORY SYNCYTIAL VIRUS (SUBCACOUP B / STRAIN END)	8		1						
MORE PRABY	CLYCOPROTEIN O PRECURSOR	EQUING HELVESTYRUS TYPE 4	27.1.2	1							
PVOLO HSVED	OLYCOPADTEIN O PRECURSOR	EQUINE RECESSION TITE 1 (STACK ABAT)		1							ļ
PVOLO JALIVT	SPIKE OLYCOPROTEIN PRECURSOR	RABIES VIRUS (STIALN STREET)									
PVOLD VSVIO	SPECIAL OF VCOPROTEIN PRECUISOR	VESICULAL STOKATITIS VIXUS (SEKULTYE INDIANA / STRAIN CLASSON)	Т	177-019							
PVOCH EBV	CLYCOPIDITIN OPEN PRECURSOR	LA SALA POPOLACIA DI MALIA REPARA A DI ADI	Т	270.297	Ī						
AND IT IN	CA VCOPERTIES IN PRECUREDA	MUMAN CYTOMEDAL DVIRUS (STRAIN TOWNE)	Т								
SVed V PRVKA	CEL VEDEROTED H PRECURSOR	HEAPES SINGLEX VIRUS (TYPE 6 / STRAIN GS)	63-89	160-403							
WITH HEWE	CEL VOOPLOTEIN H PRECURSOR	HEIDESVINUS SALMIN (STRAIN II)	388-415								
AVICE LESIVA	THE GLYCOPHOTEIN PRECURSOR	HUMAN CYTOMEGALOWINUS (STRAIN AD149)		H							
PVOLY BUNGE	M POL YPROTEIN PRECURSOR	BUNY AVIAUS GEAMOSTON	\$12.546	195716	1121-125						
PVCLM BUNCT	M POLYPROTEIN PRECURSOR	BUNYAVRUS LA CROSSE (150LATE £74)	913.950	П							
PVCLM BUNYW	IN POLYPROTEIN PRECURSOR	BUNYANWERA VIRUS	340.34		683.709						
FVOLIA DUCAV	M POLYPROTEIN PRECURSOR	bucas vixus	945.972								
STILL HANTS	M POLYPROTEIN PRECURSOR	HANTAAN VIXUS (STILAIN B-1)	8	27.76	1						
PVGLY HANTH	M POLYPROTED/PRECURSOR	KANTAAN VALUS (STRALM HOJO)			T						ļ
FW MAN	M POLYMOTEIN PLECURSOR	HAMTAAN VILLES (STRAIN LEE)	36.55	T							\downarrow
PYCEN HOUY	M POLYTHUI BUY PRELUKSON	INTO A HOLD (STORY VIEW)	628.659	1069.110							L
200	M POLITICAL MANAGEMENT IN SOME	PERSONAL VALIS	8								L
TOTAL PLANT	M POL VPROTEIN PRECURSOR	PUDDALA VILLE (STILLIN HALLINS BI)	22-110							L	L
PWCH WILLIAM	IN POLYPROTEIN PRECURSOR	PUDALLA VELIS (STRADI SOTKANO)	72-110								
PVGLV SEGUS	M POLYPROTEIN PRECUASOR	SECUL VILUS (STEAIN IS-39)	\$13-540								
PVGLM SEDUR	M POLYPROTEIN PRECUISOR	SEOUL VIRUS (STILAN R22)	73-100	\$13-540	694-731						
PVGLM SEOUS	M POLYPROTEDI PRECURSOR	SEOUL VIRUS (STITALIN SIL-11)	73.100	\$13-540	694-721						
VOLY BENY	MOHSTRUCT GLYCOPRO GNS PRECURSOR	R BOVINE EMEMEICAL FEVER VIRUS	52)-564								
PVGL BEV	PEPLONGR GLYCOPROTEIN PRECURSOR	BEANE VIAUS	÷	= 2	2-2-3	1505-1532					
PVOLY NOW	GLYCOPROTEIN POLYPROTEIN PRECURSOJUNIN ARENAVIRUS	CLUNIN AKENAVIKUS	17	1							
PVGLY LASSO	GLYCOPROTEIN FOLYPROTEIN PRECURSOLASSA VIDUS (GLASSA VIDUS (STRAIN GAUS!)	3								
PVOLY MOPE	CLYCOPROTEIN POLYPROTEIN PRECURS	CIMOPEIA VIRUS	100	316.346							
PVGLY MARV	CLYCOPROTEIN POLYPROTEIN PRECURSO PICHINDB ARENAVIRUS	I PICHINDS ARENAVIRUS	334-375		Ī						
PVOLY TACV	CLYCOPROTEIN POLYPROTEIN PRECURS	COTACALDE VIXUS	66.139	200	T						1
	CONTRACTOR AND AND AND AND AND AND AND AND AND AND	GTACAUSE VICTORIAL AND VAL									

	EURSO EURSO	JANES VRUS (STRAIN V?) ANDES VRUS (STRAIN TRV. 1199) ANDES VRUS (STRAIN TRV. 1199) ANDES SEVERE AND AND (STRAIN DC) ANDES SEVERE AND STRAIN DC) ANDES VRUS (STRAIN DS-1.)	\mathbf{T}							\prod	
	CURSO CURSO CURSO CURSO CURSO	UN DO)	301-338			\prod					
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	999		J		1	†					
	999	STATE AND LATERANCE	889-889 6	979-619		1	1				
	9		839.519	919-619							4
			Г	T							
	<u> </u>	CENIA VIEUS (STRAIN COPENIAGEN)		T	T						
	<u> </u>	VAPONIA VIRUS (STRAIN WR)	8	1	†	T					
			7	<u>1</u>		1				Ī	
	355555	THE CHARLES WINDS	30-160			1					
	>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>	A STREET WAS THE STREET WHEN	241-275		-						
	3355	VACCINIA VILUS (STIADA COPEMBAGEA)	366		l						
	3333	VACCERIA VIRUS (STRADY WR)	Т		t	1					
	>>>	PARTY VIBILIS (STEADY COPENHACEN)			1	1					
	3	The second secon	111-06	153-160	-						
	3 3		160-190								
	Α.	CONTA VILLE (STIAIN COPENHAVEN)	8						_		
		VACCENTA VIXUS (STRAIN WR)		T							
	2	OANNE A VIEUS	┪	T		Ī					
		CONTRA CONTRACTOR AND PROPERTY ACTION	296-317		593-632	1					
		VALLEY TELEVISION OF CONTRACT	280.317	548-575	593-632						
		COMITY VIRUS (3 I RALIN WA)	Ī	Г	593-632						
		VARIOLA VILUS	1	T							
	Ī	THE THIRD PROPERTY (STRAIN SMITH)	201.28	1							
	Ī	ANNUAL BEST PROTEST A LAST TICAPS DOLYNEDROSIS VIRUS									
		The Parties of the Pa	217.325	343-400							
		AUTOGRAMIA CALIFORNICA MUCLEAR POLTALIMAGIS VINCS	Т					L			
		HUMAN BORONODEFICIENCY VIRUS TYPE I (REMAT ISOLATE)	•		T						L
		WIAN BAADMODEFICIENCY VIRUS (ISOLATE AGM / CLONE GRI-1)	97.2			Ī					
	1	SECTION OF SECTION OF TAXABLE AND ARAP.	147.174								
	5	CALCADA IN CANADA / PER A TAX 113	\$01.03								
		ALTER VICES SAME CONTROL OF CONTR	31-180								
		SULFOCOBUS VICUS-LIKE PARTICLE 35 VI	5								
		ACCIPILA VIDUS (STILAIN COPENHAGEN)						L	L		
	<u> </u>	VACCORIA VOLUS (STILAIN WR.)							L	L	
	2	VANIOLA VINUS	2		1						
		COTTONITAL RABBIT (SKOPE) PAPILLOMAVIRUS (STRAIN KANSAS)	207-162								
		OF A DESCRIPTION AND MARKET SPACE.	38-65								
		TATION CONTRACTOR CONT	354-392								
		UNAN PARLAMAN WOOD STILLS	113.210								1
		CKAN PAPILLOMA VILLE 18	77.01					L		_	
		HUKAN PAPELOMAVIRUS TYPE 33						_	-	L	
		HESTAN PAPEL CALAVITUS TYPE 41	1						_		
		HENDAN PAPEL CHANTOUS TYPE 31	9								
		INVIANDA BATTANA VIRGIS TYPE SS	45.72								
		DENZAN BABRI MAZAUTRIIS TYPE IA	407-445								
ر ا ا		THE PARTY BASES AND A CORDINATION OF ALL	415-443								
		UNIAN PAILLUMATURES CONTRACTOR	130-157								
		LEOVILLS (TYPE) / STRALM DEALENCY	110.157				L	L	L		
Π,		REOVINUS (TYPIS I / STRAIN LANO)		537			L	L	L	L	
¥	Ī	TRUITA INDESCRIAT VALUS		963.00					-		L
_	THE AT REPORTED IN	PROVIDER (TYPE 1/STRAIN LANG)	290-317						-		
		PARTIES AND A VIEW AND THE ABOUT	625-662								\downarrow
Ļ	33	COVIDED IN THE STREET SCHOOL STREET	177767							į	
1	3	REDVIKUS (TYPE 37 STRAIN DEANING)							L	_	L
1	2	NEOVINUS (TYPE 21/ STRAIN DS/YONES)	207-20			27					L
TANK JEST TO SECTION TO THE PROPERTY PR	3	REGOVERLIS (TYPE 37 STRAIN DEARING)	200		Т				-	ļ	
- 1		ROVOR BESPECATORY STREPTIAL VIRUS (STRAIN ASIROS)	124-152		\int						1
1	T	GINTER PROPERTY STANDAY STANDAY CONCORDING (STEATH AL)	124-151								1
PVALS BESVA MATRIX GLYCOPROTEIN FOR		STATE SECOND CONTOUR CONTOUR (STEAD) AS 1901)	219-246				_				
		THE ASSESSMENT A THINK OF THE PARTY OF THE ASSESSMENT AND ASSESSMENT OF THE PARTY OF THE ASSESSMENT AND ASSESSMENT OF THE PARTY OF THE	219-246	L							
Г		CONTRACTOR OF STREET AND AND ADDRESS OF THE PARTY OF THE	133-165								
PVLAY DICE LATRIX (M) PLOTEIN		INTELLIGIACE C VICTOR (STROME CARROLL)	243-374								_
		CWCASTLE DEMANS VIALS (3) MAIN MOS. MOLECULOS.	15178					L			
Γ		HINKIN PALADMIUDIZA I VIRUS (STRAIM TUSMISM)									

PCGENE	10711734	All Village (My Bessel Principle)	AREAI	AREAL	ARLA 3 L	AREAL	2	3	1000	
LILERAKE	PROTEIN	PROVING BALANGELDENZA 1 VIRUS	101-101						1	+
PWAT 739	MAIRING BEANERS	MERCAN PARADOL VENZA) VIRUS (STRAIN MILL 1985)	201-231						-	+
MAT PUR	MAINT FROILER	STATE OF 15 A1	133-353						-	┧
MAT SV4	MAING FROIEN	POWER CHECKS WILLS (STRAIN MEDIUS)	175.209							+
TANKE CYBIN	ST CONTROLL OF THE PROPERTY OF	TURKEY ENTERUC COROMAVIAUS	175-209					1	1	1
100	El Concentration	AVIAN BOTECTIOUS BRONCHITIS VIRUS (STRAIN 642)	31-48	184-215			ĺ		 	+
SOUTH BOTH	ST OF VONDERS	AVAN BYECTIOUS BRONCHTIS VIRUS (STRAIN BEAUTHTE)	21-48	114-211	1			+	1	+
CKI HVB2	IN OU VOSPILOTEIN	AVIAN DIFECTIOUS BLONCIUTIS VIRUS (STRAIN BEAUTICITIC NAS)	\$	27.7			1	1	$\frac{1}{1}$	\dagger
WAG BY	LI OLYCOPIOTICA	AVIAN INSECTIOUS BLONCHITIS VIRUS (STICALY KBA123)	17.71					1	-	÷
Was CALINE	MOVEMENT PROTEIN	CAULIFEDWER MOSAIC VIRUS (STRAIN CALIBAI)	2	:		:	:			_
PWIP CALVO	MOVEMENT PROTEIN	CAULITLOWER MOSAIC VIRUS (STRAIN DAI)	3.5	7			İ	!		1
TATE PALACE	NACHENT PROTEIN	CALLIFLOWER MOSAIC VIRUS (STRAIN BBC)	227-254	273.324				1	-	-
1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	LACTOR DESCRIPTION	CALLIFICANTE MOSAIC VIRUS (STRAIN NYBLS)	120-154	273-124		İ			<u> </u> 	-
	TOTAL SECTION OF SECTI	PAIN 191 OWER MOSALE VIRUS (STRAIN STRASDOURG)	220-254	27:12						-
	MOVEMENT PROJECT	PATIENTS AND LANCAST CABIN COLONIA	220-234	273-324						
	(MOVEMENT)	A SECTION REPORT OF THE PARTY CONTINUES	18-92	100-127		 		-		-
O CERV	MOVEMENT PROTEIN	CANALISM CLOSED MINE THE COLUMN	-	11:11				<u> </u>		<u>!</u>
We sook	·	SOURCE COLUMNITY AND THE VINCE	1					l		\vdash
PANSA JOHNS	MAJOR BUTC ACT ANTICEN PRECURSOR	HERON MEZATITIS BYTHUS		777.21		-	-	!	!	<u>:</u>
WAT! DAM!	MATRIX PROTEIN !	DHON VIRUS (STRAIN INDIAN/1313/61)	6	3,117						<u> </u>
WHI WYY	M-11 MOTEIN	MYXOMA YIKUS (STRAIN LAUSANNE)	041-0			Ī				t
PVATTS MYXVI.	MILE PROTEIN	MYXOMA VIRUS (STIAIN LAUSANNE)	403-474	Ī		Ī		<u>!</u> -		:
WAS ROTH	NONSTRUCTURAL PROTEIN NSM	PORCINE ROTAVIRUS (CROUP C / STRAIN COWDEN)	:::					+		\dagger
7444	PECANAL E MONCAPSID PROTEIN NP	BOVING PARVOVIRUS	149-176							+
CONT.	LOAD ABOUT NO.	IAI EUTIAM MINIC DISEASE PARVOVIRUS (STRAIN C)	16-148				٦	-		+
200	TACACA BARNET BACK	AEDES DENSONDELEGIS VIRUS (STRAIN GRY 002 002)	14-41		411.517	515-612	780-617	179-17	-	+
THE PERSON	LOGIC ARCH DECITED INC.	INDEREM MOUTE VINUS (STRAIN MIVAL)	13-62	262-289				+		
TAKES PROPERTY	LOGIC AND DECIMAL INC.	MATERIAL MONOTE VOLUS	33-62	262-289						+
	LOCAL CARING DECITION INC.	HADALAN PARVOVILLIS BIR	236-270					-		+
200	LOAD A PRIN SECUTION ME.I	HAMSTER PARVOVERIS HI	35-62						1	†
	WANT A PER DECEMBER 185.1	POACTIVE PARVOVIAUS (STRAIN NADL-1)	24-55	96 36	316-346					\dagger
SKI DIEV	NOWSTRUCTURAL PROTEIN NS!	EPIZOOTIC HEMOREKAGIC DISEASE VIRUS ISEKOTYPE 1/STRAIN ALBERTA						1		\dagger
PWHI LALLA	HOHSTRUCTURAL PROTEIN NSI	DRILLIBORA A VIRUS (STRAIN WALASKAMIT)	171-191					\dagger		\dagger
PVNSI TANON	MONSTRUCTURAL PROTEIN NS:	INTLUENZA A VIRUS (STRAIN MANN ARBORMAN)	E					l		\dagger
NSI MON	INONSTRUCTURAL PROTEIN WSI	DIFLUENCE A VOIUS (STIGAN ACHILE/IN))	M					+		\dagger
PVISI IACKO	HONSTRUCTURAL PROTECT NSI	DIFLUENZA A VIZUS (STRAIN ACHICKENGEUMANY/N499)	24:17:				\int		+	t
PWIST TACK	HOHSTALLCTURAL PROTEIN HS!	DIFEUDICEA A VINUS (STRAIN ACHICKENIAPANTA)	107-13					\dagger	1	+
PVNS IADAZ	NONSTRUCTURAL PROTEIN WS1	DISTUBLICA A VIRUS (STILAIN ADDICIOALIBERTA/6076)	<u> </u>					+		\dagger
VNS1 IAFOM	NONSTRUCTURAL PROTECN WS1	INTLUENZA A VIEUS (STRAIN AFORT MONMOUTH/147)	171-188					+		\dagger
WASI LAFOW	NONSTRUCTURAL PROTEIN NS!	INFLUENCA A VIDUS (STRAIN AFORT WALLEWINS)								\dagger
WHS! WE!	NONSTRUCTURAL PROTEIN NSI	DIFLUENZA A VOLUS (STRAIN ALENTNORADVISUS?)	171-19					+	1	\dagger
PWNS! LAMAS	NONSTRUCTURAL PROTEIN NS!	DIFLUENZA A VILUS (STRADY AMALLARDYALBERTA/11/76)	171-191					1	+	\dagger
PVNS! LAP!	HONSTRUCTURAL PROTED/NS:	DOLUGICA A VOUS (STRAD) APOTALJALBERTA/121/79)	171-198					Ì	+	\dagger
PWKI IAND	NONSTRUCTURAL PROTECNINS	(INCLUENCA A VINUS (STRAIN APINT ALL/ALBERTA/ISU/9)	171-19					1	$\frac{1}{1}$	+
VASI LATELS	NONSTRUCTURAL PROTEDY NSI	INTLUENZA A VIRUS (STRAIN ATLINKEY/BETI-GEHEM-GLILIT/1492-B/12)	171-198					1	+	†
VAKI IATIC	NONSTRUCTURAL PROTEDNINS	INTLIBITA A VIRUS (STRAD) ATTUKEYCANADA63)	171-198						+	\dagger
WASI LATRI	NONSTRUCTURAL PROTEDNINS	DIFLUENZA A VIRUS (STILAIN A/TELIN/TURKAŒNIA/16/72)	171-198				\int		+	\dagger
VNS1 LAUDO	NOWSTRUCTURAL PROTECTION INST	INTLUENZA A VIXUS (STRAIN AUDORNIO)772)	171-198						+	\dagger
VNS! IAUSS	NOWSTRUCTURAL PROTESNINS!	INFLUENCA A VIRUS (STRAIN AUSSINGOTT)	131-136						1	\dagger
VAISI DOLLA	NONSTRUCTURAL PROTEIN NS!	DIFFLUENCA IS VIDLUS (STRAIN BIPAINS)	131-198					1	1	1
WASS LATER	NONSTRUCTURAL PROTEIN NS2	INTLUDICA A VIGUS (STRAIN A/TURKEY/OREGON/I)	1 2						1	ł
WASS DOLLE	NONSTRUCTURAL PROTEIN NS2	INFLUENCA B VIXUS (STRAIN BALESMO)	31-18							+
WHEE DEBYA	HONSTRUCTURAL PROTEIN NS2	INVILLENCE & VELUS (STRAIN BYTAXAGATAVIRI)	21:78					1		ł
WASS DICL	NONSTRUCTURAL PROTED/ NS3	INVILIBAÇĂ C VIDUS (STRAIN CLIVS)	5.					\dagger	+	\dagger
PWW CVPS	NONSTRUCTURAL PROTEDY 3-1	PORCENE TRANSMISSING GASTROENTES CORONAVIAUS (STRAIN 12/24/5/36						†	+	t
VNS4 CVR22	NONSTRUCTURAL PROTEIN 4	HUNGAN CONCONAVIOUS (STRAM 2292)	3						\dagger	t
PVNS4 PLSV	NONSTRUCTURAL PROTEIN NO	MAD STATE VALUE								l
			1	_	_	_	_	_		

PCGENE	107117814		LAND LAND	AMMA	PAIN	1	कु			
ME	PROTEIN	CONTRACTOR CONTRACTOR STRAIN 79-1643)	7	1	1					
PVNS7_CVFEJ	NONSTRUCTURAL PROTEIN?	RONAVIRUS (STRAIN FS772	34-61		Ì	İ		!	!	1
	HOHSTRUCTURAL PROTEIN 7		14-61		;					
П	MONSTRUCTURAL PROTEIN 7			1 :		1	:	!	1	
3	NONSTRUCTURAL PROTEIN 7	(STRAIN 79-1146)	Ĩ	-						1
Adla Lina	NOWSTRUCTURAL PROTEIN 7		41-75							•
	NOWSTRUCTURAL PROTEIN C	MUNICAL PARALLE FOR A CARLO CONTRACTOR CARLO CONTRACTOR CARLO CONTRACTOR CARLO CONTRACTOR CARLO	20.99		Ì					1
	NONSTRUCTURAL PROTEIN C		263-296	L						\downarrow
Ī	NOWS TREET THAT PROTEIN MS-M	OI VINOS	77:5				:		•	:
Ī	MONSTRIP TRAIL PROTECN NS-5	BUNYAVIRUS LA CROSSIS	5		Ī		:			
1100	LAMERSON THRAL PROTEIN NS-S	TOSCANA VIRUS								_
VIGIT TON	AUT MALON TO THE THE THE THE THE THE THE THE THE THE	SUBA A ARES	£					ļ	L	L
WHICE EDOY	MOCHONIC	INTITIENTA A VIEUS (STRAIN AVANAS ACUTAPRIMIORIZO9576)	178-405	+						L
PVNUC LAANA	MCGEOFFOREIN	TANA TRANS A VIBIL OF BAIN ALANN ARBORAGO	378-405							ļ
PURICE LANN	NUCLEOPROTEIN	INTURACE A MAINTENANT AND	378-40\$						1	1
WRITE LABOR	NUCLEOPROTEIN	INPLUENCE A VANCE (STEAM A SECTION DANKER A INC.) (7.3)	378-405						1	1
PVAILE MAUD	HICLEOPROTED	INFLUENCE A VICUS (STRAIN AND CONTRACTOR)	378-405					!		:
FUNDE LACAL	NACLE COPPOSED	INCUENZA A VIKUS (STRAIN ACALICONINS IN TO	107-11	İ						1
ANITE LIVE	MICH EGREOTEIN	INSTITUTION A VIRUS (STRAIN ACTIOCK EMOCRATION (1997)	700 07	-						
THE PERSON	A IN COSCULATION	INTLIENZA A VIRUS (STRAIN ACHICKENPENNSYLVANIALIS)	100 W.	†				L		
710	City the rech	BOLDENZA A VIRUS (STRAIN ADUCKVAUSTRALIA/749/30)		+				L	L	
PACE ADAU	NO. LEUN DOLLE AREN	THE LIBERT A VIRUS (STRAIN ABUCK/DELIING/I/TS)	378-403	†					L	_
WALC LABOR	MUCLEUMOITEN	INTITIONA A VIRUS (STRAID ADUCINCIECHOSLOVAKIA/S)	378-403	1						
WRUC IADCZ	MUCLEOTRUTEIN	DATITEMAN A VIETRISTRAIN ADDICKENGLANDIN	376-405							İ
WHITE INDE	MACLEOPROTEIN	AND THE PARTY OF THE PARTY AND LAND INC.	178-405						\downarrow	-
WICE INDEX	MICLEOPROTEIN	INCLUDADA A MARIA (ATA AN AMAIN'S ACADA INCLUD	378-405							1
CATE TABLE	MUCLEOPROTEIN	DELUENZA A VINUS (STRAIN ACCOMMING ACCOMMING TO THE PROPERTY OF THE PROPERTY O	378-405	-					4	4
A LANGE	MINIST ECONOTION	DIFLUDIZA A VIKUS (STILATA ADUCINATIONALIA)	338-405							\downarrow
	Later Broke Ortaba	DALLIESZA A VIRUS (STRAIN ADUCKANANI UBA1122)	707 84				L	L		
STATE IN CO.	To Post Orten	DIFLUENZA A VIJUS (STRAIN ADUCKNEW ZEALAND) (76)	200-816					L	L	L
PVPCC DADRE	CALLED TO SECURITY OF THE PERSON OF THE PERS	DOTUGAZA A VIRUS (STILAD) ADUCKĀRRAINĒZĀG)	200-01	†			L			L
WALL LADOR	NACE BOX AND THE PARTY OF THE P	INTEREST A VIRUS (STIAIN ACKGLAND/1955)	278-403	+						L
WICE INDIC	RUCLEUTION BOX	INSTITUTOR A VINUS (STEAD) AFORT MONNOUTHING!)	278-403	†				ļ	L	Ļ
WALL LAND	MULIEU STATES	INFITENZA A VIRUS ISTRAIN AFORT WARRENING)	178-403						-	L
WRUC IN OW	NUCLEOPHOTED!	THE PERSON A VIRILIA STRAIN AFOWE PLACUE VIRUS/DOBSON/DUTCING?)	378-405	1				\downarrow	+	1
FVNUC LATE	NUCLEOPROTEIN	INTERPRETATION & VIRIALISTERAIN AROWL PLACUE VIRUSAOSTOCKUM	371.405						1	ļ
WHOC DAYS	NUCL EOPTOTEIN	ANTIBODA & VISITE RETRAIN ANGREY TEALLAUSTRALIA 279)	111.405						1	1
WALLE LACKE	NUCL EOPTOTES	INTEREST A VINCE SEED AND ACTOR ACTOR AND ACTOR AND ACTOR ACTOR ACTOR AND ACTOR AND ACTOR AND AC	378.40\$						ļ	+
PARIC IACUI	NUCL ECHIOTEIN	INTERIOR A VICTOR STATE OF THE AVAILABLE AND STATE OF THE	378-405						1	1
WATE IABLE	NUCLEOPROTEIN	INTURKA A VIKUS (STANIA ANDLOMAS TOTAL	338-405						4	-
WANTE IACTO	NOT EOPLOTED	DELIDIZA A VRUS (STRAIN ACCULATION LANGELLOS)	378.405				L		4	-
ALCOHOLD TANK	NIIO POPIOTEDI	DOLUENZA A VIRUS (STEAM ANDLUMAN) LANCOTOTOTOTOTOTOTOTOTOTOTOTOTOTOTOTOTOTOT	178-406							_
TENED TANK	NATIONALOTEDA	BELLEVEA A VEUS (STEAM AGGLUAS) RACKASA (184)	707.15				L	L		_
1	ACCEPTANCE OF STREET	INTELIBRIZA A VIRUS (STRAIN AIGUEL MASSACHUSE I I SZENU)	10, 11,	1			L	L	L	ŀ
TANK MEET	SAN SAN SAN SAN SAN SAN SAN SAN SAN SAN	IDMILITERIZA A VIZIUS (STRAIN ACULLAINNESOTAMENO)	200	1				L	 -	ŀ
WALK MOUN	POCESSION OF THE POST OF THE P	INSELEDIZA A VIXUS (STRAIN AMICKOX40)	178-403	1				-	-	\vdash
PVINC IMPC	Carol Control Carol	DOLUBEZA A VIDUS (STIAM ARCOUNTIFILIBAINS)	207			1		ļ		ŀ
WACE AND	ACCEPTANCE OF THE PARTY OF THE	DATUESZA A VIDUS (STRAIN ARQUINEALONDONIA1671)	278-603			1		-	L	ŀ
PWALE LAND	POLICE OF THE PARTY	INSTITUTION A VIRUS (STEADY ARQUINE MILAMVIM))	378-403					+	-	ŀ
PVNDC IAIND	MOC FORDING	PART I PAZA A VIRLIS (STRADA ARIGNO KONOVIAS)	378-405			1	1	+	+	╀
PVNDC IAHOI	MUCLEOPHOIEM	INSTITUTE A VIRIA (STRAIN AMONG KONGARI)	374-405					1	-	╀
PVNIC IMPO	PUCI EOPTOTEIN	NAME OF STREET OF STREETS AND APPROXIME PRACTICAL STREET, 1989	378-405				-	4	1	+
PVNUC LAIPIE	INDECEDITIONS	KAHT TENYA A SPRING STRAIN AND UNE TENNESSEE/996)	376-405			_	\downarrow	+	-	+
PYNUC LANTE	INDELEGRICATED	INTELLEGISTA A CHAIR (STRAIN AIX ISVISOTS)	378-405			\downarrow	4	1	1	+
WHIC JAKE	MUCLEOPROTECH	INCLUSION A COSTE AND AN ENTHORNOUS AND AND ENTHOUSE AND AN ENTHONING AND AND ENTHOUSE AND AND AND ENTHOUSE AND AND AND AND AND AND AND AND AND AND	378.405				4	+	\downarrow	1
WANC WEN	NUC! EOPROTEIN	ACTION A CHAIR SETT AND AMAIL ALD ASTRACHANGE (MIS)	378-405				4	4	-	+
WARE LAKA	NUCL EOPTOTESN	INTERIOR A VINCE (STAND AND A STAND AND AND AND AND AND AND AND AND AND	378-405						-	+
PARTIE TAKAN	NUCL EDPLOTED!	DALLEYER A VINUS (SINGER AND A ACTOR (NATIONAL)	378-405				·	4	1	+
PANCE TANK	NUCL EOPLOTED	INCLUDACE A VINCIA SOFT TO THE PROPERTY.	118-405					4	1	4
POND TANK	NUCL EOPLOTED	DOLLINGA A VILLE (S. M.C.) MARCHES	378-405					-	-	-
1000	LACT BALL AND ATTEN	INGLUENZA A VILLIS (STAAIN ANTINOSS)				-	ļ			_
			13140	_	_	_	_	_	_	4

					A LOFA 1 LABEA 4	S Y S Y S Y	- C			
THE HAME	PROTEIN	VIRIAL CONTRACTOR OF STREET	107		-		Т			
WALC IN A	NUCL EDITIONED		178-405							
PARCE LAND	A CALL STATE OF THE PARTY OF TH	REW JERSEYATAS)	371-405			$\frac{1}{1}$	4		1	
WATE LAKES	KIKL EDMOTEIN	Ī	378-405	1		1			Ì	1
PYNUC JASHII	MUCLEOFROTEIN	USTRALIA/72)	2		1	<u> </u>	1	İ	1	3
PVNUC IASH	NUCLEDPROTEIN		10 AN	\dagger		<u> </u> 	-			•
PYNUC LATE	RUCLEOPHOTEIN	INCLUENZA A VINUS (STRAIN ANTEAL/ICELANDZ/930)	197	\dagger	+	-	-			
WHILE INTO	NUCLEOPICITED		197.11	l		-				
WING TATES	NUCLEOPROTEIN	5				l				
WHUC LATHS	NUCLEOPROTEIN	***************************************	į	:		· -		_		
PVMUC LATRIT	NUCLEDMOTEIN	STRAIN ATERMINIKAIR/IR/18/72)		†	+				Ī	
PVAILE LATES	NUCLEOPROTEIN		200		1				Ī	
PVALLE LAIDO	NUCL EOPLOTED	173)	9	+	1	1	1		I	
PVARIC LAISE	NO EDMOTEN		5071	1	1	1				
PVARIC TAVIS	NUCL EGPEGTEIN	INVELUENZA A VIRUS (STILAIN AMICTORIA/5/48)	2				<u> </u>	1	: :	:
PVNIK LAWRY	NUCL EDPROTEIN	INSTITEMEN A VIRUS (STRAIM AWITALEMAINGDINMA)	31.483	1						
PANIL IAWA	NUCLEOPEOTEIN	INTLUENZA A VIRUS (STRAIN ANMALEPACIFIC OCEAN/97%)	ê	1		1	+			
PARTIE TAVIL	SELECT BOPROTEIN	INTITIENZA A VIRUS (STRAIN ANNESON-SMITHO))	24.63	1			+			
SOUTH TANK	MAINT KOPROTRIN	INTLUENZA A VILUS (STILAIN A-WISCONSINVASIANO)	371-405	1	1	1				
1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	NEW EOPLOTEIN	INSTITUTION A VIRUS (STRAIN A/SWINE/29/17)	371-403	1	1					
17.7	MENCH BOOK OFFINE	INTLUENZA A VIRUS (STRAIN ASWINEWINS)	376-405		+	<u> </u> 	-		:	
TO STATE OF THE PARTY OF THE PA	MACHED BORD TOWN	INFLUENCA A VIRUS (STRAIN ASWINDCAMBRIDGIVIDS)	378-405				_			
VIII 1	March Bose Of High	ING. LIENZA A VIRUS (STRAIN ASWINEDANDONGWA))	118-405							
TYRUE INCLIN	March Police Pol	INVESTMENTA A VIRUS (STRAIN ASWINEGERMANY/2011)	378-405							
PVRUE MANOR	NOTE THE PARTY OF	MET DENZA A VIALIS (STRAIN ASWINERONG KONGENS)	378-405		_					
PWCC LAZAII	NOTE PASSING	FAST TENTA A VIELS (STRAIN ASWINEMON KONO 12612)	175.405							
WALE LAZIO	NAME OF STREET	PART TENZA A VIRILE (STRAIN ASWINE/HONG KONG/12/N2)	376-405							
PVPC DALIS	THE CAMPACATION	INSTITUTALA VIETZ (STEATH ASWINGTOWA! 570)	378-405					-		
THE WEST	CHARLES THE STREET	BRT I HOZA A VIRLIS (STRAIN ASWINEROWAII)	378-405			-				
PVNV.	AND SAME PARTIES.	INFILITIONAL A VIRUS (STRAIN ASSWINGTOWANS)	378-405							
PARIS MEDI	NAME ASSESSED.	INVITURIZA A VIRUS (STRAIN ASWINENTALY/43776)	378-405							
TO THE PERSON NAMED IN COLUMN 1	NIC FOR BOTTON	DOLUMAA A VIRUS (STRAIN ASWINGATALY/2/79)	374-405			1				
HI THE	NINCE EGRECIELY	DELUERZA A VIRUS (STRAIN ASWINEATAL VII 1/10)	378-405					1		
PUNIT 14214	NUCLEOPEDTED	INT. UBICA A VIRUS (STRAIN A/SWINE/ITALY/N)949)	200	1	1					
PVALC IAZIA	NUCLEDPROTEIN	INTLUENZA A VIRUS (STRAIN ASWINE)/ANGSBURG42)	9	1	$\frac{1}{1}$	+		\downarrow		
PWRUC IATAKA	NUCL EDMOTED	INTIDEAZA A VIRUS (STRAIN ANSWINGMAYIM)		1						
PWECE LASHE	NUCLEOPROTEIN	INFLUENZA A VIAUS (STRAIN ASWINE/NETHERLANDS/12/5)		1	$\frac{1}{1}$					1
PVNUC IAZOH	MUCLEOPROTEIN .	DATUE (STRAIN ASWINE ONO 2333)		1	1	+		\downarrow		
PVNUC IAZON	NUCLEOPHOTEIN	INTLUDIZA A VILUS (STRAIN ASWINEAUN ALAULUS)		T			+	ļ		
PWADE TATTE	NUCLEOPHOTEIN	DATLIERZA A VILUS (STRAIN ASWINETENMENSEEZATT)		1			+	1		
PVNUC MEW!	NUCLEOPROTED	DAPLUE A A VICUS (STRAIN ASSERBLY SCOUNTY)		T				ļ		
PVNUC IAZWI	NUCL FORESTEIN	DOLLDOZA A VICUS (STRAIN ASSAURE WISCONSINVINE)	75,136	1777	147157			ļ		L
PVNUC DICCA	NUCLEOPROTEIN	DO LUBRIA CARIOS (STRAIN CONTROLINO) (S)	166-407	Т			-	L		
PWIC MABYN	NUCL EOPROTEIN	MANAGORA CARACA CARACA BODDS	166-407					L	L	
TWICE MANY	MUCLEOFICIES	DARCENTA VIBITA STRAIN COPENIAGEN	15.	109:131	381-608	-				
WOO! VACK	MOI EIN OI	VARIOT A VIEW	150	103-131	109-115					
PVOS! VALV	PACIETA OI	BOYTAT MORAIC VIRIS	1023-1056			-			L	
PVOR1 FXDAV	1152 KD PROTEIN	STATE OF THE STATE	996-1023	1327-1561		-	 -	L		
PVOR1 NOV	ING KO PROTEIN	PAPAYA MOSAIC POTEXVIRUS	941.978	1481.1532						
PVOR PARY	170 KU TAULEIN	POTATO VIRUS IL (STRAIN RUSSIAN)	397-627		_					
PVOR! PVICE	ZO KO PROJEKA	POTATO VIRUS X	68.733	1017-1044						
PVOR! PVX	163 FOUR SECTION	POTATO VIEUS X (STEAD) X3)	T	1017-104			_			
3	TOTAL DE CALLE	STILAWBERRY MILD VELLOW EDGE. ASSOCIATED VIRUS	312-342	124.169			-			
	BIA PROTECTION	AUTOCIAPHA CALIFORNICA NUCLEAR POLYHELDROSIS VIRUS	141			_		_		
PVP10 KPVAC	PIOPEOTEDA	GRÖYLA PEEUDOTEUGATA MULTICAPSID POLYIH:DADSIS VIRUS								
	VIOLENCE IN THE PARTY OF THE PA	Control of the Contro		7.1						_

POCENE	107s178s4		_	4						_
Į	1	VIA.	_		1					ļ
	1		181-181	127.154		1	1	1		1
Ī			53-60							1
Γ			100							1
T	LALLE THE PROTEIN PRISTS		2	T	T					<u>ح</u>
NATION AND ADDRESS OF THE PARTY	CALCOCAL PARTS AT BEIOTETN PAST			1	T					
Ī	MOTES INCOME OF SECTION AND SE		31.7	1	1	T			-	-
٦	COMB FROIGHT IN	TOUGHT MINNY STUNTAVISUS (STRAIN CHERRY)	301		1	1	†			L
WHIS THIS YC	COME PROTEIN FIS	CHES SOCIALITY (A LIVER / STRAIN 1)	1.29	j	1			1	-	<u> </u>
VEW HEVEA	PROBABILE CANEED PROTEIN VP23	TOTAL DESCRIPTION OF THE PARTY AND PROPERTY AND PROPERTY OF THE PARTY AND PROPERTY OF THE PARTY AND PROPERTY OF THE PARTY AND PROPERTY OF THE PARTY AND PROPERTY OF THE PARTY AND PROPERTY OF THE PARTY AND PROPERTY OF THE PARTY	36-63		1	1	1			1
PVP24 HUVEB	CAPSID PROTEIN VP26	EUCLIE MENTE CANON CONTROL OF THE CO	48-75							1
Γ	CAPELID FROTEIN VP26	MERCESVIRUS SAUMING (STRAIN 12)	277.304	110-013	6)2.661	901.934		-	1	ļ
I	WHY CAPSID PROTEDY VP:	APRICAN HORSE SICTINESS VIRUS (SEAULTIFE ASSISTANCE OF THE STANCE OF THE	Ť	Г						
Ī	ATHER PASSED BEATTERN VP2	BLUETONOUE VIRUS (SEXOTYPE 13 / ISOLATE USA)					İ		-	
I		RETENDACHE VALUS (SEROTYPE 17 ISOLATE AUSTRALIA)			-	-	-	· -	_	
WY BTVIA	OUTER CAPAID PROJECT VICE	₹	\$ 							
VP1 BTV18	OUTER CAPSID PROTEIN VP.	HELICI CANADA VINA CANADA CANADA CALICATORIST IN	2.103	115-413						i
WHY BILLY!	CATTER CAPSID PROTEIN VP2	EPIZOOTE HEMOREIAGE DISEASE VINCERIAL OF THE STATE OF THE	200	25.15						_
	BALL WINDWARD BROTEIN VP2	BOVING ROTAVIRUS (STRAIN IS)	1							_
VP. KOIBA	MANAGEMENT OF THE STATE OF THE	ADVINE ROTAVIRUS (STRAIN UX)	1				İ	<u> </u> 		_
PVP2 ROTBU	MA-EDUNG TUDIELM TO	CANAL DESCRIPTION OF THE PRINCIPLY STRAIN WAS	20-02	533-567	╗		j			-
PVP2 ROTHW	INA-BENEAR PROTEIN VP2	A STATE OF THE STA	52-99	128-156	518.545	704.746		1		<u>.</u>
	ENALS DOORS PROTEIN VP1	PORCEME ROTAVIRUS (GROUP C.) STRAIN COMPLY.	76.75					_		
	A LA MINISTER PROTECTIVE VP.)	SINGAN II ROTAVIRUS (STRAIN SAII)		·			:	•	_	_
2 2013		APPLICATIONS PROFIL VIETS (STRAIN 1-73)	14.73	1						L
VPX ALES	MIOSPHOPHUTELIN P.JO	CALLES CO. CO. CO. CO. CALLE PARIS PARIS CO.	39.75	1						1
CONT. ASTRO	PROSHIDMOTED P11	Wilder Fred State Control of the Con	611:11							+
ACC.	THE VIOLET COLOR BY PROTEIN VP35	EBOCA VIRUS	Τ	31.36						-
	THE COMPANY PROPERTY VP.35	MARIEURO VINUS (STRAIN MUSOKE)	T							_
VP35 MARVA	THE PARTY OF THE PARTY COLUMN	MANIETE VIETS ISTRAIN POPP	┪	• (7.17)						L
WAS MADVE	POLYMENANA CURCLES PROJECT 1777	A PROPERTY OF THE PRINCE NAME AND POLYHEDROSIS VIRUS	270-297							+
VP35 NPVAC	SALLY 35 KD PROTEIN	ACCOUNT AND ALL BAN WIENBACK VIRILE	101-103	1						+
WANT HOWEN	EALLY 15 ICD PROTED [®]	TONGSTANDAR POLITICAL TOLINGS THE CONTROL OF THE CO	126.205						1	+
740	PARTHEDON DIV PRO PS	VACCIDIA VIRUS (31 MAD) WA)	197	264-201				_		$\frac{1}{2}$
170000	MANAGE SAND MOTERA	AUTOCRAPHA CALIFORNICA PUCLEAR POLITICUADAIS VINCE	Т						_	-
	MANUEL PAPERS PROTEDY	OKOTIA MEUDOTSUGATA MULTICAPAID POLITIEUROSIS VIROS								_
	CAL YOUR BACKEN	APRICAN HORSE SICKNESS WAUS (SEAUTTPE 47.5) KAIN TALLING						ŀ		_
	SALE PARTY BETTER	BLUSTONGUE VIRUS (SEROTYPE 167 ISOLATE USA)							L	-
	THE PART DAYS	BEDETONGUE VIRUS (SEROTYPE 1771SOLATE USA)	****						-	-
2 1417	VED COMPLETE	THE THE FOREITH VIRUS (SEROTIVE 1/150LATE AUSTRALIA)	167-117						-	-
PVPS BTVIA	VP) CORE PROTEIN	PERSONAL PRINCIPLE BISEASE VIRUS (SEROTYPE I)	209-243	798-832				1	İ	+
INCHE ENDIN	VPS CORIL PROTEDI	THE STATE OF THE LAB BUT AND THE A TE WALLS (SEROT PE 2 / STRAIN AUSTRAL	1 796-832					1		+
MAN PLONA	VPS CORE PROTEIN	EVECOIR, NEWSCOOL	90.13							
	EN DE CATERIA	GRAMMER FANCEAS VIRUS		20.00					L	L
2	AND PASSED BOOTERS VOI	POSCHOW ROTA VIRUS (CROUP C / STRAIN COWDEN)			,,,,	610 403				L
My) ROTH	INTER CASE TAXABLE CO.	TOURISH IN BOTAVIAUS (STIVAN SAII)	2	1200.7	1					
WP) LOTS	INNER CORE PROTEIN VIS	CASSAGE AND CHAIN (STRAIN BOLD)	440-470							+
Who EBV	CANSID PROTEDY PRO	Land State Land Annal (4 th Alb 11)	205-232	344.373				1		+
VP-0 HGWA	CAPSID PROTECT NO	PRINTED TANKS AND	\$15.549	L	L				_	1
200	CANID PROTEDING	INTEGRAL LATINGUI ANCHELII S VINOS (STICE)	174.200	405.522						
W. C.	CAPERS PROTEIN PRO	VALLET LA ZOSTER VILUS (STIVAIN DUNIAS)		410.410				-	_	_
	CATHER PAREN MOTERN VP4	SDKIAN II ROTAVIRUS (STRADN SAII)						-		L
200	COLOR DE PARTIE DE LA COLOR DE	ENGLAN I I ROTAVOLUS (STILADY SATI)	2	770						ŀ
TYPES ROTS	OUT COMPANY	10.1 PORTIN VIETE AND CHEENAGEN	4 13		_					+
WAL VACOC	MAJOR COSE PROTEDNINA PRECURSOR	YALLING TOTAL COLOR OF THE COLO	£ 75	L	L			-	-	$\frac{1}{1}$
VALLA VARAV	MAJOR CORE PROTEIN PAR PRECURSOR	VACCINIA VINUS (STANIA WA)	15.3							
0010	LAYOR PORE PROTEIN PAR PRECURSOR	VALUOLA VIRUS	911,49							-
	TAY IN MARK PROPER IN MAR PRECURSOR	FOWLYSX YOU'S			\downarrow				-	-
A LONG	THE PARK THE PARK IN THE PARK CHIRCOLD	VACCINIA VILUS (STIAMN COPENYAGEN)	2					1		-
AVE VALLE	SOUTH TOWN TO THE PART PRESCUENCE	VACCENTA VIDUS (STRAIN WR)				1			-	╀
VINB VACT	MAJOR CORE PROTEIN NA SECTION	VANDELA VIII.	7.77							\parallel
VP48 VARV	MAIOR CORE PROTEIN THE PRECUPIOR	STT STANDER CONTRACE DITYPE 10/ ISOLATE USA)	34.61	\$76-603						+
WAY BIVID	VIN CORE PROTEIN	STITUTE CONTROL OF THE CONTROL OF THE USA)	34-61	\$76-603						$\frac{1}{1}$
WH BTVII	VIN CORE PROTEDY	CONTRACTOR CONTRACTOR STATE 115A)	34-61	(09-945)						1
VAN BYVII	VP4 COLE PROTEIN	BELLETONCOD VICTOR SECTION SEC	552-622							-
	AN MARKET PARKET PROPERTY OF	NEBRASKA CALI DAMONEA VIANS SIECEM			-					
									_	

07.400	1189.198.4	All Virginia fan hecterine he pes				-		-	-	Γ
TILERANT	PROTEIN	YIRUS	AREAL	П	ARGAS	AREA 4 AREA 3	\$ 728 5	মত তেমত	NV FV3HV	4854
PVN ROTE	OUTER CAPEID PROTEIN VPA	BOVING ROTAVIRUS (STRAIN C486)	8-35	1M-622			1		+	T
PVP4 ROTHC	OUTER CAMID PROTEIN VM		П	П			1		1	
PVN ROTHU	OUTER CAPSID PROTEIN VP4	EQUINE BOTAVILUS (STRAIN H-3)	46	135-269	552-629		-		+	
PVM ROTEH	OUTER CAPSID PROTEIN VP4	ROTAVIAUS (GROUP B / STRAIN IDIR)	٦				7	1		1
PVN ROTOL	OUTER CAPSID PROTEIN VP4	HUMAN ROTAVIRUS (SEROTYPE 1/STRAIN 1076)	T	272.628				1	1	7
PV74 FOTHI	OUTER CAPSID PROTEIN VP4	HUMAN ROTAVIRUS (SEKOTYPE 2 / STRAIN RV.3)	T	27.5	2		1	\dagger	1	
PWA ROTHS	OUTER CAPSID PROTEIN VP4	HUMAN KOTAVIRUS (SERIOTATES) / STRAIN 69M)	T	11 2-1 Ju	A70-917		+		+	
FVY ROTH	OUTER CAPSID PROTEIN VP4	HUMAN ROLAVIRUS (SEMO) TPE (1) STRAIN 69h)	T	3	70.00	:				
PVY ROTIES	OUTER CAPSID PROTEIN VP4	INUMAN ROTAVIRUS (SEKOTYFI: 2 F.STRAIN 1951)		Z.7. KIN		:			.	
PVP ROTIU	OCTER CAND PROTEIN VM	HICHARY BOLA VIRGO (STACKIN RE)	Ť	2	ANT OFF	167 663		+	+	T
PYN ROTHE	OUTER CAPSID PROTEIN VP4	HUNDAY DOTA YINGS (SINGLE NO)	Ī	7	200	,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,	1		1	T
WY ROTH	OUTER CAPSID PROTEIN VIA	HUMAN KUTAVKUS (STRAIN LIA)	T	T					1	
WA ROTTON	OUTER CAPED PROTEIN V74	HUMAN ROTAYOUS (SEXULT PE) STRAIN M)?)	T	216.9/2				\dagger	1	1
PVP4 ROTIDS	OUTER CAPSID PROTEIN V74	HUMAN ROTAVILUS (SENOTYPE 3 / STRAIN MCN1)	7	2000			-	i	1	:
PVM ROTID	OUTER CAPSID PROTEIN VP	HUMAN ROTAVIRUS (SEROTYPE 3 / STRAIN P)	1	577-621					1	
PVP4_ROTHER	OUTER CAPSID PROTEIN VP	HUMAN BOTAVIRUS (SEROTYPE 1 / STRAIN RRV)	1	200	335-262				+	1
PVP4 ROTH	OUTER CAPSID MOTEIN VPA	HUMAN ROTAVIRUS (SEKOTYPE 4/STRAIN ST. THOMAS 1)	1	11:53			1	1	1	1
l	OUTER CAPSID PROTEDN VPA	HUMAN ROTAVIRUS (SEXOTYPE 4 / STRAIN VAYO)		279.306	Š		1		1	
	OUTER CAPSID PROTEIN VIN	HUMAN ROTAVIRUS (SEXOTYPE I / STRAIN WA)	╗	27-621			1		1	Ī
	OUTER CAPSID PROTEIN VPA	PORCING ROTAVIRUS (SEROTYPE 57 STRAIN OSU)	ž	25.625					1	
	OUTER CAPSID PROTEIN VPA	PORCING MOTAVIRUS (GROUP C / STRAIN COWDEN)		- - - - - - - - - - - - - - - - - - -	293.330				1	
	OUTER CAPSID PROTEIN VPA	FORCING NOTAVIRUS (STRAD) GOTTFRIED)		7			7		1	
	OUTER CAPSID PROTEIN VPA	PORCINE MOTAVINUS (STILAIN YAK)			584-625					
WAY ROTHER	OUTER CAPSID PROTEIN VP4	INESUS KOTAVIKUS		584-622						
PVN ROTS	OUTER CAPSID PROTEIN VPA	ISDADAN II ROTAVIRUS (STRAID SAII-FEM)		319-619						
PVM LOTES	OUTER CASID MOTEON VM	ISDAIAN II ROTAWRUS (STRADI SA11-SEM)		2012	584-622				1	
VIN WIV	NONSTRUCTURAL PROTEIN PASA	WOUND TUNIOR YIRUS	1						1	
PVPS AUBVA	OUTER CAPSID PROTEIN VPS	APPICAN HORSE SICKNESS VIRUS (SENOTYPE 4/ STRAIN VACCINE)	_	=				1	+	
PVPJ BTV10		BLUETONGUR VIRUS (SEACTYPE 10/15OLATE USA)	Τ	92.56				1	1	T
PWF! BTV!	CUTTA CAPSID PROTEIN VPS	BLUBIOROUS YINDS (SEROTYPE 1171SOLATE USA)	Т	4Z-Z4		1	+	1	+	Ī
		BATTER OF COURTS AND TANK AND AND AND AND AND AND AND AND AND AND	1	10.134						T
MAN BLANS	CHIES CAPSID PROTEIN VPS	BLUETOWOUE VINUS (SENOTIVE 3 / ISOLATE SOUTH AFAICA)	Τ	T	148-182				-	T
PAPE BITVIA	OUTER CAPEID PROTEIN VPS	BLUETONOUR VIRUS (SEKOTYPE 37 ISOLATE USA)	Γ	Ī					-	
IADA PAN	COTTEX CAPSED PROTEIN VPS	EPIZOOTIC HEMOAUHAGIC DISEASE VIRUS (SEROTYPE I)	Γ		399-426				-	
WHI WIV	OUTER COAT PROTEIN PS	WOUND TUNIOR VIXUS	648-675						H	
PVP61_BTV10	VP4 PAOTEEN	ISLUETONGUE VIRUS (SEKOTYPE 10 / ISOLATE USA)	[161-193						_	
PVP61 LOUDV	PROB NONSTRUCT 41.0 KD PRO	INALES ROUGH DWARF VIRUS	153-202				-			
PVMI POVAC	61 KD PROTEIN	AUTOMATHA CALFORNICA MUCLEAR POLTHEDROSIS VIRUS	G C					1	1	T
WHO BTY10	VM PROTEIN	BLUBTOROUS VIKUS (SELOTTPE 1971SOLATE USA)	137.00			+	+		+	T
ADALY MAA		TATESTANDA DATE THE PROPERTY OF THE PORTY PROPERTY OF THE PORTY OF THE	7,7			+	T	l	\dagger	T
PARK BEVILL	100000	BLUETOWOUR VIRUS (SEROTYPE II / ISOLATE USA)	157.189	Γ					+	T
PVP6 BTV13	V% PROTEIN	BLUETONGUE VOUS (SENOTYPE 1) / ISOLATE USA)	157-189							
PVM BTV17	VP6 PROTEIN	BLUETOHOUS VOIUS (SELDTYPE 17/ISOLATE USA)	187-189							
PVP6_BTV18	VP6 PROTEIN	BLUETONGUE VOLUS (SEROTYPE I / ISOLATE SOUTH AFILICA)	161.193							
PVM BTV2A	VM PROTEIN	BLUETONGUE VIXUS (SEROTYPE 2/15OLATE USA)	21.51				1	+	+	
ANA NOV	STRUCTURAL PROTEIN PA	JUCK DWALE VELIS	11.74			1	1		\dagger	T
TATA MANACA	PACKET IN LINE AND ANTICIPATE	KOT COME TO COME CONTROL OF THE CONT	1	070.077					\dagger	
PVF/3 CSVSV		JAIPPORABBLE CALIFORNICA MICHER MY WIEDERS! CVIRUS	T	70.107			<u> </u>	+	\dagger	Ī
UNA BEING	VP1 CORS PROTEIN	EPIZOOTIC KEMORAHAGIC DISEASE VIRUS (SEROTYPE I)	3						+	Ī
VIV VIV	MONSTRUCTURAL PROTEIN PMST	WOUND TUNOR VILUS	458-485					$\frac{1}{1}$	\vdash	
FVPED NPVAC	CANSID PROTEIN PEÓ	AUTOGRAPHA CALIFORNICA MUCLEAR POLYHEDROSIS VIRUS	101-143	140-201		_			H	П
PVP87 NPVOP	CAPSID PROTEIN PIT	ORGYTA PSEUDOTSUGATA MULTICAPSID POLYNEDROSIS VIRUS	2					-	1	
VPI BTV10	NONSTRUCTURAL PROTEIN PA	PLUETOWOUR VIXUS (SEXOTTPE 1073/OCATE USA)	10413	Ī					+	1
PVP FOUR	STRUCTURE PROTEIN VIETNESSON								$\frac{1}{1}$	7

VILLERANE VVI WTV VVI WTV		YRU				•					
A MARY WIN			2,5	113-143							
AN MIN		WOUND TUNIOR VIRUS	197-224								
ALA L	I PNS 9	NICE DWANE VIAUS	37.56					ļ			
		WOUND TUNOR VIRUS	975								1
		WOUND TUNOR VIRUS (STIAIN NO)	105.331								1
	LOPE PROTEIN	AUTOGRANIA CALIFORNICA MUCLEAR POLTHEDROSIS VINOS	Т	318.264							
THE PARTY	5	ORGYTA MEUDOTSUGATA MULTICAPSID POLYNEDROSIS VIRUS	Т								
1000	Ī	MOUSE ADENOVIAUS TYPE?									
		HUMAN BOADWOOFFICIENCY VIRUS TYPE I (ARVOSF2 ISOLATE)				1111	:		:	: :	
אואוא		THE MAN HARDSONE FICE ENCY VIRUS TYPE ! (III III AND LIXII) (SOLATIES)	7.							L	
PVPU HVIBI		THE TANK MANAGER PRINCY VIRUS TYPE I (DITE ISOLATE)	21-41								
MAN HAIR		THE STATE OF THE S	22-49				j				-
AU HOLES		MONAN DOGGRADOR SALENCE VINCE VOE 1/601 APE	7							1	
SOUTH BOTTON		PROVAN BOALDOOFFICENCY VIRUS 17TH 16AC 12CCCC	97.7								
210012		HENGEN BOARMODEFICIENCY VINUS 177PE I (CUC-3) I BOLATICA						L			
		HADAAN INGADINODEFICIENCY VIRUS TYPE I (ELI ISOLATE)							L		
PAPEL HAVEE		LANALS HANNESS HANNESS VIEWS TYPE I (HX02 ISOLATE)	5-48								L
WYU KWIKE	VPU PROTEIN	CONTRACTOR CONTRACTOR CONTRACTOR (CAMPING TOWN) SOLATE)	3:39								ļ
MAN HAID	WHU PROTEIN	HUNDAR BENCH CONTRACTOR OF THE	23.40								1
STATE STATE	VPU PROTEIN	REDIAN BORUNOSE ICLEMENT VINOS I VINOS VIN	ŝ								
1	VMI PROTEIN	HOMAN BOADSON PICTENCY VIRUS 17 PB 1 (MAL 130LATE)						L	_		
WINE OF	CartesAven	KIDAN BARINODEFICIENCY VIRUS TYPE I (NDK ISOLATE)								L	L
MAN HANG	VIO PROTEIN	MANAY NAMINODE FICTENCY VILLUS TYPE I (PV22 ISOLATE)	7								L
WEU HAIDY	VPU PROTELIF	THE TANK THAT THE PROPERTY VIETS TYPE ! (SF162 (SOLATE)	12-49								L
PVPU HVISI	VPU PROTEIN	CHARLES HANDOCENTER VIEWS	11-18								ļ
PVPU SIVEZ	VPU PROTED ⁴	COUNTY AND THE CONTRACT OF THE	3.3								1
UNIT (100)	VEX PEOTEIN	LACTATE DENYTOCOMANDELE VALINO VIANA	101.101					_			
	AT BUA. A BRATEIN	BARLEY STILTS MOSAIC VIDUS	ļ					L	L	-	
	That he Avenue	BOYDA ROTAVBLIS (GROUP C/STRAIN SKINTOKU)						_	L	L	L
VSO MOTOR		TEGTAVIOLIS (CRICUP BY STRAIN ADRY)	1							-	L
VEDS ROTOR	YP FRUIDA	BOTAVILLE (CROUP S / STRAIN IDUX)	24-33				1		-	-	L
VEO LOTO	VP PROTEIN	LA PAN ROTAVILUS	Ţ								L
PVSS LOTHC	VPS PROTEIN	PARTONE BOTA VILLUS (GROUP C./ STRAIN COWDEN)	Ĭ								L
PV506 MOTIFIC	VM PROTELIN	BANDAR BATAVIRUS (STRAIN KNA)	2-29			\downarrow					L
VIOT ROTEL	G. YOURSIN YOU	BACHAR BOTAVIRUS (STRATH UK)	91-146	22.30		\downarrow			-		ļ.
VSc1 LOTBU	NONSTRUCTURAL PROJECT PACE	CASTAL BATA WHIM (CEROTYPE 3/STRAIN OSU)	91-146	202-236						-	ļ
VSOT ROTTS	NOWSTRUCTURAL PROTEIN PLAN	PERMITTION AND ACCOUNT OF THE ADMINISTRATION	91-16	199-336				1		1	1
PVSc7 ROTS!	NOWSTRUCTURAL PROTEON MCVP3	SUPPLY TO A SUPPLY SUPP	164-201	L.							1
Vend Lone	NOWSTRUCTURAL PROTEIN NS2/VP9	BOVER KULA VIOLE (STINON ON)	164-201	1217-251	L						4
West Long	NONSTRUCTURAL PROTEIN NOVM	SDAAN II ROTAVILUS (SIKAM SATI)	ę,				L				4
TOTAL PARTY	CHACOPROTEIN VP7	BOVENE ROTAVIOUS (SEKOLYPE 67 31 KALM BOYL)	!		-	L	L				į
	CA VANNE CHEEN VIV	BOVING BOTAVIRUS (STRAIN AJ)			\downarrow		-		L		L
200	As Devemonted USA	BOVING ROTAVIRUS (STRAIN UK)				1		-			_
VSD KOTBU	CALL COURT OF THE WAY THE CALL	POTAVIRES (GROUP BY STIADY ADAV)	210-237		1			-		-	ļ
rvsoo tronda	CLYCOPICIEM VET PROCESSOR	LANJAN BOYAVIBLE (SEROTVPE 4/STEATH RVA)	3.70						-	-	╀
PVS09 NOTHA	GLYCOPROTEIN VP7	CHROLID BATANDING CORDITATES 2 STEATH HUS)	1.29				-		\downarrow	1	4
PVESS ROTHA	CLYCOPROTED VP7	NUMAN ROLL STATE CONTROL OF THE AMERICAN	3.29	L	_	ļ.,					-
Vene British	CALYCOPIOTEIN VP?	HUMAN KOTA VIKUS (SEKOTITIS OF STANON)	85.					-			
COLUMN STATE	ra ycopanten VP7	HUBGAN ROTAVIRUS (SEROTYPE 2/31RAM D31)			ļ			L	L		_
	CA CONSECUTION VP?	HUMAN ROTAVILUS (SEROTYPE 2 / STRAIN HULZO)		1				L		-	L
5	ALTERNATION OF THE PROPERTY OF	INTEXAN BOTAVIOUS (SENOTYPE 1/STRADY NOT)	47.7					ļ	-		L
VEO 20170	OLIOPAN OF	MUMAN ROTAVORUS (SERIOTYPE I / STRAIN INO AND STRAIN D)	2-29			\downarrow	1	1	-		-
PVSOP ROTHO	OLTUMNAM VE	LAPLAND BATA VIETE (SEE OT YPE 3 / STRAIN P)	1-29								1
PUEDS BLOTTE	CLYCOPROTEDY VF7	THE STATE OF STREET OF STREET STREET STREET	1.39	L						_	4
VSO LOTTE	GLYCOPAOTED VP7	RUNGAT HOLE VINES (MENO) 110 E 1 STORE AND WAY	1.79	_	L					4	4
WHICH BOWN	Of ycoenoten ve?	HUMAN KUI AVIAUS (SENO 175 175 175 177)	2.2				L		_	-	
AVENS P. PTTP2	GL YCOPROTEDN VP7	PORCINE RUINA UNIO (SCHOOL 176 STREET) AND THE STREET	2.30		-		L	L	_		_
Tally Both	CLYCOPIOTED VP7	PORCONE ROTAVIAUS (SELICIT FEB.) / STRAIN CAMPS)	**		-		L	L	-		
11200 0 0001	PALVOOPEDITIDI VP?	SDEAN II ROTAVICUS (STRADA SATI)					-		-	L	_
TANK WATER	IN PROTEIN		200	1	-	-	-	ļ.	L	L	L
0100	ACCOMPLETE TO BAL OLYCOPROTEIN NOVYS				-	-	L		L	L	L
1000	LESSON CUTTER CAPED PROTEDY	BOVING ROTAVILLE (STRAIN UK)			+	1	-	L	_	L	L
Calco III	1	BOVING ROTAVILLS (STRAIN YAQU)	3		-	-	1	-	ļ		ļ
W11 1011	1	INPERVISE (CROUP B) STRAIN ADRY) (ADULT DIABULEA ROTAVIRUS)	\$								ļ

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CCENT	107217014	AB VIVISO (NO DECITIONELLE)	1 740 4	AUVA 2	ARFA 3 A	ARFAI	AWEAS IA	ARFAGIAR	S VANY L VANY	2
CILE KAME	PROTEIN	HORAZAN BOTA UTBIR (SEROTYPE 2 / STRAIN RV-5)	Г	Т		т-				
TABLE BOTTON	Union Office Cabeth Profited	HENCEN BOTA VIBLIS (SEKOTYPE 2 / STRAIN DS!)	Г	111-143				-		Н
PVEIL BOTTOM	WINDS OFFER PARTY PROTEIN	MIDAAN BOTAVIRUS (SEROTYPE 1 / STRAIN WA)	111-145							
PVS11 BOTEA	MINOR OUTER CAPGO PROTEIN	AABBIT ROTAVIRUS (STRAIN ALABAMA)	118-145							i
PVS11 NOTS	MINOR OUTER CAPSID PROTEIN	SIMIAN II ROTAVIRUS (STRAIN SAI?)	111-146							1
PVSH MUDGE	SMALL HYDROPHOSIC PROTEIN	INTUNES VIRUS	9740			1				1
VSH MADON	SMALL HYDROPHOSIC PROTEIN	IMUNOS VIRUS (STRAIN MATSUYAMA)	13-41					1		7
PVSH MAN	SMALL HYDROPHOSIC PROTEDY	HUGGPS VIDUS (STRADN BELFAST)	Į				1			-
VEH LABOR	GAZALL MYDROPHORIC PROTEIN	MOMOS VILUS (STILAD) ENDERS)	97-6							4
1973/27 1787	64.411 Lymbreacher Pentrin	LATALITY VIRIAS (STRADA JERYL-LYNA)	976					 		
	MANUEL IN I DANCE I MANUEL I PARTICIONI	Calle and Charles about the lite Let	*				ļ			
PVSI MEDITA	SMALL HTSRUPHOUSE PROJECT	AUGUS TINES (STANDARD MACANA)					İ			
PVSH KUMPL	SALALL HYDROPHORIC PROTEIN	MUMPS VIRUS (STRAIM BULSTOL I)	9		†		Ţ	1		ļ
VSH BOBON	SALL HYDROPHOBIC PROTEIN	INDIONS VIRUS (STRADM MOYANIARA VACCINE)	12.4		1			1		1
PVSM MIDNOR	SMALL MYDROPHOBIC PROTEIN	MONOR VILUS (STILAIN RW)	Ī					1		4
PVCH LATERORY	SMALL HYDROPHORIC PROTEDY	MUNOS VILUS (STRAIN UNABE VACCINE AM9)	15-61		Ţ			-		
DVC: BEOVE	STOME I PROTEIN PRECURSOR	RESVIRUS (TYPE 3 / STRAIN DEARING)	26-63	11-122	137-168 2	452-222				_
INCOME POOR	GIGLIA I PROTESIA PRECINCOR	REDVIALIS (TYPE 2 / STRAIN DS/ONES)	3	130-193						
100	TINGS I BECTANISHED TO THE COM	REDVIELE CTYPE I / STEALY LANG)	4.52	18:104	112-160				_	_
Vall REUVE	STATE OF THE PERSON	BECOME A CHARGE OF PERINATION	150.184						-	L
PVSI2 NEOVO	SIGMA 2 PROTEIN	ACCURAGE A CONTRACT COLORED	114-114				T		-	-
PVSI3 REOVJ	SIGMA 3 PROTEIN	ALCVING (TVPS 21 PIRAIN DATONES)	1				T	1		ł
VSII PEOVO	SIGMA 1-5 PROTEIN	RECYINGS (1178) (31 KAIN DEAGING)					1			ļ
PVSIS_REOVE	SIGMA 1-S PROTEIN	MEOVIRUS (TYPE I / STRAIN LANG)	Š					1		-
PVTA COVI	PROTEIN TSA	CAPAIPOXVIRUS (STRAIM INS-1)	124-158							4
MATERIAL A	PROTEIN TA	SHOPE FIBROMA VIRUS (STRAIN KASZA)	250-277							_
VALUE BAV	PROPARITY NAV PACKAGING PROTEIN	FPSTEIN BALK VILUS (STRAIN B95.4)	234-290			Γ		_		
	TACABLE BILL BACK TONIO BEOTER	INDIAN PYTOMECAL OVIETY STRAIN ADIAN	4 7.451						<u> </u>	<u> </u>
VIEW HOWA	PROBABLE LINA PACKAGING PROTEIN	CONTRACTOR OF CHAIN PROPERTY AND ACCOUNTS AN		!	:	:	:	_		
PYTER JISVED	PROBABLE DRA PACKACING PROTEIN	THE THE PERSON AND A STREET OF STREET OF STREET	710.313			T				ł
PVTEA MSWII	PROBABLE DRA PACIACINO PROJEIN	ICLALOND REPORT VACANTAL AND AND AND AND AND AND AND AND AND AND		\int		Ī	Ī	-		+
PYTER VZVD	PROBABLE DNA PACKAGING PROTEIN	VAUCELLA-COSTER VIXUS (STRAIR DURINS)	77.07					$\frac{1}{2}$		+
VIPS TTVIV	VIRAL PROTEIN TPX	INEMOCROTEUS TENAX VIRUS I (STRAIN V. 3)						-		1
MIN TIVE	VIRAL PROTEIN TPX	THERMOPRUPEUS TENAX YIKUS I (STRAIN KINA)	2			Ī	1		1	+
PW PANA	V PACTEDA	HUNGAN PAKAINTLUENZA 4A YIRUS (STRAIN TOSIIIBA)	3					+	<u> </u> 	<u> </u>
17101 SSVI	HYPOTHETICAL 10 1 KD PROTEIN	SULFOLOBUS VIRUS-LIKE PARTICLE SSVI	25.65					1		-
PY168 15V!	HYPOTHETICAL 161 KD PROTEIN	SULFOLDBUS VIRUS-LIKE PARTICLE SSV1	4-61							4
IVIII EEVI	HYPOTHETICAL II.9 KD PROTEIN	SULFOLOBUS VIRUS-LIKE PARTICLE SSVI	36.78							_
PVIII TABUA	HYPOTHETICAL 11.2 KD PROTEIN	TOBACCO YELLOW DWALF VIRUS (STRAIN AUSTRALIA)	19:45							
AND ALLA	NAPOTA 11 LKD IN 16 KD STEGION	AUTOGRAPHA CALIFORNICA NUCLEAR POLYHEDROSIS VIRUS	1175							
1011	HAPOTHETICAL 13 2 KD PROTEIN	SULFOLOBUS VIRUS-LIKE PARTICLE SSVI	39.86					1		1
2012	LVANTARICAL 117 KD PROTEIN	SCHIPCLOBUS VIRUS-LIKE PARTICLE SSVI	8-38					-		_
AVIAL VAVA	HAPPOTH IN 19 KD PROTEIN STECION	AUTOGRAPHA CALIFORNICA NUCLEAR POLYHEDROSIS VIRUS	10.107					_		_
1033 47100	KYPOTHERICAL (\$4 KD PROTED)	SULPOLOBUS WAUS-LIKE PARTICLE SSVI	161-24							_
1012	WYNOTHWAT IT IND PROTEIN	SULFOLDBUS VIXUS LIKE PARTICLE SSVI	9:36	119-153					_	L
200	INCOMPRESENT 14 5 WITH PROPERTY	MANZE STREAK VALUS MICERIAN ISOLATES	16-61							ŀ
TOTAL MANAGE	WASHINGTON IN THE PROPERTY	MAIZE STREAK VINUS (SOUTH-AFINCAN ISOLATE)	34-61							H
1011	LOGICALISTICAL MAIN PROTECT	SIM FOR CRUS VINUS LIKE PARTICLE SSVI	76-103							L
	ALCONOMINATION OF THE PROPERTY	SER SOLOBUS VIRILE, THE PARTICLE SSVI	93-164					-		l
VZIK NOV	HATOLIES AND AND AND AND AND AND AND AND AND AND	COVERAN CHI CANTI MATTER VILLE	11514					-		-
772 500.0	HYPOTHETICAL PROTEIN .	NA POLICIA CALLA TARRANATA DE CENT	67.5				Ī			+
PYJIK SSVI	HYPOTHETICAL 31.3 KD PROJEK	SUCCOMBINED VINCENTIAL PARTICIPATION STATES	311.343					l		\downarrow
PTIK SSVI	HYPOTHETICAL 31.3 KD PROTEIN	SULCOLOGOS VIACOCIONE PARCILLES SAVI			1					+
PY31K NOVAC	HYPOTHETICAL 11.1 KD PROTEIN	AUTOGRAMA CALIFORNICA PUCLEAR POLYPEDRUSIS VIRUS	137-184		1		T	\dagger	+	+
VICO2 CY	HYPOTHETICAL PROTEIN 3	SOYBEAN CALOROTIC MOTILE VIKUS	122-143				1	+	1	+
PYT SOCIAV	HYPOTHETICAL PROTEIN?	SOYBEAN CHLOROTIC MOTTLE VIRUS	Z .					1	$\frac{1}{1}$	+
PY1SK 15VI	HYPOTHETICAL 85.9 KD PROTEIN	SULFOLOBUS VIRUS-LIKE PARTICLE SSVI	121-121	26.57	836-700			+		+
PYE SOCIAV		SOYBEAN CHECKOTTE WINUS	13-40				Ī			$\frac{1}{1}$
PYBOI FOWPA	HYPOTHETICAL BANGE ORFI PROTEIN	FOWLACK VIRUS (ISOLATE IN A SIGNORICH)	74-108	152-179				\dagger	$\frac{1}{1}$	\downarrow
PYBOS FOWTH	HYPOTHERICAL BANGE CRUS PROTEDI	FOWLIOX VIXES (ISOCATE NEASIGNORMAN)	62-29		_			1		-
									_	

2KG SAC	167117814	All Viveies (no bacteriophages)	AREAL	ABEA1	AREAL	4864	ABEAS	ABEA	ABEA:	VBEA1	1 1
NAME OF THE PERSON NAME OF THE P	٦	VIRIAL CONTRACTOR TO SERVICE AND	#:-CI								
PAZADO SIEVA	3	FOWLYOX VIXUS (ISOLATE IN THE MANAGE)	128-167								
MANON LINA		FOW DOX VILLS (150LA 18 PV-154 MUNICH)	13:116								1
VALANT FINAN	AFLS PROTEIN	KOLAN SPOMARETROVINGS	161.183								‡
CONTRACTOR OF STREET	HAYARTH SA I KD IN DAGA STREGION	HEIDERSVILLS SALMIN (STRAIN 1991/7)	17:55			L				ļ	
	MONTH THE IN THE LEGICIAN	RESPECTABLE SABORU (SUBGROUP C.) STAALIN 494)									
PYCHI HOVE	ALCOHOLD IN THE SECOND	VERPERVILLE SANGRU (SUBGROUP C./ STRAIN 488)							L	L	-
PYDHA HSVSC	MYPOTH 9.9 KD IN DRUK J KENION	TAWA BAY WELL (STEATH PE.I)	2								
PYFE FOUR	HAYOTHETHEAL 23.9 KD PRUIEDA	CALLS DOC (ASTR ATTA ATA PS.1)	1.70-204								L
PATO FOUNT	HYPOTHETICAL 36.9 KD PROTEIN	POWLFUL VIEW AND A PARTY OF THE	37-64	921-56	144-17					1	ļ
VALUE VALCEV	HYPOTH 21.7 KB KD NOW PRO	VACCINIA VIKUS (STICKLES WAY	3.5	179-206							
	DOMESTIC BANCH 17 4 KD PRO	AACCINIA VIRUI (STRAIN WA)	2				L				
	THE PERSON NAMED IN COLUMN TWO IS NOT THE PERSON NAMED IN COLUMN TWO I	EPSTEIN BARR VINUS (STRAIN B95-8)							L	_	
PYICE EDV	HYPOTHER INC. PROJECT	SPECIAL BANK CHRIST (STEAT) BOS.5)	19.53								
PYXXA EBV	HYPOTHETICAL BICUTA PROTEIN	EL DI ELITATION I DE LA CALLANTINA DE LA	47-16								ļ
PVL15 ADEA!	HYPOTH 12.4 KD IN 33 KD REGION	MUNAN ADEMOVING 11 CE 41	27.54								1
2	DOWNSHIP ALLES PROTED	EPSTEIN-BALL VICUS (STRAIN BY-4)	17.70			L					
	THE PROPERTY OF THE PARKET.	CONDICTION VELLOW MOTTLE VIXUS									L
PYOR! COTACY	HYPOTHER ALL DESCRIPTION	ANA ANTENIA VICTORIA MOTTE E VIRUS	35-76							L	L
PYOLI COYNY	HYPOTHETICAL 15 KD PROTEIN	CONTRACTOR STATE STATE STATE STATE AND IN IN	K-3								ļ
TWO INCOME.	LAWOTHER LA IS KD PROTEIN	WHITE CLOVER REGALL VINUS (STEWART M)	10.00		L		_				
	T	WHITE CLOVER MOSALC VIRUS (STRAIN O)				ļ					
PYON WOMA	٦	A CALN APPROVIDE GAL I (STRAIN PIELPS)	74-117							-	L
PYON ADEOL	HYPOTHETICAL 31.3 KD PAGILED	TOWNS CHECK TOWN VIRING ((STEAD) KIKA!)	23-57							-	ļ
PYORA TIVI	INTEGRAETICAL 8.1 KD PROTEON	CONTRACTOR SECTION OF THE AND PRIVATE AND	74								
0 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	TANNOTHETICAL 26 NO PROTEIN	THE MONITOR LEADER VIEWS I (STRONG TOWN)	=		L						
NAME OF TAXABLE PARTY.	NAMEDICAL 13 KD PROTEIN	THORNACPROTEUS TENAX VIXUS I (SI INAIN ALAN)	9		L	L					4
	CONTRACTOR 12 KD MOTERN	THERMOPROTEUS TENAX YELDS I (STICKIN MAN!)	,			L	L	L			
W	STORY OF A PROTEIN	DICE TINGLE BACELLFORM VIRUS				ļ		L	L		
PTP12 KIBV	A LOUIS CONTRACTOR OF THE PERSON OF THE PERS	TRICE TINGLE BACHT IFOOL VIXUS (ISOLATE PHILIPPINES)				-	ļ				L
PYP12 LYBVP	HYPOTHETICAL PIA PROBLEM	BICK WINGED BACKLI BORN VINUS	29-101	ŝ		\downarrow	1		-	-	L
PYP24 RTBV	HYPOTHETICAL PRINCIPLE	TO THE THE PARTY IN THE PARTY PROPERTY OF THE PHILLIPPINES)	101-16	2		$\frac{1}{4}$					-
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TABLE VII

107 X 178 X 4 SEARCH MOTIF RESULTS SUMMARY

(PREFERRED VIRAL SEQUENCES)

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PVCLC VZVD	ICL VCOPROTEIN GPV	VALICELLA 2031ER VIROS (SIRAIN INVINAS)		1	İ	İ	1	İ	İ		ŀ
TO ST. ST. ST.	PANIS BANTER PAS	VALICELL A TOTTER VIRE STRAIN DIDIAS	74.70		<u> </u>			1		j	
	Track to his safe action banks	CARIFFEE A. PASIER VIRUS CHEAN DONAS	10.4					j		İ	i
		A 3 Street vient rein	2 2								
PVCLC VZVS	GLYCUPILDIEM UPV		1 100 100							-	
POPOL MAN	DRA PALTAGRASE	WOULD MAKE THE ALLESS THE STATE OF THE STATE		-	İ	İ		ĺ	İ	Ī	
PARTY MANAGE	INMA NOT WAREASE	WOODCHACK MEPATITIS VIRUS ST	Ž.	j	j	İ			Ì	Ì	ĺ
	AU. 504 506 100	WOODCHACK HEPAFITIS VIEUS 1	72.24	=				j	j	ا	
JOHOT WHAT	JUNE POLITICALISE	LAXIA COLOR COLOR COLOR		91.10					_	_	
POPOL MAY	DHA POLYMERASE					Ī					
SPANN WATCH	PAIN POLYNORASE	WOODCINGE HE PATTIS VIRUS I			1	1				1	1

TABLE VIII

107 X 178 X 4 SEARCH MOTIF RESULTS SUMMARY

FOR ALL PROCARYOTIC PROTEINS

ı		Back sayante Secuences	٦	7	ι		Т	0 7 7 7 7 1	LANGE A PARA	A I AREA 9	-
PCCCNE	16717824		Į	A LATA	J			164.1202	Т	т	1
-	PROTEIN	RICKETTSIA NICKETTSII	Ţ	†			Т	+	-	-	Ī
	A VAN A LANGE OF THE PARTY IN CO.		7	7	100	1	958.06	904-931	1220-1254 1544.	1544-1571 1723	1723-1750
	LA TOTAL TENEDEST NO SECTION OF LAST ACE.	TTSII		-	1	Т	T	1		-	Γ
- 1	W. A.D. A.D. HULLAN PRESCRIPTION (1977)		ŝ	4		1	T	\dagger		-	
- T.	OBILIS	7				1		-	-	Γ	
	A PART OF THE COLUMN TO A PART		2	1	†	Ī				-	
200	A VENEZIA VENEZIA ANT PROTEIN		21:338	1	1						
	PODE EUR AND THE WASTERNESS AND PROTEIN		٦		1		Ī		-	-	Γ
	WALL DANKS AND THE STATE OF THE	Lis	_	444.524	1					-	
200	SALVEROIEM		٦	218-246	1	Ī		+		-	
POW SAC	MOB BETWEEN THE SECOND CONTRACTOR		203-232	1	Ì			+			Ī
MAD ECOL	6-PHOSPHOGLUCURATE DEATUROUSINGS	HUNDINGM	205-232					1		+	Ī
PerCO SALTY	PARCO CALTY APPROSPHOGLUCONATE DEHTUROGENASE		450-477							+	Ī
PAACA STAAU	6.AVENOCL YOOSIDE N.ACETYLTRANSFERASE		1_	185.712				4		1	
PAAT BACSP	ASPARTATE AMINOTRANSFERASE	BACTILLUS SF	T							-	
7	A CPARTATE AMINOTRANSFERASE	ESCHENICHIA COLI		1	Ī			-	-		
	ATT PROTEIN		1	70, 90	111,000			ŀ	-	-	
	ABON TICH BUACH RESISTANCE PROTEIN ABIC		┪	Т					-	L	
	A Vectorial	ACROBACTENUM TUMEFACIENS	2	1	Ī				-	L	Γ
	V Transfer	ESCHENICHIA COLI	196-032	1	1			-	\mid	-	
TO COMPANY	ACCOUNT OF HYDRATASE	BACKLUS SUBTILIS	T		Ī				-	-	Γ
2000	A CANADA TO LANGE A TAKE	ESCHENICHUA COLI	1	1						-	
NOV.	PACON ELLE INCOMINATION OF THE PROPERTY OF THE	ALCALIGENES EUTROPHUS	2 2	1						-	
TACOR ALCEU	ACBIOLICA CALABORISM ACCOME	ESCHERICHEA COLI	7	1						t	Ī
VC ECOL	ACYL CAULER PROTEIN	PSCSGRUCHIA COLI	213-247							+	Ī
PACIA ECOLI	ACIDIAVIA RESISTANCE PROTEIN A PRECUEST	PECNERICHIA COLI	1850-081						+	\dagger	
PACE ECOL	ACKERLAVEN RESISTANCE PROTEIN B	Tescional Cod 1	512-550	726-75)						+	
PACK ECOL	ACRUFILAVIN RESISTANCE PROTEIN P	STREET STREET STREET STREET	153-114							+	Ī
PACTS STRCO	PUTATIVE KETOACYL REDUCTASE	THE MONOCATO	33.264	376-603						+	I
PACTA LISMO	ACTINIASSEMBLY DIDUCING PROTEIN PACCORNO	WAS ABIA LACTANDURANS	1129.3163							1	I
PACVS NOCLA	ACV SYNTHETASE	10 C C C C C C C C C C C C C C C C C C C	136-170							+	Ī
PADAA BACSU	METPHOSTALISTEL DIA ALKTLIAANS EAASE	The Arman Lie 41 m Titles	341-425		522-556	1005-1032		*		\dagger	Ì
PADDA BACSU	ATP-DEPENDENT NUCLEASE SUBURIL	PACE 1/5 SUBTILIS		106-048	941.977					+	
PADDS BACSU	ATP-DEPENDENT MULLAASE SUBURIL B	IC DETRIBUTA ACETOBUTYLICUM	116.71						+	+	
PADHI CLOAS	NADPIR DEPENDENT BUT AND DENT DAOLER AND	P. OSTEINING ACETONITY LICENI	346.125					j		1	
PADITA CLOAD	NACH DEPENDENT BUTANCE DERFORCEMASE	CONTRACTORITY ACETONITY LICUNI	291.325							+	
PADING CLOAD	PADIM CLOAS NADIL DEPENDENT BUTANOL DEHTUNGGAASE	CLOSTATIONAL ACETORUTYLICUM	034-159	179-806						†	
PADHE CLOAL	ALCOHOL DENYDROGENASE	TESCHELICHIA POR I	171.291							+	١
PADME ECOLI	ALCOHOL DESTRUCCIONASE	ESCHEDISTRA COLI	12:							+	
PADIY ECOL	PUTATIVE REGULATORY PROTEIN AUT	LANCON ASSIA GENTALILAS	80:13	607-724	059-620	990-1017	1169.1190	1317-1416		+	ļ
PADPI LAYOUR	146 KD ADHESEN PRECUESOR	ACCOUNT ACUA DISTRICTION AF	1557-1564							+	
PADY KYCH	Abhte sol Principalson	BICKETT CIA DEOWAZEKII	176-107							+	
ADT TOX	ADPATP CARLER PROTEIN	A PERSONAL WOOD PARTY A	278-305						-	1	
PAELA AELAY	EROLYSON PR	STREET CONCESSION OF ANY	419.483	107.05						+	١
PACIAL STRUK	THIA-GALAC	STREET TO COLOR AND AND TO A	2								١
PAGAK PERAT	LETA AGALAS	PATERNA OCOCCIIC AIMERIC	129.159	165-192						1	
PAGE STANU	ACCESSORY CENT REGULATOR PROTEIN	SIACHTECCONOCIONAL STREET	9.46			L					
MARCH VENES	ATTACK ENVAS LOCUS PROTEEN PRÉCURSOR	YESDIA EVIENCULIUCA	9	466.493	503.530	L					
TOOK HINTO	ASPANTOKONAKE	ESCHERICAR COLL		401.635					-		
12.0		ESCHEDICHEA COLI							-		ŀ
	A COARTATE KINASE O ALPHA AND BETA SUBUNITS	I SPACELUS SUBTILIS								-	
	A STANDER STRANGE ALPHA AND BETA SUBUNITS						1			-	
	THE INTERIOR ALDOLASE		286.7				1	<u> </u>	-	t	
	1000	PSEUDOMONAS AERUGINOSA	3					1	-		
N C	ALCUMA TO BE STATE OF THE PROPERTY ALGE PRECURSO PSEUDOMONAS AERUGINOSA	O PSEUDOMONAS AERUGINOSA	9								
2017	THE A WEST PHINNAL REGULATORY PROTEIN ALG	П						1		 	
	ATEANE, I MONODYYGENASE						1			İ	
	TALLS TALL THE STOCK NADA TEDUCTASE			201				-	-		
	AT A CHANGE A CONTAST CATABOLIC PRECURSOR	ESCHEATCHIA COLI									
NAME AND	ALANania ini										

a mary		Prohestic Segments							Γ	
THE MAME	BOTCIN			1414	7115	SEA CH	AK TENE	28:34 08:32	L AREAL	1
PALA SACST	LANTHE MACENAISE	HIERMOMILLUS	2	1		1	1			1
PALSE BACKU	ALS GPERON ALCULATORY PROTEIN	BACULUS SUBTILIS	19.146				-	1	1	
AND BACK	IT OF YSIN PAR	BACELUS SP	183-183				<u> </u>	<u> </u>	1	-
VALYS BACSU	LHOLYSIN PRECINSOR		161.51				-		1	_
1144 44 144	Cholysby		П				1			
PALES ATLAN	AUA PROTEIN PRECURSOR		3	797.114	446.473		1			
ALCO HELD	AMMASE	PSEUDOMONAS CHILQAORAPHIS	13.99					-		
MALE SERVICE	OLIOPEPTIDE TRANSPORT PROTEIN ANIE		103.214			1		-	: :	:
DULL AND A	ALIMOPEPTIDASE AN			282-661						
ALLES SERVICE	BEALL ACT ALLACT PRECURENT	CENS	231-250		 					
	AND DESTRUCTION OF THE PROPERTY OF THE PROPERT		Т	72.80		-				
		SCHEENING AND I	655.682				L			
	MINORET I IDASS IN			T	Ì		-	<u> </u>		
100 COT	LATO AMENOPE TEDASE			T			-			
PAINT THEAD	JAINOPEPTIDASE T		201.100					<u> </u> 	1	1
PALY DICTH /	L'HA-AMYLASE I		╗				<u> </u>			
PALY: DOTA	LPHA-AMYLASE 3	-CIV	131-17	\$07.534						-
A IV	YTON A SURE AL MALAMY ASE	SALMONELLA TYPHIMURIUM	10.104						-	
TO IATE	I PHA. AMYLASE 1	UAL	280-307							
	TARKA ANAMA TAR BERTINGON	52	18:19							
	20000000000000000000000000000000000000		Γ	266.303	141.1184		ŀ	_		
- N	PANTE BACKUBERA-AMILIASE	San account of the Country	Ţ	Т	410.416				-	
ANTE CLOT	ACLUA3UA		T	Т						
PANO CLOSP			1	20.310						$\frac{1}{1}$
PALMY BACS	RECURSOR	EAROTHERMOPHILUS	į	٦			$\frac{1}{1}$	1		-
PAMYE BACS	3.6			435.465	615-643					
A16.2			(51-51)			_		4		-
		IX TIS	166-193			-		_		_
			102.136		Ì		L	L		L
PAMY MACAN			Т	11.7.11	T		\mid	-		-
E ANY	ALPHA-AMTLASE PIECUISOR		Т		T		+			ļ
AMY MORE	ALPHA-AMMLASE PRECUISOR		Ţ,		Ì		+	1		-
PANY MCSU	ALPHA-AMPLASE PRECURSOR	BACILLUS SUBTILIS	T	Т	777.00	100	\dagger		1	
PASS BUTTI	ALPHA-AMMASS PRECURSOR		T	Т	Т]		
PANY CLOAD	PUTATIVE ALPHA-AMOTASE	Ī	T					$\frac{1}{1}$	1	
PAMY CLOT	ALPHA-AMYLASE PRECONSOR	LFUROGENES	1	29-219		1	1			
PALMY STRUM	THIS WALLS		27:300				+	1	1	
PANTA AZOVI	WITE OCEN FLU	AZOTOBAČTER VINELANDII	<u>\$</u>		1	-	1	-	1	
PANTO AZOM	ATTROCENASE		95-122							$\frac{1}{1}$
PANOTA AZOVI	NITE COENASE DION-DON PROTEIN BETA CHAIN	NOIL					_			
PANCK VIBAN	ANGR PROTEIN		93-130	169-203					_	
PANCE PREDICTION	HYCOST ISON	NOH					_	_		
PANCE SYNCE	HYCOBILISON	SYNECHOCOCCUS SP	11-64	\$19-615						
PAPCE SYNYS	PHYCOBIL ISOM		53-79				-	_		
PAPIC SALTY	ALKYL HYDROPEROXIDE REDUCTASE C11 PROTEIN	SALMONELLA TYPHIMUMUM	63-69							
PAPI AGAY	PROTEKSE I PRECURSOR	ACHOROMOBACTER LYTICUS	478-505							
PAPE PCOL	PROBABLE CYTOCHRONE OXIDASE SUBUNIT I		116.148				-			_
NAME OF ASSESSED.	AT KAT THE PROTESSE SECRETION PROTEIN APRO		416-450							_
AVAM - 94 V9	AT YAT THE PROTECTE SECRETION PROTEIN APRE		13.193	201.235	247.277		-	-	-	L
	ANSWERS PROVPHORIZORYL TRANSFERASE		121-148				-	_	_	L
10271	AI PHA ALM ASE MILLIT ANASE PRECURSOR	ACTER ETHANOLICUS	176-303	347.374	916-912	987-1014 12	1210-1254 13	1311-1408	-	-
	A PENGAGE THE PARTY OF SE		T	318.345	T	-	-			<u> </u>
	A PRODUCE DESPERATION CONTROL PROTEIN ABOR		٥	Ī.	30436	-				L
	ACON AND AND	ERUGINOSA	Т	Т		-			-	L
300	TOBABLE AND		Т			\mid				-
WAY.	A CLICA COLOR	recharge Coll						-		-
PAROL ECOL	YS-ARC-UICE	Silvent Coccession					+	+	-	\downarrow
PAKOA STAAU	HOSPHOSHIK		30.07		Ī					+
MOC ECOL	HOMENATES								<u> </u>	1
PAROC EALT	CHONISMATE STATINASE		20,00	Ī			+	1		1
PAROD BACS	DENTOROGUE	BACILLUS SUBTILIS		bracket	1	1	1	1		$\left \right $

					AREAD	c					
CGENE	10111781W	DRGANISM		Т				1	†	†	
	SUIT MAKE WINAKE	ESCHENCHIA COLL		131.151	266-324		_			1	ļ
WACK ECOL		STREPTOCOCCUS PYOGENES	Τ	Т			-	 		1	
ALL STRUCK	IGA RECEVIOR PAC	ESCHELLICHIA COLI	737-767	1				-	-	_	
Att tool		FICHERICKIA COLI	201-23	1	1	Í		-	\mid		
ALSA ECOLI	ABSENCAL PUMP DRIVING AT PASE	FSCHERICHIA COLI	_		1	T					
ALSE ECOLI	ABSENICAL PUNG MCMBRANG TRUSTER	STAPHYLOCOCCUS AUREUS	1		1	İ			ŀ		
PAUSE STAAU	ABSENICAL PUMP REMERANG PROTEIN	STAPHYLOCOCCUS XYLOSUS	1	27.5	1	T					
TALES STANCY	ALSENICAL PUND MEMBERANE PROTEIN	KTAPHYLOCOCCUS AUREUS	66	1	Ì	1	T	T	-		
FAKSK STAAU	ARSENICAL RESIST OFFICON REPRESSOR PACIFIC	ECCHERICHIA COLI	П		1	1	†				
PALTA ECOL	ALTA PROTEIN	REPURPICHIA COLI		213-240		1	1	t	İ		
ARTI ECOLI	TILANSPORT SYSTE	ESCUEDIONIA COL		┪	٦		1				
PART ICOL	TRANSPORT SYSTE	EXTREMOCION SECALIS	195.781	110.505	33.67	20.5	1	1	1	İ	١
1.	ACCRECATION SUBSTANCE PRECURSOR	ENIEM COL	137.158					_		_	
	A COALTATE ALONONIA LIGASE	ESCHERICIUM COLI	5	- !				_			
	ACT A CONTINUE SYNTHET ASE IS	ESCHERICINA CTR.					_		1	1	
	THE PERSON AND ASSESSMENT AND ASSESSMENT OF THE PERSON ASSESSMENT OF THE PERSON AND ASSESSMENT OF THE PERSON ASSESSMENT O	ILISCITICATION CON.1			Ī						
YSW. ECO.	ALCONOMIC TO SECURE IN A SEC	BACULUS SUBTILIS			Ī			ŀ			
PASPA BACSU	ASPANIA I BARNIONINE I NEC	ESCHEDICHIA COLI	20.23		T						
TOOT VISVA	ASPARTATE ALCHONIA LIANE	GERRATIA MARCESCENS	104-231	Ì	1		İ	Ì			
ALCO ACCUAN	ASPARTATE ALCHONIA-LYASE	TAPET CITATION OF STREET	152-211		ļ	-		:			
PASPO BACL	L-ASPARAGINASE	SACRETA CHECKANITING	115-216					1	Ì		ļ
PASPO SAVCH	CASPARAGINASE	SEAWINING CITY OF THE ANALYSIS AND	9					1	1		
CUV VIEW		ACINE 108ACTER OLOTANITADI	154.31					1			ł
200	A COMPOSUCCIO	ESCHERICKIA COL	387.314								١
	ACKANOSTICCDA	METHANOSARCINA BAUNEN	1	301.345							١
	ATTENTION ATTO	STAPHYLOCOCCUS AUREUS									Ī
N N	POT A SUITA CONTINUE AT A SECONTINUE AT PASE A	ENTEROCOCCUS FAECALIS	41.41								1
ATTA CALL	TANAMED THANCOURTING ATPASE B	ENTEROCOCCUS PAECALIS	7								1
PATKS ENTRY	THE PERSON OF TH	SALMONELLA TYPHIANUNUM	2000								
PATION SALT	T MALL STORY OF THE PARTY	SYNECHOCOCCUS SP	3								
1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	AIT SINIES A CHAN	VIBRIO ALGINOL YTICUS		41.7							
ATA VIOLE	CALCACTURE AT BUA CHAIN	ANABAENA SP									
PATPA AMAS	ALL STATES OF ALBUM COLLAIN	BACILLUS MEGATERIUM									
ZYTY WOR	PATPA BACME (ATP STRICTURE AND STREET	ESCHELICHIA COLI	110-000								
PATTA ECOLI	ATP STRINGS ALEXA CHAIN	ENTEROCOCCUS PAECALIS	9(-)								
PATPA ENT!	ATP STATISTICS ALTER CITY CUAN	MYCOPLASMA GALLISEPTICUM	362-400								
PATPA MYCC	PATPA MYCCA ATP SYNTHASE ALTHA CHANT	PROPIONICENTUM MODESTUM	6-36								
PATPA PROM	O ATP SYNTHASE ALTHA CITAL	INDOOR BUILTON RUBRUM	165-200	2							
PATTA MOR	U ATP SYNTHASE ALPHA CHAIN	THE FOR CALLS ACTION ALL DARIUS	318-345	167-589							L
YEAN WAY	E ATPASE ALPHA CHAIN	SOUNDED ACTION OF THE PARTY OF	7								
PATPA SYND	ATP STATIONS ALPHA CHAIN	S STANCOCOCI E UP	<u> </u>	362-269							İ
PATRA STATE	S TATE SYNTHASE ALPHA CHADA	STREET, SCHOOL ST	17.9	434.500							1
VKV2 ATTA	3 ATP SYNTHASE ALPHA CHAIN	STATE OF BLANK PA. 1	6.36								1
101	ATT SYNTHASE ALPHA CHAIN	THE LOW LEADING BANK I COMMISSION OF THE PARK	464-513	L	L						1
AND ATTA	ATP SYNTHASE ALPHA CHAIN	VIBIO ALUMAN TILLOS	110.307	176.397	L						1
DANK G	UP IN STATEMENT BETA CHAIN	ANABALMA	161.180	38.385							1
	Т	BACELUS PUOMOS	175-402			_					1
	OA ATP SYNTHASE BETA CHAIN	MYCOPLASMA GALLISET INCOM	119.186	L		L					1
		PHODOSPIRELUM KUBKUM	101								_
	A THE WITH A PLASE BETA CHAIN	SULFOCOBUS ACIDOCAL DANGS	181.40		ļ						
1000		SYNECHOCOCCUS SP	1100	181.468				Ľ			
TALES OF THE	ATT EVATINASE	Synechococcus sy					-		L		
LA LA STATE	TA CATHLAST	SYNECHOCYSTIS SP	100	1	-	1					
	AS EVALUASE	ANABAENA SP	67:40		1	-			L		
ATTO ATTO	1 VALUE	BACELUS FRUKUS	2	3	\downarrow	-					Ц
PATPD BAC	STATE OF THE PARTY	BACELUS MEGATERUM	2012								L
PATPO BACKE	STATISTICS OF	ENTEROCOCCUS PAECALIS	3		1	-			L		L
IATTO CATA	THE SYNTHASE	PROPIONICENTUM MODESTUM			\downarrow	1	1		L	Ľ	Ц
LYTTO THE	PATTO PROMO INTERNATION OF TACHADA	AHODOPSEUDOMONAS BLASTICA	123-132		-	1	1	1	ļ		L
					_						_

FATPO STORE	PROIZIN	ORGANISM	Ⅱ.	AREA 3 AREA 3	F VACTOR	ABFAG	AREA SAREA		ARFAR A	ABLA
PATPO SYNO!	The second and believed persons			1	7	20420		Т	т	
	ATP SYNTHASE DELTA CHAIN	SYNECHOCOCCUS SP	100-137		-		+	+	1	
PATPO SYNTY	ATP SYNTHASE DELTA CHAIN	SYNECHOCYSTIS SP	13:43					1	1	1
PATPO VIBAL	TP SYNTHASE DELTA CHAIN	VIBIUO ALGINOLYTICUS	10-01	1			+	+	1	
PATPE BACFI	TP SYNTHASE EPSILON CHAIN	DACILLUS FIRMIUS	8					+	†	ł
PATPE MYCGA A	TP SYNTHASE EPSILON CHAIN	MYCOPLASMA GALLISEPTICUM	95-126					-	\dagger	
PATPE PROMO	TP SYNTHASE EPSILON CHAIN	PROPIONIGENIUM MODESTURI	180					+	t	
PATPE SYNFI	ATP SYNTHASE EPSILON CHAIN	S YNE CHOCOCCUS, SP.	8 :	11 14 144	,			-	\dagger	
PATP! ANASP	ATP SYNTHASE B CHAIN	ANABALNA SF	T	T		I			†	
PATPF BACFI	TP SYNTHASE B CHAIN	BACILLUS FIRMUS		9.					t	
PATPE BACME	TP SYNTHASE B CHAIN	BACILLUS MEDATEMUM	T	20.00	1				t	
PATPF MYCGA	TP SYNTHASE B CHAIN	MYCOPLASMA GALLISEPTICUM	_	140-141	+			 	\dagger	
PATPE SYNDI A	TP SYNTHASE B CHAIN	SYNECHOCOCCUS SP	7	25	1			+	\dagger	
PATPE SYNDS	TP SYNTHASE B CHAIN	SYNECHOCOCCUS SP	1	128-155				$\frac{1}{1}$	\dagger	
PATP! THEP3	TP SYNTHASE B CHAIN PRECURSOR	THERMOPHILIC BACTERIUM PS-3	50-77					1		
PATPG ANASP	TP SYNTHASE GANOUA CHAIN	ANABAENA SP	176-310						1	۱
PATPG ECOL	TP SYNTHASE DANDA CHAIN	ESCHENICHIA COLI	253-283				-	1	1	
PATEG MYCCA	THE SYNTHASE CIANDLA CHAIN	MYCOPLASMA GALLISEPTICUM		07:140				1	1	1
PATPG KHORU	THE SYNTHASE GALDA CHAIN	RHODOSPIRILLUM RUDRUM	110-291							
PATPO SYNPL	17 SYNTHASE DAKONA CHAIN	SYNECHOCOCCUS SP	280-307						1	
г	LADA CHAIN	SYNECHOCYSTIS SP	96.126	100.307				1	1	
	ATP SYNTHASE PROTEIN I	MYCOPLASMA GALLISEPTICUM	133-167						1	
PATPX ANASP	TP SYNTHASE B'CHAIN	ANABAENA SP	129-156			_			1	
PATPX BACK	IT SYNTHASE BETA CHAIN	BACILLUS FIRMUS	162.119	156.313					1	
PATPX RHORU	TH SYNTHASE B	AHODOSPIALLUM RUBRUM	40-74					1	1	
PATPX STAP! /	TP SYNTHASE B	SYNECHOCOCCUS SP	37-110	28-155					1	l
PATTEX SYNOW	ITP SYNTHASE B	SYNECHOCOCCUS SP	8	-				1	1	
PATPX SYNY3	ATP SYNTHASE B' CHAIN	SYNECHOCYSTIS SP	108-135						1	١
PATPZ BACAGE	ATP SYNTHASE PROTEIN!	BACELUS MEGATERUM	14-62						1	
PATTE SYNPI	ATP STATINASE P	SYNECHOCOCCUS SP	Т					$\frac{1}{1}$	†	ļ
PAYLE PEESO	AVINULENCE B PROTEIN	PSEUDOMONAS SYRINGAE	_	233-760				ł	1	
PBAN EURSP	7.ALPHA-HYDROXYSTEROID DEHYDROGENASE	EUBACTELUM SP	20-22	1				1	\dagger	
PBATE EUBSP	3.ALPHA-HYDROXYSTEROID DEHYDROGENASE	EUBACTERUM SP	20,70						\dagger	
PBACE EALER	HALORHODOPSDN	HALDBACTERUM HALDBIUM			1		Ì	$\frac{1}{1}$	1	
PBACH HALSO	HALORHODOPS DY PRECURSOR	ALCOACI CALOM ST	153.184		+				\dagger	
PBAES ECOL	SENSOR TROITED BARBO	STREPTOCOCCUS AGALACTIAE	93.119	138-204 267-306	06 343-385	487.524	\$62.589	1014-1041	-	
COVE CANA	BACTERIAL DEVICE DEN	VITREOSCRITA SP	119.146	Т	Т		<u> </u>		l	
PRAIC HIMSP	PRAIC HIMS BILE ACID-DIDUCIBLE OPERON PROTEIN C	EUBACTERIUSASP	423-450							
PBAKA ECOL	SENSOR PROTEIN BARA	ESCHENICHEA COLJ	134-361	415-455		_				
PBASS ZCOLL		ESCHENCHIA COLI	123.156					_		
PBAT HALHA	PUTATIVE BACTERIO OPSIN ACTIVATOR	HALOBACTERUM HALOBIUM	408-442							
PBAX ECOLI	AX PROTEIN	ESCHENCHIA COLI	3.					1	1	
1900 1000	NOTIN CARBOX		3		+				1	ĺ
PECHE INDCA	METHYLTRANSFEALSE	ANODOBACTER CAPSULATUS	1000-1032		+			1	1	
PBCHOW MIDOCA	ROTOCHLOROP		249.276						1	
PBCNS CLOPE	SACTEMOCON BO		8	585-646			j	1	1	١
PBCPA PROAE	BACTENOCHE	PROSTIGECOCHE, CIUS AESTUARII	61.93	****				+	1	
PBCSC ACEXY	CELLULOSE SYNTHASE OPERON C PROTEIN	ACETOBACTER ATLIMUNI	10.13	1033-10112				+	\dagger	
PBCSD ACEDY	CELL MOSE SY	ACETOBACTER ATLINON	111	1	1	\downarrow	1		1	l
PBENA ACICA	BENZOATE 1.2.	ROUGESTON COLUMN	241.330		 	1			t	
TOTAL ECON	DGH APPINITY	UNACCOUNT OF SET I TENTA E	9.15		+				t	
VEXA MEDI	BEXA PROTECT	WANTED BY THE STATE OF THE STAT	157.114	236.243			ļ		t	
THE ALL PACES	Carona Control	HAEMONII US DIFLUENZAE	205-239		L		İ	l	l	
Party Mirve	BACTENOFERATION	MITROBACTER WINGGRADSKYI	<u>:</u>							
L	EVOLVED BETA-		955-918							
PBOAL BACST	BETAGALACTO	BACELUS STEAROTHERMOPHILUS	100-633							

		The state of the s									
CENE	8711751		4	1						1	1
T.W.	BETA OAT ACTORIDASE	CLOSTRUDIUM ACETOBUTYLICUM		T	ĺ	ĺ				-	
TOTAL TOTAL	SET A CALL AND CONTRACT	1			Ť	Ī	-		<u> </u>	-	
PROPE CEOIN			7	1	1	İ	İ		-		
OAL RUETA	UE IN LANGE OF THE PARTY OF THE		30.332	1	1			l	-		
	BEIN-UNITAGE OF THE PROPERTY O	SO	7		1				-	-	
OAL STRTE	BETA-GALACIOSIDASE		┪	29.700	1	Ť	T			r	
PBOAL SULSO	DETA-GALACTOSIDASE		20.5	1	Ì	Ì	1		-	r	
SOAM LEURA	BETA-GALACTOSIDASE SMALL SOBOWY		9-1-90	j		1	!		i	_	
OF DOS MYDE	BETA-GALACTOSIDASE		153-360 4		1		1		-	t	
ACA CLOTA	DETA-CLUCOSIDASE A		159-216		154-581	99-169		+		t	١
PECLE CLOTM	THERMOSTABLE BETA-GLUCOSIDASE B		464-494	\$36.563				9		†	l
DOJ TING	BETA-GLUCURONIDASE		ī	T						1	١
62 (27)	RFFA.CLUCOSIDASE		Т	414.462	693.719	138.765		-	<u> </u>	Ì	-
	THE A CLUCKING TO	2	T	Т	Т						
1150	SELACE CONTRACT		3	-				•	:	_	
PBIND STAND			163.197	1				-	-	T	
DIME STAND	_	STAPHYL OCOCCUS AUREUS	163-190							Ì	١
PERME STANU	DNA-INVERTASE BINR		33-60					†		Ì	
PRION BACSH	AMINOTRANSFERASE		145-173					+		T	ļ
BIOS BACKH	BIOTIN SYNTHETASE		130-137					Ì	1	1	١
TOOL HOLL	BIOTEN SYNTHETA	EXCHENCE AND THE PROPERTY OF T	144:131						+	1	1
MACAN DAIGH	DETHIOSIOTON SY		Ţ	315.305					-		1
	BETALL ACTAMASE PRECUASOR, TYPE	BACILLUS CEREUS	Τ.	10,70							ļ
	WALL A CALLAND	HAEMOPHILUS DIFLUENZAE	Т					ľ			
NEW IVE	13471471	BACILLUS CEREUS	T								
PB.V. IACCE	BELIA-LAL AMON	BACH LUS SP	Ţ					r		Ī	l
NOW WITH	BELACIATION CONTROL TO THE CONTROL T	EACH LUS CEREUS	٦	621-66							١
PBLAJ BACCE	BETA-LACTAMAN	PERTINOACINAS AFRUGINOSA	2					Ì	1	Ī	l
PBLA4 PSEAE	BETA-LACTAMASE	D. A. C.	95-02 20-02	200-227					1	Ī	١
PBLAB BACCE	BETA-LACTANASE	BACKLOS CONCO	Γ								1
PRI AB BACFR	SETA-LACTAMA		93.120	276-303						1	١
BUT NATION	BETA-LACTANASE PRECURSOR, TYPE!		Т	\$11.91							١
TOTAL STREET	SETA CACTAMA	BACOLUS LICHEMPORMIS	166.39								1
CACAGO A POR	RETA-LACTANA	PROTEUS MINABLES		740.767							Ì
SOUR JE IN	BETA-LACTAMA	PROTEUS VULGAUS	,								Ì
	INETAL ACTAMANE PRECURSOR	STREPTOMYCES ALBUS G	2,1								
1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	201744	KLEBSIELLA PNEUMONIAE	12						-		
200	BEIN-CALINO	STAPHYLOCOCCUS AUREUS	19-74	2							1
BLAI STAN	PLANCELLIA ASS. Marchan	ESCHENORA COLI	116-146	200					t		١
PELAO ECOL	BETA-LACTAMASE PRECUASOR	BECKERICHTA COLL	1155-196						1	Ī	١
FELAP ECOLI	BETALLACTAMASE PSE-2 PRECURSOR	DACT LICE POPULISONAIS	129-156	115-512							١
PELAT BACK	RECULATORY PROTEDIBLARI	STATES ACCOUNT AT BEING	87.114	122-161	134-161	261-312	503-539		1	Ī	1
PELAK STANI	PECULATORY PROTEDI BLAR!	STATE STATE OF THE PARTY	312.346	L							1
PALE TREPA	BASIC MEMBRANE PROTEIN PRECURSOR	I NETONEMA PALLICOM	337.304	L		L			1		Į
PRIME BACSU	MAIL TERUO RESISTANCE PROTEIN	BACILLUS SUBTINIS	1991				L		-		Ì
DESTA PARE	BENZENE 13-DIOXYGENASE ALPHA SUBUNIT	PSEUDOMONAS PUTIDA									
THE PARTY OF THE P	RENTENE 1.2-DIOXYGENASE BETA SUBURIT	PSEUDOMONAS PUTIDA									
Mark Value		PSEUDOMONAS PUTIDA		10.		141.425	50:33				
1		DESULPUROLOBUS AMBIVALENS									
PBPS URSAM		PSEUDOMONAS AERUGINOSA	360-21		1	1					L
SKA PAK		PSEUDOMONAS AERUGINOSA	2		1	1	1		İ		
NEW PARTY	I WAS TO SEE THE	PSEUDOMONAS AERUGINOSA	7.]				Ì		1
PBIAO PAN	BIAU PAULEN	t	419-466		1	\downarrow	-				L
910	THE WAY	┲	ŝ	1		\downarrow		\prod			
PBTUE ECOL	NI THE NAME OF THE	F	174-205		1						
PBVQA BOILTE	TICKSC MC 100	٢									
	THE ASSESSMENT OF THE RANGE PRECURSOR	BORDETELLA PERTUSSIS	2			\downarrow					L
PBVGB BOX	TAIL SALLE	BONDETELLA PERTUSSIS	8	207		1	1				L
PBVCC BOUVE	THE PART BY	BOXDETELLA BRONCHISEPTICA			Т	678 719	15	500.000	1156.1207		L
VBVGS BUTTER	SALE STREET STREET OF TANK A PRECURSOR	CLOSTILIDIUM BOTULINUM	313-340	- 1	7	7		1041 1001 1000			L

POGENE	100517314	Prekaryetit Sequentes			П	П			П	п	
ULEKAME	ROTEIN		ARIAL	7	J	3	7	Z Z Z	S VINC	3	Z Z
Pexci CLOBO	SOTULINUM NEU	CLOSTADIUM BOTULINUM		Т	ł	т	741-00	178	1961	1	
78XD CL080	SOTULINUM NEU		_[Т	2/:/	Т	760-110	٦,	1001.0001	1	
0907D EX84	SOTULINUM NEU	1	ı	T	3	Т	2	-	A .	1	
PBXE CLOBU			- 1	╗	704-733		, (A	_	A 11 - C 11	Ī	
PBXF CL080	BOTULINUM NEU		669-710	235-772	802-919	1013-1040	27	0171-611	1	1	
PCS NGCAE	CYTOCHROME CS	MCROCYSTIS AERUGINOSA	1.30			-			1		
CON MODE	PROBABLE CADACUAL TRANSPORTING ATPASE	BACELLUS FERNUS 1 .	30-57	100-131	165-192	276-306	533.567				
PCADA STAND	PROBABLE CADM	AUREUS	113-309	065-965					1		
MADE BOOL	PRANSCRUPTIONA	ESCHENICHIA COLI	\$1.15	(00-210					_		
PCARA VERSE	CAPRIES AND	YEASDUA PESTIS	203-240	416-457	\$30.559	619-646					
PCABA BACAN	WISHOUGH VAN.	BACULUS ANTHRACIS	101-138					ř			
	CASE IN CASE		14.70								
	CAN PROTEIN	AUA74648 DISTRICT	196						ļ		
3	PHOSPHOENGL TRUVALE CARBOALLASE			791 631	4.01 334				t	Ī	
3	PHOSPHOENGLPYXUVATE CAXBOXYLASE								İ	Ī	
100 SEC	PHOSPHOENOLPYRUVATE CARBOXYLASE	M GLUTAIICUM	77-6								
PCAP ECOL	PHOSPHOENOLPYRUVATE CAMBOXYLASE	ESCHERICHIA COLI	15-62						1		
PCARA BACSU	CARBAMOYL-PHOSPHATE SYNTILASE		274.319					•	İ		
PCARE IACSU	CALBAMOYLPHO	SACILLUS SUBTILIS	190-031								
PCARR PON	CARBAMOYLAH	-	180-181								
PCATE HAAL	CHI DRANDHEDAD		7.34	11.11							
PCATT FTAAU	CHI ORANOHENICOL ACETYL TRANSFERASE	STAPITY DEDCEUS AUTEUS	*	17:114							
ACAY APA	CATTOHOL 12 D	ACINETOBACTER CALCOACETICUS	Ş ∓								
	BEST VILLE LE	BACKLIN STFAROTIFERIOPHILLS	440-470								
	TENOMESTICAL CONTINUES.		170.404						ļ		
	CAIALASE INT	TOTAL STREET	907						1		
NA VOC	CATALASE	18118		144.44	Ī					Ī	
MATA SALT	CATALASE IOI	MACHELLA I PRINCIPALINI									
77 E 500	CATALASE IOII	ESCHENICHIA COLI	70.01						İ	Ī	
7CT CA100	CHEORANDMENICOL ACETYL TRANSFERASE	CAMPYLOBACTER COLI									
PCAT CLOBU	CHECKLANDINEOL ACETALTRANSFERASE	CLOSTILIDIUM BUTYTICUM							1		
PCAT ECOLI	CHECKANOPIED COL ACETYL TRANSFERASE	ESOREMONIA COLI									
PCAT PROM	CHLORANDYENICOL ACETYLTRANSFERASE	PROTEUS MIKABICIS	2							1	
74 TA	CHLORANDY@MCOL ACETYLTILANSFEILASE	STANTED OF COS INTERNATIONS									
MAT STRAG	CHLORANGMENTOL ALETTLINOWSPERASE	STIEVING CUSTOM							Ť		
PCINE COLD	CONTROL	COXIELLA BURNE TII	2							1	
MOUNT THEIR	PCBFT THEIN CAMBOXYPEPTIDASE T PLECURSOR	THE LINGUITIES VUICANUS							†	1	
CCV ECOL	THAY MUCLEOTIDYL TRANSFERASE	ESCHENCHIA COLI	2						1		
PCOK SYND	COJ CONC MECH PROTEIN CCAIX	SYNECHOCOCCUS SP	ž.								
MODEL STATE	NO CONC MECH	SYMECHOCOCCUS SP	32.23	2:12	\$				1	Ī	
KOAL THEE	YCLOMAL TODE	THERMOANAEROBACTER ETILANOLICUS	20.22								
PODE BACK	I CYCLOMAL TODEXT GLUCANOTRANS PRECURSOR	BACKLUS MACERANS	439.466	616-643							
PCDG! BACK	I CYCLOMAL TODEXT CLUCANOTRANS PLECUASOR		210.251	436.466	615-642						
PODGY BACK	CYCLOMALTODEXT GLUCANOTICANS PRECURSOR		217.244	442-47]	594.651						
MODEL BACK	CYCLOMALTODEST GLUCANOTRANS PRECURSOR	BACILLUS LICHENIFORNIS	217.244	442-472	594.647						
PCDCI EACOH	I EYCLOMALTODEXT CLUCANOTILANS PRECURSOR	BACETUS ORBENSIS	410-431						-		
PCDOT BACK			110.33	415-461	299.519						
POOT BACK			409.47								
DATE TOWN	CYCLOLAL YODEXT OLUCANOTIVANS PRECURSOR	BACELLUS SP	210-217	433-462	18 51				ľ		
DOM:	CYCLOMAL TODEXT OLUCANOTRANS PRECURSOR		110-217	433-465	615.642						
PCDOT BACE	CYCLOMAL TODA	BACELUS SP	27.744	443-472	394.651						
PODOT BACK	CYCLOMAL TODEXT OLUCANOTRANS PRECURSOR	픚	316.646								
MADE KIEW	CYCLONALTOD	-	212:33								
MON ECOL	COLICEN EL PROT	ESCHENICHIA COLI	44.3	215.326							
SOLVE STORY	COLICON ET PRO	SHICKLIA SONNE!	16.34	284-535	41140						
MEN ECOLI	_	ESCIEDICHTA COLI	134-361						Į.		
אכנאי ונכסרו		ESCHENICHIA COLI	196-366								
KEA6 ECOLI	COLICIN ES	ESCIENCIAL COLI	34.36								
KEAN ECOLI		ESCHENICHIA COLI	283:34						1	1	

THE FAME TO THE FAME TO THE FAME TO THE FOOL TO THE F	STOLEN D		116.227	_	1					
				ļ		i				
					1	1		-		
	N ASSIS	ESCREDUMENT	10.146	13):00			-	1	i	į
	1 No. 100	ESCHENICHIA COLI	T	!	 -	<u> </u> -			j	
100 100 100 100 100 100 100 100 100 100	V MOS PUT	CITAGOACTER FACUNDII	1	-						
110 000 000 000 000 000 000 000 000 000	CONTRACT IN INCREMENAL	AVULIGERUS		41 416	178.412 413	415.452	_			١
100 ACT 100 AC	SCHOOL SECTION		Ī	T	T	(3)	 			
	CONTRACTOR OF THE PROPERTY OF		T	Ť	Τ					
	ALCO IN TRUITS	ACETOBACTER XYLINUM	20.60	1	1	 				
		ESCHEDICHIA COLI	2 6 -103	1	+					
7	MOTION CELA	ESCHENCIA COLI	╗	Т						
742 100U O	CI AN INGRIAL SUBLANT A PACCAMON	GENUBBLINE COL		38 436	561-393	1	+	+		
3/10 100U O		ESCHEDITAL COLL	137.160		_	-	+	1	Ī	
SAL ECOLI	CANTUGUAL SUBUNITO	ESCRUTCHIN	Г	344.271	Γ					
NIO ACTOR	AA HAGINAL SUBUNIT 6	ESCHERICHIA CULT	Т	-		-		_		١
	TO CALL DE D'ANNA	ACVITHOSIPHON PISUNI SYNIDIOTIC BACTERO		t	+	-				
	TO ALL CONTRACTOR	SACULUS SUBTICIS		†			-	-		
	ID CIATERUM	CH ALYDIA TRACHOMATIS	5	1	1	1	-			
	KD CHAPERUMIN	I CHERTHA COLL	57-14		1					
	10 KD CHAPEROPIN	Livery Company 116 Pale In IV II VI	\$6-19				1	1		
	10 KB CHAPERONIN	TAMENOT THE STATE OF THE STATE	23:05							
	16 KD CHAPERONIN	TANK BETTER THE INCANCING	65.92							
24.10	ED CHAPETONIN	MUNICIPAL ISSUED IN THE PARTY OF THE PARTY O	10.99					-		ļ
SALA NICES	TO KED CHAPERONDA	THE LACTHURE BACTERIOR 13:3	141.141					-		
	WIN CHANGE DONN	ACYRTHOSTPHON PISON STMBIOLIC BACICAS	T.	110.110	421.466		L		-	
2		ACTOBACTEDUM TUME! ACIENS	Т	Т						Ĺ
CHAS ACREES &	L. C.	AMOEBA PROTEUS SYNBIOTIC BACTENUM	7		1					
CHIO AND	SED CHARLES	BACKLUS SUBTILIS	┑	8				-	_	
CHAO BACSU	S KD CHAPEKOPIEN	ROBERTIA BURGOON EN		294.362						
CHAS BORLEU IS	ND CHAPEROXIN	DESIGNATION AND PRINT	1117.144)	339-366						
OLIO BRUAL IS	A KD CACABLONIN	PART AND PARTITIONIAE	16:3			1	1	-	-	
STORES OF THE PERSON NAMED IN	O KD CHAPERONIN	COLCAN LONG THE ACHONG TIS	6.31			-				
SHE GATH	O KD CHAPLEONDA	STEAM TON TOWN ON THE	300-327				1		$\frac{1}{4}$	
CHES CORY! IS	6 KB CHAPERONIN	AL STRUMENT APPROPRIATION		137.364 4	455-483		-	1		
See Closs	O K D CHAPEKONDA	TO SECTION AS DESIGNATION OF THE PROPERTY OF T	137.366	417-444						
S C C C C	O K.D. CHAPERONIN	CLUS I KINING FEW MINISTERS	Т	348.318				-		
THE COME	O KED CHAPERONIN	COXILLA BUNCE III	T.	417.466						
THE PARTY AND	SICE CHAPELONIN	PAEMOPPILOS DOCUETO	11.00							
THE LEGISLA	STATE OF THE STATE OF THE PARTY.	LEGIONELLA MICLANEL	Τ	452-479	-					
	OF STATES ON THE	LEGICMELLA PREUMOPHILA	Т	T	113.164		-		_	
	A PA PARONO	MYCOBACTERIDA LEPRAE	Т	T				-		Ц
	STATE OF STA	INTCORACTERUM TUBERCULOSIS & BOYIS	Т							L
DEC MICIO		PSEUDOMONAS AERUGINOSA	Т	7						L
ONO PEAR	O KD CHATEACHE	INSTACH TECHNOSARUM	7	П	73-400			 -	-	L
POSSO BUILV	60 KD CHAPELUMON	IRICKETTSIA TSUTSUGAMUSHI		7	20.38		1		1	
POSS NCTS	IN ICD CHAPTERORIES	EVARIONOCOCCUS SP	104-335	337.380	1		1		+	
PCHES STAB!	SO KD CHAPERONON	CONFORMACY STIRES	338-365	485-419			1	+		1
CAN SHOW	66 KB CHAPEROPIN	PURE WINDOW IC BACTEDIUM PS. 3	337.364				1	1	-	1
PCHO TIEPS	66 KD CHAPERONDA	CHEEPTOACYCES AL BUS G		117.364			+		-	1
	60 KD CHAPELONIN 2	VIRBIO HABVEY	17-12	172.199					-	1
	N.X.DIACETYLCHOOLASE PIECUNON	MACHINISTELIS	_	190-617			1	1	-	1
a	CHEMOTAXOS PROTEIN CHEA	Gentlemonta COLI	136-206							1
DOLLA ECOL	CHEMOTAXIS PROTEIN CHEA	CALLED TO POPULATION	162-197							1
PORT SALTY	CHEMOTADS PROTEDY CHEA	2 - Car 1 12 - C15 - C1	134-151							1
POLES EACEU	CHEMOTAIS PROTED! METHAL TILANSFELASE	BACKLOS SOCIETOS	611.53					$\frac{1}{1}$	$\frac{1}{4}$	1
PCHEW ECOL	PUSING BORDON CHEMOTANDS PROTEIN	TATABLE A TABLE OF THE	1							
POLICY SALTY	PUTENE BINDING CHEMOTAXIS PROTEIN	SALMONETA LITERATURE	22.40							1
POEY ECOL	CHEMOTAXS PROTEIN CIGY	PACKET A POPULLATION	11.49					-	4	1
PORY SALTY	CHEMOTAXIS PROTECT CHEY	SAY SUBSUITE STATE	401.518	166-341				1	\downarrow	1
PCIG: BACCI	DUTONASE ALPR	AL TEROMONAS SP	345-572			1	1	+		1
PORT ALTO	CIGHOLASE A PRECURSOR	COMPATTA MARCE CENS	146-373			-	$\frac{1}{1}$			1

TILL NAME NONID BACK! NONIT SACE NOUT STUL NOUT STUL	PROTEIN CHITIMASE D'RECURSOR	OHGANISM CHIEFTER ALE	HALA LAND	ARIAL LABOA	A.J. AREA	ARIA ARIAS	ARIO 408IA	-1	1	T T
NONID BACK! NONIT SAGE NONIT STIVE.	CHITINASE D PRE		ľ					•		
POST SACEA POST STAL POSAU BACSI		BACILLUS CIACULARS	Т	•	+	1			Ī	
PORTU BACSI	CHUTCHASE	SACCHAROPOLYSPORA ERYTHRAEA	411.24	+	$\frac{1}{1}$					
PCIONU BACSI	CHITINASE & PRECURSOR	STREET CONTRES PLICATOS	17.40							
	CHORSMATE MUTASE		100	<u> </u>	<u> </u> T	1		İ	i	:
OHOD BYEST	CHOLESTEROL DAMASE PRECURSOR		100	+					Ī	
Y ALC	CHOLLEGA ENTEROTOMIN, A CHAIM MELOASOM		T	181.208	1	-				
THAT AGE	THE CREATE PROVED CAN BE FOUND TO	AGROBACTERION TO BE ACIENS	≘	-						
100	PCIAL CHEE CITIOLYSIN PROTEIN		435.441	L						
100	COLICINI RECEPTOR PRECURSOR		[46-17]	-						
MACKE ANDE	PUTATIVE DNA RECONGINASE		178-405	-	L					
AVUV AND	CITEATE SYNTHASS		143.170							
MOSV BACO	CITEATE SYNTHASE	BACILLUS COAGULANS	16.55							
POTEN CALTY	CITEATE-PROTON SYNDOR!	SALMONELLA TYPHIKIURIUM	134.181	-				j		
	CITEATE COULTY EVAPORT	KLEBSIELLA PNEUMONIAI:	194.328							
1412	CITEATE COMING SYMPORT	SALMONELLA BUBLIN	14.331	<u> </u> -		 				
	CITED TRE COOK TO COMPOSE	SALMONE! LA PULLORUNI	184-321				Ĺ			
2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	THE CONTRACTOR IN THE CANADEMASE	PSEUDÓMONAS PUTIDA	5.50							
	WAINT BADTH DETERMINANT PROTEIN	ESCHELOCHIA COL.	113-169	<u> </u> -						
	CHAIN LENGTH DETERMINANT PROTEIN	ESCHERICHIA COLI	136.317 350	130-177						
ACL SALTY	CHAIN LENGTH DETERMINANT PROTEIN	SALMONELLA TYPHINGRUNI	96-127 151	151-212						
PCI OF CLORE	ALPHA-CLOSTRIPAIN PRECURSOR	CLOSTRIDIUM HISTOLYTICUM		197.524						
NO NA POR	ATP-BROOKS SUBUNIT CLPA	ESCHERICHIA COLI	655.695							
PCH A THORI	CLPA HOMOLOG PROTEIN	INHODOPSEUDOMONAS BLASTICA	Г	Γ						
PCL PR BACNO	CL 28 HOMOLOG PROTEIN	SACTERGIDES MODOSUS	116-137 442	642-476 558-505	303					
	1 PR PROTEIN	ESCHENIONA COLI	Г	363-590	L					
	OUT OF A L		Τ	332.350		_				
A POST	A TO ANDING SUBLINIT CLOX		355.382		_					
NOW YEAR	TY CYCLIC NIC		30-77							
MODA COO	YTOSDAE DEAN		103-139							
PCOM! BACSU	COMPETENCE	SACILUS SUBTILIS		186-213						
PCOMO BACS	CHOSTSNCS NA	BACELUS SUBTILIS	154-239							
PCOP6 STAAU	OP & PROTECN	STAPHALDCOCCUS AUREUS	1.33							
ACOPB PARKA	COPPER RESISTA		140-167							
LOOK ECOL	MAGNESILIMICOBALT TRANSPORT PROTEIN CORA	_	134-161							
PCOLA MALTY	AGNESILE MODE	_	134-161	$\frac{1}{1}$	1	1				
PCOTE BACSU	PORE COAT PRO	BACILLUS SUBTILIS	26-25							
PCOXI BRAIA	CYTOCHRONG C OXIDASE POLYPEPTIDE I	BRADYRECOBIUM JAPONICUM	380-407	1						
PCOXI PAIDE	CYTOCHOROME C	PANACOCCUS DENITUBICANS	307-40	1						
PCOXI MOST	I CYTOCHRONG COXIDASE POLYPEPTIDE I	AHODOSACTER SPHAEROIDES	38.423	+						
PCOXX BACF!	OXIDASE ASSEMBLY FACTOR	BACILLUS FIDMUS	9			+				
PCOXX BACS	J OXIDASE ASSENDLY PACTOR	BACILLUS SUBTILIS	7		1	+				
PCPPB NEICO	CRYPTIC PLASAED PROTEIN B	NEISSEUA COMOUNIOEAE	7	602:48		<u> </u>	1			
NOTE ECOL	MANNOSE: 1-PHOSPHATE GUANYLYLTRANSFERASE	ESORETICADA COLI	304-336	+						
PCFSB_SALTY	MANNOSB-I-PHOSPHATE GUANYLYLTRANSFERASE	SALMONELLA TYPKOMUUM	11:33			+				
PCPXA_ECOL	SENSOR PROTESY CPXA	I SOME JULY COLD	192-62	$\frac{1}{1}$	1	1				
PCFXG STR.SC	CYTOCHICAGE PASS 105C1	STILEFTONYCES SP	N-18	$\frac{1}{1}$		1				
KOYU SACEA	LDEOXYEAYTH		233.360	1	1		1			
NO TO THE	U CYTOCHROME PASS 109	BACILLUS SUBTILIS	240-287	-		1				
PCPXXY ANAS	PROBABLE CYTOCHRONE PASS	ANABAENA SP	81-123			1				
PCR37 BACTI	27 KD CRYSTAL PROTEIN	BACILLUS THUMINGIENSIS	137-110	1	1	1				
PCR17 BACTM	27 KD CRYSTAL PROTEIN	BACILLOS THUMORENSIS		+	1		1			
PCK41 BACSH	1 9 KD INSECTICIDAL TOXIN	(BACII LUS SPICAERICUS	376-308	+	+	+	\downarrow	brack		
PCA41 BACSH	II 9 KD INSECTICIDAL TOXIN	RACHEUS STIVERICUS	100.00	+	+	+				
PCR43 BACSH	ALE MAN CHAIR STATE TO COLUMN TO COL	DACTI LIK TOTA CHOISENSIS	Т	252-270 479-461	1	+				
PCR70 BACTO	т	DACT LIST THE BUSINESS	7	1	13					
PCR 70 BACTO	-7	משקורות וווסשווים וויים	1	1	-					}

PEGENE	103217824	Probaryotle Sequentice	VAREA !	AREAJ	SHEAT A	ARIA	177110	OREGE SANKA?	1	1011	2 AXXA
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	16 KD CRYSTAL PROTEIN	BACIT IN THE ENGINE IS	61.133	П	\$3.615			1	T	Ī	
CRTI BACTK	TO KD CRYSTAL PROTEIN	BATH 115 THORNOIENSIS	14-111	П		1		1	1		
CRT2 BACT!	23 KD CRYSTAL PROJEIM	PAPELLIS THEMOTENSIS	161-19		552-593	1		1	Ì	Ī	
CR72 BACTK	TO KD CRYSTAL PROTEIN	BACILLUS THURINGIENSIS		52.57		1	Ī	1	T	Ī	١
PCR77 BACT	11 KD CRYSTAL PROTEIN	FCHERICHIA COLL	103-130			1		T	1	Ī	
CILEC ECOLI	SENSOR PROTEIN CREC	FC-MS RICHIA COM	94-121		1	1		1			
TION GROW	DOCE MEMORANG PROTEIN CRED	ESCHENCHIA COLI &	34.53	2:12					1		
100	CATABOLITS GENE ALITATION	SHIGELLA PLEXMER!	7					Ì	İ		
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PCN SALTY	CATABOUTE GENE ACTIVATOR	KLEBSIELLA AEROGENES			1		T		T		
	STATE SECOND CONTRACTOR	EXWINIA HELBICOLA	231-258		T	T			T		
PCRTI ERWIG	PHYTOENE DENTUROPENASE	RHODOBACTER CAPSULATUS	389-416						Ī		
CATI MOCA	PHYTOENE DEHTUNGENASE	SHODOBACTER CAPSULATUS	133.160	134.361	3				:	;	
CATI MOCA		BACH LINE THE BUILDINGS	721-755	175.0m2	1						
PCAYS BACTA	133 KD CRYSTAL PROTEIN	BACK THE VILLENSIS	736-77	165-192	1053-1050						
CAYS BACTB	PCRYS BACTB 110 KD CRYSTAL PROTEIN	EACH LIFE THE PROJECTS	136-170	190.913							
CAYS BACTE	IN KO CAYSTAL PROTEIN	DAPET CATILITY MODERNS	218-252	121-101	175.R03						
CRYS BACTI	PCRYS BACTI 130 KD CRYSTAL PROTEIN	DA CHILLIPINGIENSIS	137-771	865-892	1053-1080						
CAYS BACTK	IN KD CRYSTAL PROTEIN	DATHERNOIS	736-770	16-061		į	-	:	:		
CAYS BACTS	130 KD CRYSTAL PROTEIN	BACH THE THERMONENES	170-011	16.18.18.12	1051-1000	j	! 		ļ		
CRYT BACTA	130 KD CRYSTAL PROTEIN	STATE THE THE PARTY OF THE PART	145.779	926-66							
CRYT BACTE	134 KD CRYSTAL PROTEIN	SACRETA THE PLANTISENSIS	217.251	334-316	101.728	775-102					
CRYT BACT!	IN KD CRYSTAL PROTEIN	STATE OF STA	111.111	165.892							
PCAYT BACTX	130 KD CRYSTAL PROTEIN	A CONTRACTOR OF THE PROPERTY O	136-770	16:068							
PCRYU BACTA	135 KD CRYSTAL PROTEIN	AND THE PLANT OF THE PARTY OF T	117.251	120.00	101-16						
KAYU MACTI	135 KD CRYSTAL PROTEIN	BACILLOS INDESCRIPE	136.772	866-893	1054-1081						
KERYU BACTK	151 KD CAYSTAL PROTEIN	MACHINE TRIPINACIENSIS	111.111	165.492	1033-1080						
PCRYV BACTA	130 KD CRYSTAL PROTEIN	BACH CUS THURBOCIENSIS	116-151	145-771	10-140						
MAY BACT	INSTRUCTION PROFESSION	BACILLUS THURMGIENSIS	136.770	8							
MAYN BACITA	TO BUILD ON SEAS	SACILLUS THURINGIENSIS	745-778								
MAN BACIA	THE PERSON AT PROPER	BACEL US THURINGIENSIS	401-63e	9			7,07.10				
PORTO BALLIN	PORTO BACATA INDICATION OF PROPERTY	BACILLUS THURINGIENSIS	63:116		3 3						L
A STATE	THE PARTY ENGLISHED PROTEIN	ESCHERICHA COLI	\$								
	THE PAT EVALUATION OF IND PROTEIN	ESCHENICHIA COLI	2				1				L
	THE BAY CONTINUES IS NO PROTEIN	ESCHENICHIA COLI	0.4								L
		HALOBACTERIUM HALOBIUM	*				-				L
		HALOBACTERUDA VOLCANII	2								L
		METHAMOTHERNIUS FERVIOUS	20.00						-		L
		NETHANGTHERANDS SOCIABILIS			1						L
	CALIFICATION SUBUNIT B PRZCURSOR	ESCHENICHIA COU						L			L
A G DA	COA. TRANSFERASE SUBUNIT A	CLOS MUDIUM ACETOBUTYLICUM	14.30		-			L			Ц
XCTS CLON	COA. TRANSPERASE SUBUNIT B	CLOSTNOIUM ACETUBUTA COM						_			
ACTIC NEDGE	BNGSLAGMORANE MOTEUN CITUS	MEISSEALA MENINGHIMIS	11.11	151.52	3	117.251	L				
PCTX PAEAE	CYTOTOXIN PALL	Particular Court	3.3	161.219							_
PCVAL BOOL	כסרוכטי ע גבכת	STORESTON OF I	151.178		L						
PCVAS ECOL	COLICIN V SECR	EACH THE BENEVIS	197.224	=======================================	1010-1044						1
PCWPM BACBA	A SOCIAL CELL WALL PROTEIN PRECURSOR	STATE OF THE PROPERTY OF THE P	178.216	\$60.517	943-948						1
PCWPO BACER	A COUTER CELL WALL PROFESS PARCONSON	PORDETRILLA PERTUSSIS	40.75	633-659	961.96					1	1
PCYAL BOLT	ADDMIATE CY	VERSONA INTERNACOIA	343.387	193.430						\downarrow	1
CYAA YEND	DOMAIL CT	BOADETELLA PERTUSSIS	341-36			_	1	\downarrow	\downarrow	1	\downarrow
7748 007	CAMPAGISTA	BONDETELLA PERTUSSIS	178-212			\downarrow		1	\downarrow		1
	CTAD PROJECT	BOADETELLA PERTUSSIS	 			\downarrow		1	1	1	1
TAL BOOK	TOORDE	RHODOBACTER CAPSULATUS		2		1	\downarrow	1	-	-	
		ESCHENICHIA COLI	2	\$	1	\downarrow	1	-			ļ
		44 0000									

PCGENE	07517464	Proharyotic Sequences	П		П		. 1401			
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PCYNT SYND	ALBONIC AMIYDRASE		300						Ì	
PCYNX ECOL	YNX PROTEIN		3 :		+		-	1	t	T
ACYON ECOL	YTOCHROME O UNIQUINOL OXIDASE SUBUNIT !			+					t	1
PCYPH SYNP?	EPTEDYL-PROLYL CIS-TRANS ISOMERASE		100	1		1	+	1	1	
PCYSA ECOLI	SULFATE PERME				1			\dagger		T
PCYSB ECOL!	CYS REGULDN T		2		+				İ	
PCYSB SALTY	CYS REGULDA	HINTURION	2						İ	Ì
PCYSI ECOLI	ERINE ACETYL TRANSFERASE		164-191		\parallel		†	1		1
PCVSI SALTV	SECTIVE ACETYL TRANSFERASE	HINDUM	16:191	-			-		1	
- ACA BON	CHANGE LYNTHALE		405-432						┆	
	STOCKE STOCKE	HINDRICK	605-432		_					
	THE THE ANGESTS ASSESSED.		2.3	-	_					
STATE OF THE PERSON	IE IMMONIEMOSE SOSOWII I		0,0 10,0	-				ľ	-	
CYSW TOOL	E W PROTEIN				 	T			T	
PCYSW STORY	E W PROTEIN	SYNECHOCOCCUS SP	٦	7			1	t	İ	
DOM ALCO	STEM PROTEIN C2CB		╗	211.120 104.14	-			1		
TISCH ALCOHOL	STEM PROTEIN CZCD		139-169	_			•			
	C PROTEIN S' PRECURSOR	BACULUS SUBTILIS	10-101					1		1
	SALES SEEDING		127-154							_
NOADA ECOLI	D-ANGING ACID DEAT DROVEDANSE	2000	166.00	+		F				
PDACA ALTIKA	PDACA ALTHA MAC-PLINKED D'ALANINE GLYCINE PERMEASE	TOLCARIIS	Ť	91, 91					T	
PANA ECOL	DANCE PROTEIN		1					t		Ī
POAR ECOL!	(ATE SYNTHASE		1						†	
PDAY! BACSU	DHA - PROTEIN-CYSTEINE METHYLTRANSFERASE		3.43	-					1	
	THE PROPERTY OF		12-39				_			
1	CHOCKION	FIREMAN	8.5							
	DAS-BINDING PROJECT NO		141.141						-	
	SECALBOXYLASE PROENZYME	CACHEMICHIA COLI			1	-		1		
POCDA CORGE	NAMINOPINELATE DECARBOXYLASE		194-16					+	İ	
POCOA PERAL	DIAMONOPORELATE DECAMBOXYLASE	RUGINOSA	**						İ	
1001 1004	EUTAKATED		4.31					1		
PROME BOTA	HISTIDDAE DEC	ENTEROBACTER AEROGENES	101-138							
National Property	MATTERNA DECARBOXYLASS		161-111				•			
CALL VILLA	MATERIAL DEC	ANII	10:111							
	ACCOUNTS TO A SECURITY OF A SECURITY OF A DECIMENT OF A DE		188-222	-	_			1		
			105-332		_			ľ		
7	LTSINE DELAUGUAT LASE	VELN COMITAE	L	149.160	l				T	
POOP KIEPY	XALOACETAT	34	T	142.169						
PDCOA SALTY	XALOACETAT		Т		 			t		Ī
PDC08 EALTY C	XALOACETAT		275-469	+				İ	1	T
POCTS THE	TRANSPORT SE	OSAXUM	114/1					1	T	I
POCT BURGE	TRANSPORT SE	ori	П	-				1	1	
Post design	ATP-DEPENDENT MAN HELICASE DEAD			518-545						
POSTA CASA	ATP. DEPENDEN	MONIAE	18 767.192	319-346			_	-		
WENT SCALE	DEDA MOTEON	ESCIENCIA COLI	106-133					_		
117/11	CONTON DECITEDADECS		54 02-16	12.139 120.33	133					
	UNITED AND TARE	MORAXELLASP	114-141	L	-					
100	PECONOMINATE OF THE PERSON OF	FCHERICHOA COLI	- - - - - - -		-					
3	DEUA I ALBUSE	NA SCOOM	15.7						Ī	
PDKAL PSECU	ALDEHTOR DE		,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,			 -		l		
PDHAS BACSU	į		Ţ				1	Ì	T	
PDHAS CONCL	ASPARTATE-SE	CONTINEBACTERUM GLUTNICUM	Т	712-339		1			1	
DOM: SAMON	ASPARTATE SEMINIDERYDE DEHYDROGENASE		22.62			\downarrow	1		1	Ī
PDHAS VIDEN	г	VIBNO CHOLEIAE	309.336						1	
PDSA BACSH	_	BACELUS SPHAERICUS	149-176	_		-				
POLICE RAPES	ALANDOZ DEM	BACELUS STEAKOTHERMOPHILUS	94-131							
NO D SANGE	MAIN SPECIFIC CLUTAMATE DEHYDROGENASE	CLOSTALDIAN DIFFICILE	116-143							
PURET PERAS	S. SPECTF CAL	PEPTOSTREPTOCOCCUS ASACCIIAROL YTICUS	2	345.380	-			İ		
Phre. 10150	CLUTANATE D	SULFOLOBUS SOLFATARICUS			L					
POST CORGE	NADP-SPECIFIC	CORYNERACTERIUM GLUTMICUM	18	952-622						
POLICE ACTION	Ca LICOSE DEHI	ACDRETOBACTER CALCOACETICUS	110-59	190-217				1		
1										

4000000	Probaryolic Sequences	1 7307	ABEA?	ABEAL	AREA	ANEAS	ARTAL	ARIA?	AREAL	SHEA.
		Т	Г							
THE MORTH COME LINE HYDE COCENASE B	KUUM		Ī							
PORCE SALVE GLOCOSE SECONOS CONTRACTOR DE CO			T	İ	!-					
DHO COOL IGLUCUSE DENTITION CONTROL		3	1	İ	Ī					
DIK! STRVN KETOACTI, REDUCIASE!		102:219	1		Ì					
DIEL BACST LEUCINE DEITTORIGENASE							Ī			
PHALO ACINTA DALYSOPINE DEHYDROGENASE		181-181	186-224				1			
POPER KETEX KETHANOL DEHYDAOCENASI SUBUNIT I PRE-	THE PARTY OF THE PROPERTY OF THE UNIT	133.187	190-124							
PORTI VETOR METHANOL DESTYDROGENASE SUBUNIT I PREL	A CONTRACTOR PROPERTY AND	195.222								
HANNI BABRE INFTHANCE DEHYDROGENASE SUBUNIT I PREC	Ī	314.314								
COLUMN TO THE TOTAL THE										
TRUM BACK TAND BELLENGEN AND				Ì	Ī					
POPON ECOL INADA DENT DE COLORADE		73-167	406-433							L
PERCENT BACSULHOMOSERINE DEMYDROCENASE	A STATE OF THE STATE OF THE PARTY OF THE PAR	108-132								1
AND AND TARGET HOMOSERING DEHYDROGENASE	CONTRIBATION	91.5								
STATE OF THE STATE OF A SANDE DELIVERANCE NAME OF THE OWNER OWNER OF THE OWNER OWNE	BACILLUS SPHAEMCUS									
DATE LACOR PRESENTED STREET STREET STREET	_	482.312			Ī					
PDHSA ECOLI SUCC DEHYDROLOGENASE FLATOPAGE	т	=======================================	130-16							
	Ť	133.160								1
THE PARTY SALL SUBURIT	_									
PURIS STRUCTURE AND PRINCIPALSE	METHYLOTROPHUS METHYLOPHILUS									
PORTING TIME IN COMPANIES OF THE PARTY OF TH	FECHELICHIA COLI	384-611								L
PONG ECOLI IPROBABLE ATP-DEPENDENT RELICASE MINO	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	54-83	14.14].		1
PRIVE BACSU DIVISION INTTATION PROTEIN		93.120								1
THE REPORT INHAMENT POSICIONE DEPTOROGENASE	PSEUDOMORAS PUTEDA		354.334					-		
1000	AZOTOBACTER VINELANDII							L		
POLINE AZOVI SERVINE WENT SPACE TO SELECT SERVINE SELECT S	BACH 1115 STEARDTHEAMOPHILUS	12-124								L
LIPOALHIDE DEPO	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	13.109								
POLYMOR DEAD	BALLETO'S BOTH INTO	5								1
THE THE TRICKING OF THE LAND DE LANDROCENASE	ESCHENORY COLI		111					عا		_
POUR ELUI DONI DE CASA DE COMPONINCE	PSEUDOWONAS PLUORESCENS		95.55							L
DUNTOKOLLOW	BERTHOLDANA & PUTIDA	3 8							ļ	L
POLON PSEPU MENOL HYDROXYLASE PI PROTEIN	735000000000000000000000000000000000000	447.524	188.805							1
PESAL BAPELL IBNAK PROTEIN	BACULUS SUBTINIS	456.483								1
POULS BAPELL INVAR PROTEIN	DACTILUS SUBTILUS	14.186								
PLANCE CONTROL & SECTION	SACILLUS SUBTILIS		366	141.183	436.463			_		
POWA SALED LONG FROM	BORDELLA BUNGDON'ERU			91.13						
PONAA BUMBO IDAAN PROTEST	BUCIOCITA APRIDICOLA	3								L
PONAA BUCAP DINAA PROJECT	IF SCHERICHIA COLI	166-400								L
PDNAA ECOLI DNAA PROTEIN	TOWNS CONTROL LITTER US	38712								1
PONAA MICLU DNAA PROTEIN	100 100 100 100 100 100 100 100 100 100	3.	15.112	274.310	350-389					ļ
TOWAR LANCE A DRIVE PROTEIN	MICOLANDACA	201			L			_		-
SECTION AND PROPERTY	PROTEUS MIKABILIS	917.005				L			_	
POWA FROM CONTRACTOR	PSEUDOMONAS PUTIDA						-	L	L	
POWAL PSETU DRIVA PROJECT	SPUROPLASMA CITTU	43.72	2	2					-	L
PONAA SPICI DWAA PROTEIM	CHI AMONDIA TRACHOMATIS	312-353								-
PONAB CHLTR DNAB-LIKE PROTEIN	SCOUNTING COLU	13.109								1
PHYAN ECOLI IDNAS PROTEDI		13.100				_				4
PONAS AATTY DAME PROTEIN	SALMONELLA I TERRITORIOM	97.77	L							
THAT PART DAY PROTEIN	ESCHENCIAA COLI	753	187.45			L	L	L	_	
THE PROPERTY	BACK LUS MEGATERUM							L	L	
POWAK BALME DIVANTA TO THE	BORNELLA BURGDON'EN	15.3								L
	BRUCELLA DVIS	248-275	\$12.546					1	ļ	ļ
PONAX BALLOV IDNAK PROTELIN	CALIS CRESCENTUS	101-195								4
POWAK CAUCH DNAK PROTEIN	P. DEST THE ACT TO RESTORE THE LICENSE	499-526	L						1	1
PINALY CHOAB DIVAK PROTECN	CLUSIA MACENTAL CONTRACTOR	404.423			L	_				4
SHALK PLANK PROTEDY	CLOSTRUIUM PER PUMPENS	93				L	L			_
PROTECT CHANGE PROTECT	METHANOSARCINA MAZEI	2								L
PURAN PER PROPERTY AND PERSON AND	MYCOBACTENINA TUBERCULOSIS	\$ 25.7%						-	-	L
PONAK MICIOLOGIA PROTECT	STREPTOMYCES COELICOLOR	?			1	1	ļ	-	-	-
PONAK STREE DRAW PAULEN	ESCHENCIAL COLI	114-14				1		\downarrow	1	+
PONTR ECOLI MEGULATORY PROTECTIONS	ZYMOMONAS MOBILIS	651.712			\downarrow			1	1	1
POKI ZYMONO DNA LIGASE	•	14-51						1	+	1
PONIL STIPE TRANSOUCTION PROTEIN UNIC	-to	- 3 - 3	L					4	-	+
POOCK SULSO PROBABLE SIGNAL RECOGNITION PARTICLE PROT		2	417.444	1382-1416	9				4	4
POPJA BACSU DNA POLYMERASE III, ALPHA CHAIM	+	11.10	L					4	4	+
POPTA ECOLI DNA POLYMENASE IIL ALPHA CHAIN	-	230-257		-	L	L		_	4	-
POPTA SAFER DRA POLYMERASE III, ALPHA CHAIN	SACCHARUPULTSPURA EN LITTOREA								ĺ	İ

CCENT	107817310			Т		7 7 3 9 7	7.101	ABFA 6 JAMFA?		7.2	
THE MANE	PROTEIN	CALLONGITA TVENILLIBILA	4 z	0	1	Т	т			Т	
DESK BALLY	DIA POLYMENASE III	BACILLIS SUBTILIS	212.239								
CAN BALSO	DIA MI VISEA	BORRELIA BURGDONFER!	(16-3)	İ							
POPUS BUCAP	INA POLYMERASE	BUCHWELL APPRIDICOLA	31.62	301-350							ĺ
DINB MICEU	DNA POLYNERASE	MICROCOCCUS LUTEUS	1101-210								
POPJB MYCCA	DNA POLYNGRASE	MYCOPLASMA CAPRICOLUÑI	5					Ì			
DATE PREPU	DNA POLYMERASE	PSEUDOMONAS PUTIDA	9	T			1		Ť	T	
PDP18 SPICE	DNA POLYNGRASI	SPIROPLASMA CITRI	78-112	R.			Ī	T			
DPIX BACSU	DNA POLYMERASE	BACILLUS SUBTILIS	212-112		Ì		T				
PDPC2 ECOU	DNA HUMASE TRAC-1	ESCHELICHIA COLL		Ī	Ī			Î	Ī		
DACE ECOLI	DNA PRDÁSE TRACA	ESCHEDICHIA COLI	2 . 5			Ì	Ī	1	T	Ī	
HUTTE STATE	DPMD PROTEIN	STREPTOCOCCUS PNEUMONIAL					1	T	1		
DIOI BACCA	DNA POLYXERASE (BACILL US CALDOTENAX	201-202	Т	Т			Ī	1		
POPOL STRUM	DNA POLYACIASE I	STREPTOCOCCUS PNEUNIONIAE	100	П		22.0			Ī		
POPOL THEAQ	DNA POLYMERASE	THE LANDS AQUATICUS	22	201.024				1			
DOI THEFT	DNA POLYMERASE	INCINUS AUDA IL US	70 47	Ì					Ī	Ī	
POPOZ ECOL		ESCHEROCIIA COLI	144.		I			Ī	ľ		
200	DNA POL TALENASE	STANDARDS COURT AND STANDARDS	170-404	Т	625.650	747.774			Ī		
200.50	DINA PULTMENASC	TAR BLOCKETIS LITTRALIS	200	581.188	Т	TΞ	1153-1194				
2		1 AFTOCOCCUS 1 AFTIS	716.753	Т							
	DOESTIMATE TO ASSET T	LACTOCOCCUS LACTIS	116-753					ſ			
מיניים ביינים	DOESTIMATE TEXT TO SECURITION DESCRIPTION DESCRIPTION	REC'HE BLOKEN COLL	3								
Ore Church	SEC YOUR DOWN I'V	STREPTOCOCCUS EQUISIMILIS	3.60	291-316							
1000	AINMINICIPAL	STREPTOMYCES PEÙCETIUS	166-313								
DVA MAA	DENTOROFOLATE	STAPHYLOCOCCUS AUREUS	63-10								
ELIB BACCI	OLUCAN ENDO-1	BACILLUS CIRCULANS	134-161		150-020		П				
PEAR ECOLI	ATTACHENO AND	ESCHENICHIA COLI	99-100	188-185	\$25-525	681-725	102-136	20.00			
PERGR ECOL!	EBG OPERON NEPRESSOR PROTEIN	ESCHERÁCHIA COLI	131-13								
EBR STANU	ETHEROUN BROW	STAPHYLOCOCCUS AUREUS	61-91								
SCIENT PROCE	ENOYL-COA HYT	EMODERACIES CAPOLATOS	447.777								
000	OKAPEKONE PROTEIN ECPD PRECURSOR	ISVACATOR VIOLETTE				Ī					
TAY THE	BETTER LAND CELL	STAPHYL DOOCCUS AUREUS	2.3	119.146							
PERSONAL PROPERTY.	PLONGATION PAC	DESULPUROCOCCUS MOBILIS	427-461								
THE PERSON	•	HALOBACTERUM HALOBIUM	166-213								
PET METVA	ELONGATION FACTOR 1	METHANOCOCCUS VANNIELII	409-436								
PET SULAC	ELONGATION FACTOR 2	SULFOLOBUS ACIDOCAL DAKIUS	3	45.180							
EF1 THEAC	ELONGATION FACTOR 2	TREMONIASMA ACIDOPHILUM									
EFO ANAM	ELONGATION FACTOR O	ANACTORIS MEMOLANS	14.36					T	T		
70.0		AVOCALCISE IN THE PRAF	1	316.157							
		SALMONELLA TYPHDAURUM	116-261								
EST LYON		SPIRULINA PLATENSIS	114.174	115:11							
PEFO SYNTS	ELDNOATION FACTOR O	SYNECHOCYSTIS SP	7								
WITH STUDY	-	STREPTONIYCES RANOCISSINIUS	221-258								
PETT STUCK	-	STREPTOMYCES ALMOCISSIMUS	221-258								
PETTY STRUM	ELONDATION FAC	STREPTOMYCES AAMOCISSINIUS									
PETTS ECOLI	ELONGATION FAC	ESOEMORA COLI									
7575 STG	ELONGATION FA	PARTICIPATION CLINE		336.354							
PETT MOR	ELONGATION FACTOR TO	PACIFICIAL US SUBTILIS		230-237		I	Ī	I			
DOME OF THE PARTY	TELONOATION SACTOR TIL	BURKHOLDERIA CEPACIA	36.53								
	FI DWGATION FACTOR TU	CHLAMPELA TRACHOMATIS	218.245								
SEAL DESCRIPTION	EL BNOATION FACTOR TU	DEDIONEMA SP	130-251								
	ELOHGA HON FACTOR TU	FLEXISTIPES SINUSARABICI	111-141								
		the Creation of the Court of th									

47.4	1026130.4	Proharystic Sequences	1400	AREAZ	AREAS	AREAS	AREAS	AREAS	1	1	
_	NI LI COG	ORGANISM	Г	Т					j	1	ł
TO THE PERSON NAMED IN	EL ONDATION FACTOR TO	MICROCOCCUS LUTEUS	***								
	7 V 1014 V 1010	MYCOPLASMA HOMINIS			į	:	:				
2	DRUALICATAC	MYCOHACTERNIM I I PRAI	20.00						_		
PEFTU MYCLE	DACIA FILM PACE	ANY COMPANION TURNER ULTONIS	120-247					Ì	Ì	Ì	١
TU MYCTU	LONGATION PAC	CHEWANELLA PUTREFACIUNS	3.5					1	T		Ì
	ELONGATION FACTOR 10	THE PTOCOCCUS ORALIS	133-359				Ī	T	Ī		
	ELONGATION FACTOR TO	PERIDOMONAS ARRUGINOSA	141-169				Ţ		1		
	PSEUDOL YSIN PIECUROUS		20.10	;	:						
	T-LABOLE ENTEROTOXIN A CHAIN PICCOASON	SECTION COLUMN C	7.18								
	7-LABILE ENTEROTOXIN A CITAIN PRICCURSON	THE PROPERTY OF THE PROPERTY O	223 36V				1	Ì		Ī	
_	1-LABILE ENTEROTOXIN B CITAIN PRECURSOR	CCOSTROLOGICAL COLOR	154-188								
	ENTEROBACTIN SY	EXCREMENTAL COLOR	14.41								
	ENVAL PROTED	SALMONELLA I TPRIMIUMUM	,	100	20.13	387-421	447.889				
	THE WASTERNAME ASSOCIATED PROTEIN	STAPPINLOCOCCUS EMBERCHIDIS	2								
2	THE PERSON OF TH	STAPHYLOCOCCUS EPIDERAIIDIS	11.40						ŀ	:	
PEPIC STAEP			7.58	197.174	į	1		1	i	•	:
	SERINE PROTEASE ENP PRECURSON		70.105								١
	INVESTMETICAL 16 P KD PROTEIN IN EPIA SAFUIUM		201								
PEDIZ HAEP	HYPOTHETICAL PROTEIN IN EMA S'REGION	MANAGERICA	2								
	GTP-BINDONG EAA PROTEIN	ESCREPTION	100.341								
1000	CENTORY THANSDUCTION PROTEIN ERYCI	SACCHARDPOLYSPONA ERTTINACA		2							
	ENVIRONMENTERASE TYPE	ESCHERUCHIA COLI		100	17.11.44						
	The second line	SACCHAROPOLYSPORA ERYTHRAEA	2								
PLAYS SACEA	EXTINGUISM.	STREPTOMYCES SCABIES	2								
STA STRSC	ESTELASE MALUA	PERITOGRAPHAS FLUORESCENS	162-119								
PESTE PSEAL	ANTESTERASE	BEANING OCOCCUS AUREUS	76-119	135.206							
ᆫ	ENTEROTOXEN TY	10 M.	76-117	155-206	L						
TO STAND	ENTEROTOXON TITE C.2 PRECURSOR	SIAMILLOCOCOS ACRECO	36.113	1155.206		L		-			
THE PERSON NAMED IN	ENTEROTORY TY	STAPHYLOCOCCUS AUREUS	1	164.102							
	TI VOXOLUTI	STAMMY OCOCCUS AUREUS									
	THE OF THE PARTY	CLOSTIUDIUM PENFILINGENS	207								
	SUPERIOR IN	STAPHYLOCOCCUS AUREUS	2								L
	TOTAL POPULATION IN	STAPRYLOCOCCUS AUREUS	3								
	VICEOTORN TV	STAHMIOCOCCUS AUREUS	A 0 - 0 7								L
TELES SING	THE PARTY AND IN	SALMONELLA TYPHIMIURIUM	2								
	DINA THUS TO ANY	ESCHENICHIA COLI		,	17	137, 101	130.916				
N. W.	CAN STATE	ESCHENICHIA COLI	2	7							
TACK TOTAL		ESCHERICHTA COLI	226-23)				1				
	AUGUST AND THE	ESCHENICHIA COLI	80-107								
	OPPLIES IN	NUMBER OF THE PARTY OF THE PART	180-207				1				
EXOA MONE	UCCUMOLI CON	STREPTOCOCCUS PHEUMONIAE	ž		\downarrow						L
EXOA STRUT	ACCES A PARTY	PARZOBIUM MELELOTI	236-270	27.16				ļ			L
EXOL NO.	EXOP PROTEIN	THIS COULT MELLIOTI	252-279								
PEXON DODG	UCCBOOK YCAN	RHIZOSIUM MELILOTI	211.242	173-299	356.391						1
	UCC DOCK TON	ECHERICHIA COLI	36-63	7.0							ļ
TADS ECOLI	ATTY OXIDATIO	E CONTRACTOR A COLI	120.247								1
HALL ECOL	ATTY ACED TRA	FECHERICAL COLL	133-359	421-453	501-541						
HAZD ECOLI	OUTER MENDIAME MUTELIN FALL PRESCUENCE	RECUESIONA COLI	\$ <u>7</u>	L				_			1
TAEF ECOLI	KIS MONOR FOR	ESCUEBICITA COLI	160.194	36433	396-623	730-757		_			
FAND ECOL	AND PROTEIN	Berties Cut A CO. I	23-58		L						1
PFANG ECOLI		ECHEDICHTA COLI	20.50								1
PFANG ECOL	FAMO PROTEIN	ECCIPATION COLL	1								1
PEANN ECOL	П	PEET TOWN AS PRACE	<u> </u>	263-322							1
PFAOS PEUR	FATTY OXEDATIO	WOLDNETT A SUCCINOGENES	2.2								1
PEDITO WOLSE	51	ESCHENICHÍA COLL	613-640				1				1
1001	FORMATE DESTI	PSEUDÓMONAS SP	49-76	364-393		-	-	1			1
POH PSESA	FORMA IE DENT	ESCHENCIBA COLI	306-315	<u> </u>	2	1	-		1		ļ
100 E00	-	ESCHENCHIA COLI	3	\rfloor		1	1	1	ļ		L
2	TANASION IN	ESCHENICHTA COLI	202	\downarrow	1	1	+		1		ļ

PCCENT	107217814	Probacyotic Sequentes				4	40744	AUVA 6 SARFA 3	-	• VARV	AREA 9
FILE NAME	MITTONA	ORGANISM STANSSOCIAL ASSESSES	┰		Т	Т			ī		
PEND STAND	CSSIBLE PROTE	STATE COLOUR ACKEDS			T						
PER SYN	PERKEDOXINAMADI REDUCTASE SERVEDOXINAMADI REDUCTASE SERVEDOXINAMADI REDUCTASE SERVEDOXINAMADI SERVEDOXINAMADI SERVESTOS CONTRACTOS C	ECUSSICHIA COLL	136.20					-			
B	FARIC ENTEROR	ESCHERICHIA COLI	Г	201-108							
THE PLANT	BANC ENICACED TRANSPORT PROTEIN FER	ESCHENCHIA COU	23:133								
	SOUT NAVAGE EN	ANABAENA SP	3.29								
PERSON ANARE	TREE PROTEIN IN IN ILEGION	ANABAENA SP '1	61.Pt								
TARVE BURNE	H AVENTOUS HEMACOLLITINON	BORDETELLA PERTUSSIS	1120-1150	1120-1130 1359-1386	2063-2114	2041-2868 3	3051-3085	167.28	Ì		
PHAN PARTY	HAEMOLYSPALIKE PROTEIN FHAC PRECURSOR	BORDETELLA PERTUSSIS	342-369				<u> </u>	1			
PANA A NISA	ORMATE HYDE	ESCHERICHIA COLI	16-63	350-384	401-428						
1000	A STANDARD IN	ESCHENICHIA COLI	438-485								
1 XX 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	NOTION THE	ESCHÉNICHIA COLI	127-254								
	WIND VENDENCE DECEPTOR	ESCHERUCHIA COL.	317-610								
THE ELOCI	COLEMBRATION MALES TON	SPIROPI ASMA CITIU	161-195	136.367							
	THE CLASS AND A SINK BOOKEIN SIC	ESCHERICHA COLI	131-13								
יייי בייי	CELL TILAMENTA FION BROTEIN FIC	SALMONFILA TYPIRMURIUM	131.13								
١.	A HER LIEUTEN AND BEATERN BILLY BERTINGS	ROADETELLA PERTUSSIS	30.33	140-367	618-645						į
TO BOOK	COLOR MEMBRANE TABLES THE THE COLOR	ECCHERICHIA COLI	31.3	T							
	HATERONE TRO	ESCHERICHIA COLI	33.33	\$17.15	34.561	261.590					
		ESCHERICHIA COLI	165-192								
A	UIGA STIERNIJ	SAL MONELLA TYPISMURIUM	49-76								
	TIMBIAL Y PRO	ESCHERICHIA COLI	43.69	162-192	196-230						
	BRIGHT V PROTEIN	SALMONELLA TYPHINIURIUM	175.209								
	SPACE DESTRUCTION	ESCHERICHIA COLI	145-172								
	7051044 4615	NCKETTSIA NCKETTSII	162-189								
200	KIND BEOTEDA	AZONHIZOBIUM CAULINODANS	129-136								
TIAL ACUS	CALCAS BEAGES INC.	AZORHIZORIUM CAULINODANS	247-274								
V 100 V 100 V	ENEOR PROTEIN	BRADYTHIZOBIUM JAPONICUM	37.54	253.380							
	110000000000000000000000000000000000000	ROBERTIA BURGDORFERI	10.0	171.398							
	PLACELLAS PLACEMENT AT NO COME PROPERTY OF THE PARTY OF T	HALOBACTERIUM MALODIUM	63.92	137.184							
1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	TO COLUMN AS THE CONSTRUCTION AS THE CONSTRUCT	METHANOCOCCUS VOLTAE	38.73	03):160							
	ACCOUNT OF THE COMPANY	METHANOCOCCUS VOLTAE	3								
	THE ACTUAL OF A COLUMN TO THE CONSORT	HALOBACTERUM HALOBIUM	3								
	TO TO THE PROPERTY OF THE PARTY	METHANOCOCCUS VOLTAE	15.16								
	er Acer 1 No beaching con	HALOBACTEMUM KALOBIUM	36.90	157.184							
	SPI A4 DATUA TELACELENCES PRECINCOS	HALOSACTENUM HALOBIUM	16-63	184:181							
	BI A LICEUS 23 0KD PROTEIN	BACILLUS SUBTILIS	33:149	133 186							
PELAN CANCO	FLAGELLINA	CANDY COBACTER COLI	13-41	164.191	497-535						
PRIAN CALIF		CAMPYLOBACTER JEJUNI	220-266	310-337	20.28			1			
A VETTO	PETAN LATTO IN ACEL IN A PRECORSOR	METHANOCOCCUS VOLTAE	29-62								
PRIAN PERAN	FACELLIN	PSEUDÓMONAS AERUGINOSA	141	11-16	97.124						
PILAA NUDAR	FLAGELLIN	NHIZOBIUM MELILOTI	111.219	221-265	360-391						
PILAS SPINU	PLACELLAR PRANCHT PROTEIN PRECURSOR	SPINOCHAETA AURANTIA	162-119								
PILAL TREPY	LAGELLANTIL	TREPONEMA HYODYSENTENAE	23.40	219-285			1	1			
PFLAA TREPA	FLAGELLAR FILANDAT OUTER LAYER PROTEIN	TREPONEMA PALLIDUM	20.23					1			
PILAS CAUCO	I PLACELLIN B	CANDYLOBACTER COLL	44-19	2	,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,						\downarrow
PFLAB CANGE	FLAGELLINS	CAMPYLOBACTER JETUNI	95.0 0.0 0.0 0.0 0.0	16.01	8						
PFLAB NUMB	FLACELLIN	NULTOBRIM MELLICITI		27.6	2	200					
PLAV GOLD	NIX OCCON YT	CLOSTRUCKINA MP	2								
FLAY CALC	REGULATORY PROTEDY FLAY	CAULOBACTER CRESCENTUS	<u>=</u>	<u> </u>							
PILA BACSU	LAGELLIN	BACELUS SUBTELIS	103:139	38-33							╛
PFLOG BACSU		BACELUS SUBTELIS	63.19								
PFLOK SALTY	FLAGELLAN HO	SALMONELLA TYPHUMURUM	13-10	133.360	436-540		\int				
PFLOL ECOLI		ESCHENCION COLI	\$:- i	239-766							
PICAL SALTY	FLAGELLAR HO		6	87.47							
TOS OTIA		SECURIODIA COLI	91,313	\downarrow					Ī		1
PFLIA PSEAE	FLAGELLAR OPERON RWA POL SIGMA FACTOR		178-625]				

l	100-100-1	tle Sequences	1054 1	AREA 2		AREAS	ARIA			Į	
PCGEAL.	MILLIAN		Г	Г	Г						
	SI ACSULIN			Г	26.50		П				
3	FI JOST IN	Sinis	Ī	Γ	Г	232-359	272-299	176-401			
	PI ACET IN				711-76						
	EL AZELT IN	SALMONELLA PALATYPHI-A	T	Γ	81-92						
	III ACELL IN		T	Ī	136.200						
	H ACELLIN	SALMONELLA TYPHINURIUM		Ī	ı	Т	137-164	115.211			
	21 7 CHI 10 CHI 1	SERVATIA WARCESCENS	1	Ŀ	Ļ	Т	311				
	HI CASES AND ARCOCIATED PROTEIN 2		T	Т	1	107-431					
8	TAGELLAN THOMAS ASSOCIATED PROTEIN 2	ממא	J	Т	Т						
1	FLACELLAR ROCK-ASSOCIATION STATE	PACILLUS SUBTILIS	₹		T						
BACSU	FLAC HOOK-BASAL BOOT PROTECTION	BAERLUS SUBTILIS	_	٦							L
PRED BACSU	PLACELLAR M-RD40 PROTEIN	PAIR DRACTER CRESCENTUS		387.124	2						
CAUCA	FLACELLAR M-RING PROTEIN	EAT MONELLA TYPHIMURIUM	484-529								L
SALTY	PLACELLAR M-MUNG PROTEIR	18 A P. 18 18 18 18 18	33-62								
	FLAGELLAR SWITCH PROTEIN FLIU	BECKE BOHA COL	44.3	ļ		;	:				
mooa onse	FLACELLAR SWITCH PROTEIN PLIU	In Add the familiant of	19.46	105-132							1
	PRODABLE FLIII PROTEIN		=								
ı	FLAGELLAR FLIJ PROTEIN	BACILLUS SUBTILLS	1					•	:	:	!
TALES IN SECTION	FLAGELLAR FLU PROTEIN	SALMONELLA I TPRIMIONION	2	E]
	PROUADLE FLIK PROTEIN	UACILLUS SOUTHERS	1	50	109-136	L					1
	FLIL PROTEIN	BACILLUS SUBTILIS	200							1	ļ
1001	FLH MOTEIN	ESCHEDICHIA COLI	E								
	STIT PROTEIN	SALMONELLA TYPHIMURIUM									
- 6	The same of the sa	BACILLUS SUBTICLIS							L		
PFLDA BACSU	TOTAL STREET	ESCHENICHIA COLI							_		
PILDA ECOL	PLIM PROTECT	CAULOBACTER CRESCENTUS									
	1010 11 100	ESCHENICHIA COUI		72							
		SALMONELLA TYPHIMURIUM					L			L	L
1	ELVER A PROTE	PSEUDOMOKAS AERUGINOSA					L	L			
	TYPE I SILDREAL	ESCHENCINA COLI									
	TYPE, I FOORBLA	ESCRENCIA COLI		60.130	417.446			Ľ			
	GRAMMAL KUBUN	ACTINOMYCES VISCUSUS						L	L		
	TEN-MELLY PROTECN 9479 PRECURSOR	ESCHERICHIA COLI					L				
	PENDENTAL PROTEIN PRECURSOR	BACTEROIDES NODOSUS			\downarrow			L			
	ENGINE PROTEIN PRECURSOR	BACTEROIDES NODOSUS									
	SEAST BACKED SHARBIAL PROTEIN PRECURSOR	BACTEROIDES NODOSUS					_		_		
	TENAMINAL PROTECUTION PRECUTSOR	BACTEROIDES MODOSUS	5				L	L		Ц	
	PROTEIN PROTEIN PRECURSOR	BACTEROIDES NODOSUS	2				L		L		
	THE PROPERTY PRECURSOR	SACTE LOWES NODOSUS			1	1			L		L
	PERSONAL PROPERTY PRECINISOR	BACTERGIDES NODOSUS				-	1	-			
	THE WASTE DE CHEST BY SECTION OF THE CHEST BY SECTION	BACTEROIDES NODOSUS					1	-	-	L	L
	PROPERTY BEATEN PRICINGOL	BACTERODES NODOSUS	2			1	-				L
	PROPERTY PROTEIN PRECURSOR	PSEUDOMONAS AERUGINOSA			1	-		-			L
STATE OF THE PARTY	CHASE IN PROPERTY ASSEMBLY PROTEDY FOW	BACTEROIDES NODOSUS	3		\downarrow	-	L	L		L	H
THE BACK	CHOSTEL E PROBLAL ASSEMBLY PROTEIN FORD	BACTEROIDES MODOSUS	3				-	L	L		
	17100000	ESCHENCIAL COLI	27.176	 -		-	ļ	-	-	L	L
	FINANCIAL PROTECTION PRECURSOR	NEISSERIA WENTHGITDIS	ě		1	\downarrow	1	-	-	<u> </u>	L
N N	S PORTAL PROTEIN PRICINGS	NEISSENLA CONORUMOEAE	66-91		-		1	-	1		L
8	MBALAL PAC	MORAXELLA NONLIQUEFACIENS	<u>\$</u>		1		-	1	-	-	ļ
PENDA MONCH	THE PERSON NAMED IN	PSEUDOMONAS AERUGINOSA	ě	2	1		1	-	ļ	-	ŀ
PEND PRANE	THE COURT PROTECTIONS OF	PSEUDOMONAS AERUGINOSA	į		1	1		-	-	ļ	-
	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	ESCHENICHIA COLI	3		1		-	-			L
	NATIONAL PARTY	ESCHEUCHIA COLI	60.0		1	+	-	-	-	-	L
200	LA KOLE FORBEL	HAEMOTHELUS INTLUENZAE	20.20	716.881	138	137.17	517.555	652.686	711.756		
1	FIRE ONE CTON-	STAPHYLOCOCCUS AUREUS		+		Ţ	Т	Т	L		
TODE JUNE	OLY POLYGE	ESCHENCIDA COLI	136.14	-	-						+
ACC LACEA	OLYLPOLYGI	LACTOBACILLUS LASE!		 		-	-	L		-	
				•	-	_					

PCGENE		Proharyotk Sequences			11		П		П		
THENDE	CILENAME PROTEIN	ORCANISM SCHEDIONIA ON 1	1	V	T T T	1	2	TOTAL PART	Т	4	1
TO TOWN ACT	A PLANCED TEN SUBURIT	S:N:CON	T	21.314	Ī	ĺ	İ	Ī	Ī	-	i
PFRZE MYXXA	EGINATORY PROTEIN		_	471.505		Ī	T				
PITHS CLOTH	PROFOLATE LIGASE		061-691								
PFTR METTH	125	AN THERMOAUTOTROPHICU	14.0								
PITSA BACSU	INFTSA		Т				1	Ī		1	Ī
THE PERSON	IN FISA	ESCRETCHIA COM			T		T	T	T	\dagger	T
11000	127.17		8			Ì	T	T		T	Ī
				T	T	T	T		Ī	T	
	EDIEM STOR	PSCHEDICHIA COLL	331.105			T		T		T	T
	NOTE DE LES	CORRICHIA COLI	230-260								T
1003	IN ACTIVATOR	ESCHERICHIA COLI	7			Ī	Ī	Ī		T	
	IDAABATE HYDRATASE CLASS I AEROBIC	PRERMOPHILUS	290.317	Ī	Ī		T	Ī		T	
PELINGE BACKET	Т		\$ 1				İ			j.	Ī
PELIE YERM	Т		2	:	:			:	<u>:</u>		
DO I BOOK	۲		302.339			İ		ľ			Ī
POINT ANAVA	Т	BILIS	17-114			Ī	İ			T	
PGJP3 ANAVA	Т	ANABAENA VANIABILIS	162-139				Ī	Γ		l	
FOR ECO.	T		206-324	ĺ			T				
POLP BACKE	POIP BACKE GLYC 1-HOS DEHYDROGENASE	RIOM	Г	175-565	ĺ	ĺ	İ				
POJP DACSU	Т		49.76		Ī						
PGIP PYRWO	Г		259-216								
POJP THEXA	Г		Г							-	
POAPB BACST	П	THERMOPHILUS		241-268							
DOSE OFFOR			301-321								
POSPD ZYDDAO			165-192								
MACA PSEFL	┪		78-203							1	T
MALI SALTY	┰		Т	-		1	1	1	1	1	Ī
100 CTVC	UAL-1-THUS URLUTE TE TANNSFERAND	TACHORACHI IS NO VETICIN		467467			İ	Ī			T
1	CALACTORS OFFICE BEFORESCOR		2	T		Ī	T	Ī		İ	
POALL HAED	GALACTOSE OFERON REPRESSOR		113.209	Ī			T	Ī		T	
POAL PSEFL		\$	281.278			İ	Ī				
NOCHO ECOLI	OTP CYCLOHYDROLASE (I		П								
PCCRG PHOLE	OTP CYCLOHYDIOLASE II	LEIOGNATH		146-27]							
POCSH ECOLI	GLYCINE CLEAVAGE SYSTEM HPROTEIN		10-01								
TOOL SOOL	GLYCOVE DEHYDROGENASE		216-246	Ì		İ	İ		1	1	
No.	GLYCINE CLEAVAGE STREM INCORNELIVATOR	ESCHEMICHA COLI	K 5			T	T	1		1	T
1000	SECTION DESCRIPTION DESCRIPTION		T	113.316	140.184	Ī		brack		\dagger	Ī
POEN BACSU	ATION PROTECN III PRECURSOR		_	ı		Ì		Ī	Ī	T	T
PGENE_BACSU	PROTEIN GERE		9							T	
POGES STANK	ANTIBACTERIAL PROTEIN?		6-33							-	
PGGD STANA	ANTIBACTERIAL PROTEIN 3	HAEMOLYTICUS	6-33							-	
PGIDA BACSU	GLUCOSE INCESTED DIVISION PROTEIN A	8	196-423								
PODA ECOLI			233.568	1							
PGIDA PSEPU	TED DIVISION PROTEIN A	PA	319.566	1	1	1					
NGDB BACSU	GLUCOSE INGESTED DIVISION PROTEIN B	BACTLUS SUBTILIS	197	T	1		1	T	1	†	T
PCIDB PSEND	GLUCOSE DIMIBITED DIVISION PROTEIN B			T	Ī	1	1	1	1	†	Ì
PGLCP SYNY3	GLUCOSE TRANSPORT PROTEIN	ASSESSION IN	2002	Ī		Ī	1	Ī	1	†	T
TOTAL BACS	OF THE COURT CONTINUES		356.381	Ī	1	1	1	1	1	\dagger	1
1000	GLICOSE, PHOSPHATE ADENYLYLTIANSFERASE			Ī	Ī	T	T	1		1	T
TO SELT	GLUCOSE I PHOSPHATE ADENYLYLTRANSFERASE	1	1			Ť	T	T		T	T
POLYE ECOL	GLUC-TRUC 4-PHOSANGNOTTANSFERASE		200-243				П	П		T	
PGLNI METIT	GLNB-LIKE PROTEIN I	1 1	58-45								П

	PCGENE	107237864	Proharyotte Sequences	- T	Т	7			т	100
The control of the	FILE WAME	PROTEIR		4	-T	т	Z VIII		- V-190	2034
The control of the	PGLNA ANASP	GLUTAKINE SYNTHETASE			-					
The control of the	PGLNA BACSU	GLUTAMING SYNTHEIASE		413-440	-	<u> </u> -				
The control of the	POLYA CLOAB	GLUTANING SYNTICETASE		144.171						
	NO. NA. ECOL.	GLUTAMINE STRINETASE		201-130	-					
	PCLNA METVO	CLUI AMINE STRINE IASE	PROTEIN VIAGABLE	142-169		-				
	POLINA PACIFIC	COLOT ALVANDA CONTRACTOR		187-161						
This control of the	PCI NA CALTY	GLUTAMRG SYNTHETASE	KIUM	144.171	 					:
THE CASE HELELATORY PROBLEM 13-4	MOL NA STREET	OLUTAMINE SY		112:91			_	-		_
THIRDER REGULATOR THORIEN II THE COCCURS IN THE COLUMN	PGI NII AZONE	NIT ROCKY REG		13.49						
THE CALL STATE S	PULNS BHOCA	AI PROCEN REG		15.49						
DEPTION TRANSFELLER SECRETARIES SECRET	PCLNB SYNM	NITROCEN REG		П						
	PCLND ECOL	UND VIEW YE		П	17.1					
Controller Con	PGLND SALTY	UDP URIDALY	SALMONELLA TYPHIMURIUM		,					,
CLICKED POTENTIAL BUTCHED 19-11	MINE SCOL	ADENYLYLTRANSFERASE	ESCIUERICITIA COLI		_	R				
ALTONOGRAME PROGRA	MOLKH ECOL	CLUTAMINE-BINDING PROTEIN PRECURSOR	ESCHERICHIA COLI	126-153	1					
ALTONOCOLOGIA 19-10 19-1	PCLNO BACST	GLUTAMINE PENNEASE OPERON PROTEIN GLNQ		7.34			-			
ACTOR ACTO	POLYO BACSU	AEROBIC GLYC1-PHOS DEHYDROGENASE	BACILLUS SUBTILIS	194-230						
Guyeriou inverse Acutivous notes Accurd Statis Accessor (Parker Acutivous notes	MALPO ECOL	AEROBIC GLYC.)-PHOS DEHYDROGENASE	ESCHERICHIA COLI	410-437		$\frac{1}{1}$	-		1	
ACKERGE TRANSE SACREMENT STATE	PGLIF BACSU	CLYCEROL UPTAKE FACILITATOR PROTEIN	BACILLUS SUBTILIS	235-274		+		+	1	
ACTION LANGES EXCREMINATOR 19-10	POLYK BACSU	CLYCEROL KINASE	BACILLUS SUBTILIS	44.93		+		1		
CLAYER PROTECT 19-13 19-	POLPK ECOLI	GLYCEAOL KINASE	ESCHENICHIA COLI	86.90						
CLITALIDADISTALE SECRECACION 197131 1971	MILE ECOL	GLYCEROL 3-PHOSPHATE REGULON REPRESSOR	ESCHENICHIA COLI							
CLUTAMEDONN STATEMENT ST	POLIX ECOLI	CILPX PROTEIN	ESCHENICHIA COLI	297.324		1				
CLUTOMACE FORTIALS ECCENTRIAL 115.44 115	POLYX SHUT	GLPX PROTEIN	SHIGETLA FLEXNERI	297-324						
ACTIVALE NUMBER SECRETCH 18.19 16.11	PGLIX ECOU	CLUTAXEDOXIN			<u> </u>					
SECOND OF CONTROL OF	MOLTE ECOL	CLUTAMATE SY		65.50		1				
LENG HYBOXYAGENATIONALE BACKLEAN STATES 18-40 18	POLTP ECOL!	PROTON GLUTA			1	+	 			
STATE STAT	POLYN ECOL!	PHOSPHOTICAN		200		-			-	Ī
SANG PROTOCOLOGICAL PARTIES 1997	MALYA BRAIA	ENINE HYDRO		200			-			
STATE AND THE PART OF THE COLOR STATE OF THE PART OF	NOT X	EALINE HYDRO	CAN TLOOK IER JOON		<u> </u>	<u> </u>	<u> </u> -	-		
STATE STAT	PCLYA HYPM	EKINE HYDKU	PACIFIC CONTRACTOR	Ī	- 555	<u> </u>		-		
The control of the	STATE OF THE STATE	COMED OF EACH		Ī.	<u> </u>	<u> </u>			<u> </u> 	
TABLE SCENE FORTEN CHAANTOLA TACTIONALIS 15.15 15.10 15.25 15.15	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	CHARLES DE CYCEN BODI D	DAKATIS	112.35	-					
THE PROPERTY PROPERTY TACKFOOLATES 15.45 15.25		Wait Suck Profess ROPS D		97.131					 -	
PACIFIESCE FROTER FORCE CHANTOLA TACCHOLATIS 11-46 1-40 14-4		VILLE BACK PROTEIN POPS.D		25.52						
13.40 13.4	1000	VALUE DACE PROTEIN POPED		Г	1.230	-				
No. No.	10 00 OF 12	VOLUE ENCE PROTEEN FOR 2.6		3.40						
13-45 13-4	POPED CHETT	VINULENCE PROTEIN POPL-D		121.30						
CONTINUE MACLILLY BURGORAFEE 2773 2773 2774 2775 27	POULA MOR	TRANSCRIPTION ELONGATION FACTOR GREA		15.40	1		-			
SAMELIER BOAUGIA BACCOUNTIAL 12-19 12-	MOUNT INCHI	CAPILLING PROTEDS		27.73		$\frac{1}{1}$				
AMALGE STATE ALCELLIS BLEVIS ALCELLIS ALCEL	POUR BOUND	CAN LIKE MO	BOULETA BURGOUGETU	6, 79	1	+				
ACTION STATE ACTION STATE SACTION STATE	200	CALTE PRO		Ť	Т	Т	290			
SCHEDUCHA STREET LOSS SCHEDUCHA COLI STR-30 STR-30	TOTAL ST			Ť	T	Т		2162.2189		-
EXCENCIALE ESCENCIALE			ECHEDIONA COLI	Т		T	7			-
### PRECIDENT REDICTASE PRELIGIONOSA 16-114 18-29 ### PROTECTOR REDICTASE 18-29 ### PROTECTOR REALITY STATES 18-219 116-114 18-29 ### PROTECTOR REALITY STATES 18-219 18-219 ### PROTECTOR REALITY STATES 18-219 ### PROTECTOR REALITY STATES 18-219 ### PROTECTOR REALITY STATES 18-219 ### PROTECTOR REALITY STATES 18-219 ### PROTECTOR REALITY STATES 18-219 #### PROTECTOR REALITY STATES 18-219 #### PROTECTOR REALITY STATES 18-219 ###################################		THE LEASE OF THE PARTY IN	ESCIEDUM COLI	Т	=	\perp	L			
TAXVATORI-BEDUCELE PLOTEDY A BACELLU'S FUNTELLS 14-101 185-296 18-104 185-296 18-104 18-		THAT THOOPE	PSEUDOMONAS AERUGINOSA	Г	L					
FIGURE PRECINSOR EAWPRA CAGOTOVOIA 151-151 151	100	G-KOLLAVA TACK	SACELUS SUBTILIS	Г	5.2%					
PROTEIN D PLECUSCA ERWINIA CHRYSANTICEAG 191-316 151-316 131-316	POSDO DIVIC	PROTEDIO PLE			Г	Г	L			
	OWIN OND	ROTENOPLE	2	Г	П		9			
ENVORA CAROTOVOAA 131-147 131-	ACED KLEY	ROTEN D PUE		П	H					
PROTEIN I EAWONA CHRYSANTHEM 137-367 PROTEIN E KLEBSEELA PREUMOMIAE 137-361 PROTEIN E PREUMOMOMAS AERUGINOSA 137-149	POSTE BINC	PROTEIN E		139-367						
PROTEIN E NEUMOMAE 133-341 PROTEIN E PROUDOMONAS AERUGINOSA (133-14)	POSTE BLWC	PROTEIN E		329.367						
PROTEIN E (132-149	POSPE ILEM	PROTEDYE		П	+	+	+	1	1	
	POSPE PIECLE	PROTEINE	PSEUDOMONAS AERUGINOSA	-1	1.369	-	-	1	1	

POCESSE Tiesting.4										
FILE NAME PROTEIN	ORCA NIGHT	4 10 17 4	104	1		7	_			
PROTEDIE	XANTHOMONAS CANDESTRIS	100			т			9	9	4
ĕ	PSEUDONONAS AERUGINOSA	5		Ī			Ī		Ì	
S	AEROMONAS HYDROFIIILA	114				Ī		Ī	!	
PGSPI_ERWCA_PROTEIN PRECUISOR	ERWINIA CAROTOVORA	7				Ī	T		Ì	
POSPI KLEPH PROTEIN I PRECURSOR	KLEBSIELLA PREIMONIAE	140-167								
POSPK ELWCA PROTEINK	ERWINIA CARDIOVORA	28-55								
TUSTE, ELWCH PROJECT A	EKWINA CHRYSAATGEN!	10-55								
MONK KLEW PROTEIN K	KLEBSIELLA PNEUMONIAE	72.48								
PUSER PSEAL PROTEINE	PSEUDOMONAS AERUGIMOSA	262.219								
PUSH EXWCII PROTEIN	ERWINIA CHAYSANTHEM	1.42	248.216	131-158						
POST XARO PROTEINE	XANTHOMONAS CAMPESTRIS	14.73	197.334	Ī						
YOU'M ENTRY MOTERN M	ERWONIA CAROTOVORA									
POSCO ERWON PROTEDY D PRECURSOR		159-303	440-475	Г	657-684					
POTET STEDO GLUCOSTILITANSFERASE: PRECURSO		43-69	137.304	212-230	107-19	111:1416	409-1529			
PGTF2 STILDO GLUCOSTI, TRANSFERASE: I PRECURSOR		171.198	106-211	451.415	1343-1412	4		j	1	!
PULPA STEWN (GCUCUSTITICANS) ELASE.S		197.350								
COLD STIMU GLUCUSTLIRANS ELASE: PRECUISOR		42.93				313-347	392-617			
POINT STAND INCUR USST. HAM SHASE SI PRECURSOR	SOR. ISTREPTOCOCCUS MUTANS		110-131	_	330-361	614.613				
POTES STRUCT CACACOSTALINAMINERASE, SPRECURSOR	T		436-46)	211.015						
MAILE BACKLI CAS CONTINACE	T) ()	Т						i	
POLIAA ECNI ICAD ENTRACE	ESPERIOR SOUTES				Ì		j			
POINT BACK THEY AND LAKE STREET	בארבאראויא רסרו	20.60								
TOTAL CLICAL AND	3									
POUR BACKET BEET AT PARTIES BEET BEET BEET	BACILLUS LICHENIFORMIS	8								
PROGESTICANA	BATH LIKE	3 4		1	1					
MOCH INTAKE	2 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	Т		1	1	1				
POUNI BLITE BROOD DEANAGE	STEAT COME OF THE PARTY OF THE	5	103-41	1						
POUNT HACSU INDOCULIZAMATE PRECTINGOR	MACH 116 CONTROL	Т		1		1				
DEDOCT UCANAS	THE EMONORORY FILES	100	1	1	1	1				
DOOGLUCANASE	BACELUS SP	T	148.174	11.61	Í	T	1			
ENDOCALUCANAS	BACCLUS SUBTILIS	т	†		T	Ť				
SPOCK UCANASE	FIBROBACTER SUCCINGENES	342-586		†		T	Ī			
POUNT THEFU ENDOGLUCANASE EAPRECURSOR	THERMONDSPORA FUSCA	301.342						Ī	Ī	
MDOCK UCANASE	THERMOMOSPORA FUSCA	П	ļ		Ī	İ	Ī			
MOOD UCANAS	BACOLUS LAUTUS		484-481							
MOOGL UCANASE	CLOSTRUDIUM THERMOCELLUM	354.384					-			
POUR TIEST ENGINEERINGS A PRECUESOR	PSEUDOMONAS FLUORESCENS									
	NORTH COLCUS ALBUS				Ī				·	
POLINE BACE A FORMACI IN ANA COR PRECIDENT	BATH LIKE ATHER	2.00								
MOGLICANA	CALDOCELLINGSACCHARGE VYICINA	Т		1	1	1				
PCUMB_CELT! ENCOGLUCANASE B PRECURSOR	CELLULOMONAS FIMI	Т			1			1	7	
PCUNE CLOCI. ENDOCLUCANASE B PRECURSOR	CLOSTRIDIUM CELLULOVOILANS	Т	266.300	T	Ť			Ī		
PROPERTY ENCORPORANTE IN PRECURSOR	CLOSTABILM THE LIMOCELLUM	Т				†	T	T		
SADOGI (UCANA)	CELLULOMONAS FIDAI	806-186		İ		T	T		Ī	Ī
POUNC PAETL EMBOGLUCANASE CPRECURSOR	PSELDOMONAS FLUORESCENS	53-15							Ī	Ī
MOOGLUCANAS	CLOSTIMICELLU.OLYTICUM	П								
ADOCULICANA SE	CLUST MUCHA CELLUIOL YTICUNI		╗							
	CLUS I ALLION I PELMOCELLUS	<u>.</u>	7	<u> </u>						
MOOG! UCANAS	FEWORA CAROTOCAL	T		1						
KGINX CLOTA PUTATIVE DIDOCLUCANASE X	CLOSTEDIA THEOLOCELERA			1	1	1				
PGURZ CLOSA ENDOGLUCANASE 2 MECUASOR	CLOSTREDIÚM STERCORABUM	T	133.540	T	T	1	1	1	1	
POUN BACHO ENDOGLUCANASE	BACELUS POLYMYXA	T		T	T	Ť	1	Ì		
POUN BACSI ENDOGLUCANASE PRECURSOR		321.346				Ī	T	T	T	Ī
EMBOGLUCANA	BACILLUS SP		185-106	613-664		ĺ		l	Ī	Ī

PCGEAR (1074)7634	Protaryotic Sequences		П	П			,	•		
FILE NAME PROTEIN	ORGANISM	4	d	701	Т	1		Т	Т	4
	HAT ON A CTERT OF HAT ON HIM	9	Ť	Ť				İ	:	:
AS VESICLE PRO	HALOBACTERNOM HALOBRUM	100		Ì	Ī					
AS VESICLE TAC	APHANIZONE NON EL DS. ADUAE	-	99-66							Γ
POWER PRINT CAR VESTILE PROTEIN	FREMYELL A DIPLOSIPHON	17.	89.65		Γ	 -				
POVPA RALINE GAS VESICLE PROTECH	HALOBACTERUM MEDITERRANEI	11.64								
POVPA MICHE GAS VESICLE PROTEIN		99-61								
POVPA PSEAN GAS VESICLE PROTEIN		10.0	39-06							
POVEC AMBL DAS VESICLE PROTEIN C	APHANIZOMENON FLOS. AQUAE	67-1							1	
POVPC HALHA GAS VESICLE PROTEIN C	HALOBACTÉRIUM HALOBIUNI	150.749		Ì						
PRIVICE HALLAGE GAS VESICLE PROTEIN C	IIALOBACTERUM MEDITERRANEI	139.169						Ì		
POVPO KALHA GVPD PROTEIN, PLASMID	HALOBACTERIUM HALOBIUM	110.147						j	į	
VPD PROTEDI	HALOBACTERIUM MEDITERRANCI	110-147								Ī
POVPF HALHA GVPF PROTEIN, PLASMID	HALOBACTENION HALOBIUNI	13-47	135-167							
POVPE HALLAGE GOVPF PROTEIN	HALOBACTERIUM MEDITERRANEI	13-43								
VPF PROTEIN	HALOBACTERUM SALINARIUM	67-1								
POVPG MALKA GVPG PROTEIN, PLASMID	HALOBACTERUM HALOBIUM	34-65								
POVPO HALLAG COVPO PROTEIN	HALOBACTERUM MEDITERRANEI	11.72								
POVPH MALHA GOVPH PROTECTA	HALOBACTERIUM HALOBIUM	10.40								
POVPI HALLAGE GVPI PROTEIN	HALOBACTENIIM MEDITERIANEI	1.32								
POVPK HALHA GVPK PROTEIN	HALOBACTERIUM HALOBIUM	49.76								
POVPK HALME OVPK PROTEIN	HALOBACTEUUM MEDITENBANEI	13.39	16.74							
POVPK MALSA GVPK PROTEIN	HALOBACTENUM SALINARIUM	<u>=</u>	2							
POVPL HALME GVPL PROTEIN	HALOBACTELUM MEDITERRANEI	44.71								
POVPN HALHA GVPN PROTEIN	HALOBACTERUM HALOBIUM	13.140								
POVPN HALLINE GOVPN PROTEIN	HALOBACTERUM MEDITERRANEI	\$	j	1						
VPO PROTEIN	HALOBACTERUM MEDITERRANEI	98.60	200		Ì					
NA GYRASE SUE	BACILLUS SUBTILIS	1000	┱	7	1					
NA GYTASE SUE	CAMPYLOBACTER JEJUNI	01(.785	T	N 9-24	603.673					
POYTA ECOLI DNA GYTASE SUBUNIT A	EXCREMITAL COLI	144 161	107	777	Ī					
TA CTRASE SU	2	4.91	T		Ī	Ī	Ī		Ī	
TOTAL MICE DAY CIRCUS COCCUIT A		126.156	146.331	6,00.4%	647.674	113.130			Ī	T
POTAN PLANT COME OF STREET BY	BACH 115 SUBTILIS	917.19	Т	Т	Т					
DNA OYRASE SU	BORRELIA BURGDORFERJ	181-181		Ī						
POYAG ECOLI DNA GYRASE SUBUNIT B	ESCHENICHIA COLI	616.643								
POYDS HALSO DNA OYRASE SUBUNIT B	HALOFELAX SP	230-257								
DNA OYRASE SU	MYCOPLASKA PHEUMONIAE	249-283		-						
INS ESYMAD YNG	NEISSERIA CONORAHOEAE		500							
DNA OYNASE SU	PSEUDOMORAS PUTIDA		Т	7						1
POYAB SPICE DNA GYTASE SUBLINGT B	SPROPILASMA CITIC	ž	Т		341-368	340.579				
FOYNE STAND DNA GYLASE SUBUMIT B	SIAPHILLUCACION AUREOS	6/2-762			I					Ī
FIGURA ELOCAL PALARA-NIDROATSIEROE MENTUROCENASE	BACHEBICHA COLI	711,001	430.444	1						T
PIGE HAEIN LIPOPROTEIN E PRECUASOR	HAEMOPHOLUS DIFLUENZAE	31.83		T				T	T	T
OLUTAM TIV	CHLOROBIUM VIBRIOFORMES	233-259								
	ESCHENICHIA COLI	219.316								
S-ALENDE S	INHODOBACTER SPHAEROIDES	11.100								
GLUTAMYL-TRN/	SALMONELLA TYPHUMUMUM	316-316	144.371							
GLUTAMYL TRN/	SYNECHOCYSTIS SP	163-190	350-377							
DELTA-AMINOLE	METHANOTHERMINS SOCIABILIS	131-158								
PUTATIVE URDIN	BACELUS SUBTILIS	10-37								
PREMA_ECOL: UNOPORPHYRINGGEN-III SYNTHASE	ESCHERICHAA COLI	211-238								
PIEXON ECOLI HENOM PROTEIN	ESCHENCHA COLI	147-174								
PRESCHA YEAR HEADNIECEPTOR PARTORNER	ESCUEDICIA COLTICA	274-20	076.101							
PREMA ELOCA INDIALISMENTALIAMASTERASE	BACH IN COMPANIE	1	2							T
MEM BACSO MEM TROICE				1	1]

PCCENE	1109s13fin4	Park a mark for a second									
TILE NAME	PROTEIN	OPCA MICK									
PHENZ BACSU	PHENG BACSU PEUROCHELATASE	USSUBTILIS	\$ ***	T T T	7	O BEG 4		AND THE	3	PEAS PEAS	ARKAS
META ANASI	HETEROCYST DIFFERENTIATION PROTEIN	ANABAENA SP	- -	357.391	521-565					-	
MEX STEN	DNA MISMATCH REPAIR PROTEIN KEXA	STREPTOCOCCUS PNEUMONIAE	426-460								
NOTE OF	DNA MISMATCH REPAIR PROTEIN HEXE	ĄĒ	19704	Ī							T
200	POS TRANSACTIVATOR PROTEIN HEAB	ESCENTUS	98-123								1
2022	HOLC PROTEIN		111.140								Ī
TOTA COL	CIT-BINDING PROTEIN BOLX	ESCHERICINA COM	169.478			-			İ	:	
	INDSTRACTOR I PROTEIN		24.51	;							
200	PILIATION PROTEIN HIPC PRECUISOR	NZAE	15.50	- F	447.474						Ī
	THUSTHURIBUSTI-AND CYCLUMYDROLASE	:TIS	136-174								Ţ
2 1 7217	TOTAL CAMEDIA MINISTRATION		651-521								Ī
10.00	F.P.A. CARBOXAMIDE RIBOTIDE	LACTOCOCCUS LACTIS	49.10	111.22							
YALISA MELAY	P.S.A CAUBOXAMIDE KIBOTIDE		13:142		Ī						Ī
Y X	P.S.A CAUBOXAMIDE INBOTIDE		125.150			T					
HISS LACEA	AMDOTRANSFERASE HISH				Ī		İ				
	HIST PROTEIN		Ţ	371							
	HISF PROTEIN	COUNTRY	T	60.7							
PHIS? ECOLI	INITIAL SOLECT YCENOL-PHOSPHATE DEHYDRATASE ESCHENICHIA COLL		Ì,								
PHIST SALTY	IMIDAZOLEGL YCEROL-PHOSPHATE DEHYDRATASE	SALMONELLA TYPIGIMURIONI	171								
PHIST ECOLI	INSTIDINGL PHOSPILATE AMINOTRANSFERASE	ESCHEBICKIA COLL		Ì							
PHISS HALVO	HISTIDINGL PHOSPHATE ANTHOTICANSFERASE	VOLCANII		Ì	1						
PHIST LACLA	HISTIDDIOL-PHOSPHATE AMINOTRANSFERASE		100		1						
PIDSI SALTY	HISTIDINOL-PHOSPHATE AMINOTRANSFERASE	SALMONE! A TVOMINE BILL			1						
PHISQ SALTY	HISTIDDIE PERMEASE MEMBRANE O PROTEIN		27			1					
PHISX ECOL	HUSTIDINOL DEHYDROGENASE		-	1							
MESX_LACLA	HISTIDINGL DEHYDROGENASE	1	<u>.</u>								
PIESX MYCSM	HISTIDDIOL DEHYDROGENASE		7	264-303							
	HISTIDINGL DEPHOROGENASE	SALMONE! A TVENIAM WITH	Т	200							
	ALPHA-HEMOLYSDY PRECUESOR	STAPHYLOCOPPIS AIREIN		1	1						
PILY! ECOL!	HEMOLYSIN A, CHROMOSOMAL	ESCHENCIA COL	Ť	100	┱	╗			7		
	HAEMOLYSIN SECIETION MOTEIN, CHROMOSOWA	ESCHENICIÓN COLI	ŀ	T			337-380	458-492	<u> </u>	22.23	
	HENOLYSIN D, CHROMOSOMAL	ESCHENICHIA COLI	T	38.3	11.16						
PHLYA ACTEL	HEMOLYSIN	ROPNEUMONIAE	T	Ť	Т	W. 151	110	7			
PALYA ACTSU	EMOLYSON	Ī	T	Ť	Т	Т	Т	7	26.0		
HEYA COL	EMOLYSIN A, PL		T	Ť	T	Т	Т	Т	P (4-6)		
PPE.YA PROM	HEMOLYSIN PRECURSOR	PROTEUS MIRABILIS	8	T.	Т	Т	Т	T	_	Т	Ī
			T	T	T	Ę	7				147.774
THE TA SEAMA	HEMOLYSIN PRECURSOR	SEUVATIA MARCESCENS	T	Т	Ī	-	_	10.96	7011-100	100	13.27
PIR VA VERMI	- CONT. CO. C. C. C. C. C. C. C. C. C. C. C. C. C.		1316-1331		Т	T	Т	Т			0871.657
TO THE	JARVOLT SIN PREC		3	59.15				1	T	T	1
- CO. 15	MATERIAL VEN CEN	PLEUROPNEUNIONIAE	14-61					T	T	T	Ī
PHO YE PROM	HELIAN VANA ACTIVATOR PROTEST BESTERS		-			İ	Ī		T		Ī
PHE YS PROVI	KAEMOLYSIN SEC	PROTEIN MICKELLS		100.513					T	T	T
HE TO SEUKA	AGMOLYSDY ACTIVATOR PROTEIN PRECIPEOR	2	٦	₹					T	l	T
PAT'N VIDOL	HENOLYSON SECURITION PROTEIN PARTIESON		╗	╗					Ī	T	Ī
PACYC ACTIVE	HEMOLYSIN C		٦	13-447	458-524			Ī		T	
THE VOTE	REMOLYSIN SECRETION PROTEIN APPR	1	10:13			-				T	
HE YO ECOL	ME, YD, ECOLJ HEMOLYSIN D, M.ASIADD	1	7	- 1							Ī
PREV HALIF	HALOLYSIN PRECURSOR	THE CASE OF STREET		617.91	10 m						
HARG DESM	13 1 KD PROTEDY DV HOAC OPERON			1	1	1					
PHOLD LOTTEA	HIS PROBLEMS DEHYDROGENASE		B	+	1		1				
PHOS SEUMA	X H-NS			1	1	1				1	Γ
PHOLA ECOL!	LIL DEL TA SUBUNIT		Τ.		1	1					
PHOXA BRAIA		150	L		\dagger	1	1				
2000	MONEY NOOTH HOXS ALPHA SUBUNIT				\dagger	\dagger	†	1	1	+	
באסאט ארננט			96-110	l	t	t	†	†	1		
					İ	1	1	1	1	1	7

LCCEME	107117814	Probaryotte Sequences		П	1-1	-	\Box	17	П	17	
LILE RABIL	PROTEIN	ORGAKISM	T T	45154	1471	14184	3	1	3	4	AREA!
PHO CE BICADA	MOXX PROJECT	DEINOCOCIIC BADIONII ANG	(14.2)					İ		ĺ	
PICHET LACLA	PHOSPHOMBOSY	LACTOCOCCUS LACTIS	1.5	71:10				Ť		İ	
PILLOD STREO	SIGMA FACTOR HADD	STREPTOMYCES COELICOLOR	196-123					İ			
PHOUS BURSO	REGULATORY PR	BURKHOLDERIA SOLANACEARUN	111.405								
PHOUSE PRESY	OUTER REMORAL	PSEUDOMONAS SYRINGAE	631.20	110-144							
PHRYS PSESH	PROBABLE REGULATORY PROTEIN HOUS		15:51								
PHS:1 CLOAB	I K D MEAT SHO	IS.	101.0	i		1		•			
PIS70 HALMA	HEAT SHOCK TO KD PROTEIN	=									
AIS WAYOU	HEAT SHAKE TO PROTEIN	ANY CHIACTERINA LITERAL	1	<u> </u>		-	:	Î :			-
N N N N	PICAT SINCE TO AND PROTEIN			000				1			
200	MEAT SPICE PROTEIN CALS			1					Ī		-
2	PROJEKSE DO PRELUASUR					T					
THE PERSON	RIVE TRUITS PRELOGOU	N I I I I I I I I I I I I I I I I I I I						ĺ			ĺ
	SECTION MODERNIA PERIODICE	-			3		į	Ï	!		
PHILIT BACKL	HILT OPERON POSITIVE REGULATORY PROTEIN	: : !	. 19	:	i ;						
PHYTI LACIE	HELVETICIN J	ELVETICUS	174.212	10.0				-	Ī		
PHYCA ECOL!	FORMATE HYDROGENLYASE SUBUNIT I		37:100	108.13							
PHYDO ECOU	TATANSCRIPTIONA		:51.278								
PHYDO SALTY	TRANSCRIPTIONAL REGULATORY PROTEIN HYDG	HINIURUNI	251-278			1		1			
TANK CO	SENSOR PROTEIN HYDH		112.338	160.187				1			
1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	HYDANTOIN UTIL		554.58								
THE TREE	HYDANTOIN UTIL		9	2	1	1			Ì	Ì	
NAL MESS	INDOLEACETATE-LYSINE LIGASE	TUNGVE	8	111.702				1	Î	ĺ	
WAP ECOL	ALK PHOS ISOZYNE CONVERSION PROTEIN		74.101								
NICEN ERWAY		ELWINIA ANANA	101.45	A P 3 - 7 7 8	Т	Т	Т	Т	Т	Т	ž
Physical Partie	-	FRUIDA MERRICOLA	110-117	117707	114.561	Т	464.331	111.164	186.011	917. tone	
	CE MICH EATION	SE SCENS	201.301	Т	Т	100:109	Т	Т	Т		
PICEN PUESY	ICE NUCLEATION		564-402	172.647	Т	1	Т		T	Ī	Ī
PICEN XANCT	ICE NUCLEATION	PESTAS	496.534	215-515	1168-1204	1244-1275				Ī	
NCS SHOT	DITERCELLULAR		41-105	411.467							
PES BACST		HERMOPHILUS	П	101.109							
PUT BACKU	INTIATION FACTOR IF-2		П	7							
PU2 ECOL	DOTTATION FACTOR IF:		010-724	292-66				1	1	1	
FOR EATH	DOTINATION FACTOR IP-2	ENTEROCCOCOS PARCIOM	120.61		1	1				1	
	NOTE AT THE PART OF 15.1		27.54	76.97	T	Ī		T	Ī	Ī	
PUES KLEPN	DATIATION PACTOR IF 3		27.54	10-01			T		T	T	
PUT WHOTE	PAITIATION FACTOR IF-3	2	177-311					Ì			
PUT PROVU	DOTTIATION FACTOR IF-3		3-20	70-97							
PES SALTY	INITIATION FACTOR IF-3	UUM	27-54	10-91							
PUT SERVIN	PATIATION FACTOR IF-3		19.46	10.97							
PICA NEIOO	IGA-SPECTIC SERING ENDOPERTIDASE	HOEAE	247.27	¥.	3	1074-1051	177. 404	<u>₹</u>			
MCGB STRSP	1666 BINDONG PROTEIN PRECURSOR		46.76	120-150	П						
PICGO STREP	IOG BEYDING PROTEEN PRECURSOR	4	46.76	20.50	\$2.23	270-297					
7 F. COL				200			1	1	1		
PR.W. SALTY	ACETOLACTATE	שטאט	19-01	120-147		1					
A CO	ACETOLACTATE STATIKASE		20.00				1				
1008 KLT	DOB PROTEIN		2.3			Ì			1	1	
PDG ACICA	INOSINEST-MONOPHOSPINATE DEPTOROGENASE	ACINETUBACTER CALCOACETICUS	100		1			1		1	
PAC S	E-3 -MUNOTHUSTRA I E DEN I DAUGENASE	2137.45	34-180	.,,,,,			1	1	1		•
PDA BACIL	INTERNAL IN A	LISTERIA LICHOLYCORNES	171,701	141.14	515.30	Ī	1	1	Ť	1	
Organ Street	INTERNALLY B PRECURSOR		13-94	Т		T	T	1	T	T	T
PRIVA VEIEN INVASIN			301.131	Т		Ī	T	†	Ť	T	T
					1	1	1	1	1	1]

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PCCENE	10717214	Prehamatic Commence						Ī			
THE MANE	LACTEIN	PRCANISM	AREAL	AREA 3	ARFA 3	ARFAG	ABEA 6	ABEAG	\$ V48 V		
ייאי איניין	60 KD ANTIGEN	SHIGELLAFIEXNEN	Γ	Т	Т	Т	Т	1	7	Т	3
- 1	IN KD ANTIGEN	SHIGELLA PLEXMEN	95.136	437-475	493-537	396.430	l	Ī			Ī
A SEE	43 KD MEMBRANE ANTIGEN	UAE	31.55	9	480.507	\$11.336					T
TIME SHIPE	62 KD LEKBRANE ANTIGEN		Ī	Γ	Т	33:38	Ī	Ī			Ī
PIPAC SHIDY	42 KD MEMBRANE ANTIGEN PRECURSOR	UAE	1:33	19:0	ľ	324.378					
LAC SHIPL	41 KD MEMBRANE ANTIGEN PRECURSOR		Γ	Г	Т	34.372	Ī	Ī	Ī		Ī
VUAD SHIDY	17 KD MEABLANE ANTIGEN IPAD	SINGELLA DYSENTENIAE	31.5	Г	1"		T	Ī		Ī	T
איני איני	16 KD MEMBRANE ANTIGEN		Γ	Ļ	31:318	İ	İ	Ì		T	T
A 200	DOB PACTEDA	UAE	115-202	Ι		T	Ī	T		T	I
	IPGB PROTEIN		135-202		Ī	T		T			
	ISOPENTENYL TRANSFERASE	MOAE	t	141.131	Ī		Ì	T		1	
PIPTE ECOL	INCREAME PYROPHOSPICATASE		Ŀ		T	T	T	1		1	I
	VOLULENCE PROTEIN PRECURSOR	VIBRIO CHOLERAE	L	116.177	T		1	Ì			Ì
	VOLULENCE REGULATORY PROTEIN DIGB		Т			1	†	1			
_	DON. RECULATED PROTEIN A				1						
1-	INSERTION PLEMENT ISOLISID PROTEIN INSE	148		1	Ī		1	1			
	INSERTION ELEMENT ISO-ISIN PROTEIN INSE			1		İ		1			
	INSERTION ELEMENT IS! PROTEIN INSB		97.11	1	T			1			
	INSERTION ELEMENT IST PROTEIN INSE			1	1		Ì				
1	INSERTION ELEMENT IS! PROTEIN INSA		1117	1	1	1	1	Ì			
PISPI BACSU		5	Ĺ	197,334	341.980		\dagger	1			
	INTIACELLULAR SERINE PROTEKSE	3	T	Т			\dagger	1	1		1
	ISTA PROTEIN	ESCHENCHIA COLI	017.310	1	1	1	1	1			1
PISTA SHISO	ISTA PROTEIN		11.310	T	T	ı	1	1	1		
	FEALUC AEROBACTIN RECEPTOR PRECURSOR		Т	135.40	(40,40)	1	1	Ť		1	
-		S	Т	Т			\dagger			1	1
PK672 ECOLI			01.01	T	T	İ	T	Ì	1	1	T
PKAD BACSU	ADENYLATE KINASE		111.213	T	T	T	t	Ť	Ī	1	
CKAD LACLA	ADENTLATE KINASE	US LACTIS	18-21)		T			İ	T	T	
PKAN BALSE	PANAMITCIN MUCLEOIDITLITANSFERASE		69.96		r	ĺ		İ		T	Ī
PKDGT ECOL	KETO LAPORY	PENTEUCCEUS AUREUS	90.00							İ	
PKDOT EAWCH	3-KETO-3-DEDXYGLUCONATE PERKEASE	in the second		1	1						
PKDTA ECOL	DEOXY-D-MANI		6 9	†	1	1					
PKGTP ECOL	LPIA-KETOGLU		R C	1	1	İ		1			
PKGUA_ECOLI G	GUANYLATE KDVASE		987.68	1	1	1	1	1			
PKHSE_BACSU	HOMOSERINE KINASE		10.34	t	T	1	1	1	1		
PKHSE PREDI	HOMOSERDIE KINASE	NO.	2 2	1	1	1	1	1	1		
PKKA4 BACCI	AACINGGLY COSIDE T-PHOSPHOTHANSFERASE	BACILLUS CIACULANS		\dagger	t	t	\dagger	\dagger	1		1
PKOMP ECOLI	KOLD TRANSCRUTIONAL REPRESSOR PROTEIN		311-355		İ	t	t	t	T	1	T
AND AND AND AND AND AND AND AND AND AND	VEUVATE KIRAS		13:148					l		t	
PLACE STALL	CONTRACT LATE CONTRACT	HILUS	111.374			-			Ī		T
PLACA STRACT	SOMERASE LACA SUBUNIT	STATE OF COLUMN AND AND AND AND AND AND AND AND AND AN	3	1	1						Γ
PLACE STRUCT	TAGATOSE & PHOSPHATE KINASE		T								
יולנס ואפנא	4-PHOSPHO-BETA-GALACTOSIDASE		7	287-310	1				Ī	-	
ארעכו בנסח	ACTOSE OPERON			1	1						
PLACI KLEPN	ACTOSE OPERON	MONTAE	965	1	İ	1	+	1	H		
PLACK STAND	HOSPHOTICANSF		3.30	\dagger	1	1	1	1			
PLACK STRAD	PHOSPHOTRANSFERASSE REPRESSOR			\dagger	†	+	1	1			
MACY LACOE	ACTOSE PENNEA	CKII	200	\dagger	\dagger	\dagger	\dagger	\dagger	†	1	1
PLAFB VIBPA	LAGELLAR HOO		Т	SIFTIE	t	\dagger	+	\dagger	1	1	
LANG KLEPH	MALTOPORUM PRECURSOR		П	+	t	+	\dagger	\dagger	†	+	1
PLAKE CLOIM	SAUCH LANGE A AGUCANASE PRECURSOR	×	132-159		-		$\frac{1}{ }$	\dagger	\dagger	†	T
PLCCI LEUGE	ROBABLE LEUCOCH A BOADNITY PROTEIN	PREUDUMONAS AERUGINOSA	171-191		Н			\mid	t	t	T
PLCNC LACLA	ACTOCOCCIN A SECRETION PROTEIN LCHC		_			H		-			Γ
			02 461-501	207-234 38	1	1					
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		Shr. with	3		ARIA	AREA 4	3				
TE NAME	PROTUIN	CANADA PARTIE	Γ	140-203	237.307	_					
CND LACEA	FICHD LACEA LACTOCOCCIN A SECRETION PROTEIN LCND	CACTOCICES CACTOS		ı							
CRD YEREN	LOW CALCIUM RESPONSE LOCUS PROTEIN D	TERSINA CHICACOLOLICA	T	115.162							
CRD YEAVE	LOW CALCIUM RESPONSE LOCUS PROTEIN D	YEASINIA PESTIS	Т	Τ	340.363	Ī		Ī			
CRV YEAVE	VIRILLENCE-ASSOCIATED V ANTIGEN	YERSINIA PESTIS		Т				Ī	Ī		
PLCRV VERPS	VIRULENCE-ASSOCIATED V ANTIGEN	YEASINIA PSEUDOLUBEAL ULUSIS					Ī	ĺ	Ī		
CTB BACCA	LCTB PROTEIN	BACILLUS CALDOI EMAX					ļ				
PLCTB DACST	LCTB PROTFIN	BACILLUS STEAROTHERNIUMINUS		Ì					Ī	Ī	
PI MID I ACPL		LACTOBACILLUS PLANTARUM	-						1	T	
Pile BACE	LACTATE DEHYD	BACILLUS PSYCHROSACCIIAROLY FICUS	Ī	2	279.100		1	1			١
Pito avera	LACIATE DELIVE	BACILLUS PSYCIMOSACCHAROLYTICUS	1-4)	241-275	379.306				1		l
L DICK BALLS	יייייי יייייי אנייייי	BACILLUS MEGATERIUM	244-274								
BYO'G	L-LACTATE DEMTO	DATE OF THE STREET OF THE PARTY	241.268	279.313							
DH BACST	LLACTATE DEHYD	BACILLUS SI CANOI REPORTED	Τ	140.767				Ţ			
PLDH BACSU	L-LACTATE DEHYDROGENASE	BACILCOS SOBILLIS	33.46								
DH 81110	L-LACTATE DEHYDROGENASE	BIFIDOBACTEMOMICONO		Ī						Ī	
PL DAT LACK	L-LACTATE DEHYDROGENASE	LACTOBACILLUS PLANTARUM	197.23						Ţ	I	ļ
PI PU LISTA	1. J. A.C.T.A.TE DEHYDROGENASE	LISTERIA MONOCYTOGENES	42.69						1	Ī	ļ
	TATAL PERIAL	MYCOPLASMA HYOPNEUMONIAE	276-310								
	-	THE BALL & AND LATIOUS	3.30								
HOY H	L-LACIA IB DER 10	BAPITA 116 ALTER AFIE	165-192	304.331	410-314	548-578	159-619	737-764			
PLEF BACAN	킭		9								
PLEPA PSEFL	LEPA PROTEIN	PSEUDONOMAS PLOUMESCENS									
PLEP BACSU		BACILLUS SUBTILIS	2						1	I	
FULL ECOLU	•	ESCHENCHIA COUI	1								
1	2. ISOPROPYLMALA	LACTOCOCCUS LACTIS	22-49	79.4							
200	A LEVIDED ON MAIN	BACILLUS COAGULANS	111-334								
בורה פעררה	TO	1185-213									
PLEUJ CLUPA	-ISUPROFILMALA	TAPACOCCUSI ACTIS	163-190								
PLEUD LACLA	- I SOPROPTUMALA	2	107.134	676.701	344.774	785-822					
EVR BACSU	TRANSCRIPTIONAL REGULATORY PROTEIN LEVE	BACILLOS SUBILICIS	146.131					Ī			
PLEXA_ERWCA	LEXA REPRESSOR	EXWINIA CAROLOVORA									
PLIP1 MORSP	LIPASEI	MOKAXELLA SF								ļ	ĺ
PLIPZ MORSP	LIPASE 2	MORAXELLA SP									
PLIPE ECOLI	LIPS PROTEIN	ESCRETORIS COL	100								
PLIP BURCE	LIPASE PRECURSOR	BURKHOLDENA CEPACIA	2								
IP PSEFL	LIPASE PRECURSOR	TARUCCALUMAN TUCCARSURAS									
PEESS 41.14	LIPASE PRECURSOR	PSEUDOPROPASSA		777 611							
PLIP_STANU	LIPASE PRECURSOR	STAPHTLUCUCCUS AUREUS	200								
PLIVE SALTY		SALMONELLA TYPHIMURIUM	077-561								
IVE SALTY	LEUCINE-SPECUIC	SALMONELLA TYPHIMURIUM	193-222								
PLIVE SALTY	AMINO ACID TRAN	SALMONELLA TYPHIMURIUM	131-146								
IVE ECOLI	ANIDA ACID TRAN	ESCHENCHIA COLI	23-50								
101 (175)	I BIM BAAL BINDING PROTEIN PRECURSOR	CITROBACTER FREUNDII	195.222								
100	THE INTERVAL BRODNE PROTEIN PRECURSOR	ESCHENCHIA COLI	195-222								
	- SICHNE CRECIEST RINDING PROTEIN PRECUESOR	ESCHERICHIA COU	195-222								
		P SCHEDICHTA COLI	121-148								
LIVA ECUL	٤l	ACTINOBACH LIN ACTINOMYCETEMCOMITANS	10:10	113.213	198.443	451-438	193-620	655-711			
KTA ACTA	LEUKOTOAU	PACETER A VACUO VIDA	0.15	70.716	145.172	409-436	455.482	196-530	\$45.572	100	55.438
KTA PASHU	PLKTA PASHA LEUKOTOXIN	PASIEUMELLA MAZMUCI III.A									
KTB ACTAL	LEUKOTOXIN SECRETION PROTEIN	ACTINOBACILLOS ACTINOMITOS ISANOMITOS	, , , ,	,							
PLKTB_PASHA	× 1	PASTEURELLA MAEMOLT IILA	60.70								
KTC ACTAC	LTCPROTEIN	ACTINOBACILLUS ACTINOMITCE HAICUMILAND		2							
LKTC PASHA	(XTC PAOTEIN	PASTEURELLA MAEMOLYTICA									+
PLKTO AGIAC I	LKTD PROTEIN	ACTINOBACILLUS ACTINOMIYCETENICONITANS	=	2	31:30	<u> </u>					
KTO PASTU	LKTD PROTEIN	PASTEURELLA HAENOLYTICA	114-189								
TON ECOD	ATP-DEPENDENT	ESCHEUCHIA COU	=								
וויאי מלח	JOP-N-ACETYLOI		23.26								
LISPA REGUL	LIPOPROTEIN SIG	ESCHENCHIA COLI	٥								
LSPA STANL	LIPOPROTEIN SIG	STAPHYLOCOCCUS AUREUS	2		!						
LIKF STAM	I LEIKOCIDIN F SURINIT PRICLIKSOR	STAPHYLOCOCCHS AURIEUS	3		:	1					Ì
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P.C.S. 107:138.4	Probate Seconds			ſ						
PROTEIN		П	AREAL	AREAL	AREA4	AREAS	AREAS	ARCA?	AREA	AREA?
		Т								
ALKANAL MON	JM PHOSPHOREUM	╗	237.79							
LKANAL MON		23,488								
CYL-COA REDI										
ACYL, COA MED	M PHOSPHOREUM	2								
PLUXC VIBIL ACYL.COA REDUCTASE		ŝ								
CYL-LUA RED	PENCHANGEOUS LUMINGS CENS									
ACTE INVISITE		Τ								
	HA WOOD IN	144.19	1			T				
NON-FILORESCI	2	Τ	100			1	Ţ			
PECSANI FILA		T,								T
PLINE VIEWA II LINE PROFESSION			T				Ì			1
WITH VIDE CONTRACTOR OF THE PROPERTY INV.					Ī		1			
CHANGE STATES			1	Ī			1			
PLUXP PHOPO ILIBATOR BROTEIN	A PRIOSPINAL IN			Ī		Ţ	1			
I IYO BECSEN AT										
PLYE PHOLE ALKANAL MONOCYCENACE BETA CHAIN			T	Ī						
A KANAI MONE	STATE OF THE STATE	20.00	1			1	1		1	
R.FNZ VACE			1						1	
т	TOBILITY ICINI		Ì	Ī		1	Ī			
PLY CO FICELL I VERNE CHECKET DEBLUE ACE					Ī				Ì	
AMIDATE ENIA						1				
I VTR PROTEIN			1			1			1	
1		Т				1				
LICK AND AND ROLL		7	30.0	1		1				
Т		1	†			Т			1	
PACSA STREY IN PROTECT STROTYPE SAPERCIPACIE	CAMED TO COLOR OF THE PARTY OF	Ť		7	Т				1	
PASS STRPY IMPROTEIN SEROTYPE SPRECURSOR		Ţ	1.	T	Т	Т			1	
M PROTEIN SER		Τ	Т	11.14	VII 201	1	1		1	I
Ī			T	Т	97.17	1	Ī		1	Ī
듩		T	T			Ì	T			Ī
MALTOSE-NINDI		i i	T		T	T	T			T
INNER MEMBILLI		8			Ī	Ī	T	T		Ī
AALT REGULATO		622.639					Ī	Ī	Ī	Ī
PMALK STRPN MALK PROTEIN PRECURSOR	CUS PNEUNIONIAE	19:03	10.207				ĺ			Ī
PMANG DACSMI I.4-DETA-MANNOSIDASE A AND DIFFEC.		П	П				Ī			
PAIAME CALSA B-AIAMNAMASEENDOGLUCANASE A PREC	ICON	Ħ	929-865	4521-2221	1206-1323					
ANTIBIOTIC BEEF	FAXING STICKULLING AND THE WATER THE US	246-273	1							
MORI IZ ATION P										
	NOCE: NEW		5	Ī	1	1	ĺ			
MCSS PROTEIN		1			1	1			1	
NCBD PROTEIN		١,	Ť	17.1	Ì	1	1	1		
_		Т	Ϊ		Ī	T	Ì	Ī	1	
LACTHYAL-ACCEPT	E SCHENCHIA COLI	258-306	İ	İ	T	Ì	Ì	I	1	
METHYL-ACCEPT	HIMURUM	38.106	T	T	T	T	T	T	Ť	
METHYL-ACCEPT		211:312	T			T	Ť	Ī	T	T
		591:1	2 2	277.104		T		T	T	T.
HEMORECEPTO			Г	\$16.543		T		Ī	t	F
HEMOTAXIS CIT		314-348		F			T		<u> </u>	1
HEMOTAXIS AS		~	П	Ι			T	Ī	\dagger	T
PMCPS ENTAE CREMOTAXIS SELUNE TRANSOUCER	ENTEROBACTER AEROGENES		158-208	181.71	411.531					
JETHYL FOENZY	h. d. c. c. c.	-				H				
PHORA METVA METHY COSNEY N. B. BEBING ASP		607.	1	1	1	1				
	LETTANOCOCIE UNITARE		1	1		1				
					1	1	1	1	1	

PCGENE	1871784	Proharywie Sequences		17		т	П	П	, , ,		, , , ,
THE HAME	FILE NAME PROTEIN	ORGANISM	1	4	4	4	3		1	Т	
PAICAB NETTE	METHYL-COENZYNG M REDUCTASE			Ì	T	T	1	1			
PARCED NETVO	METHYL-COENZYNE NI REDUCTASE	VOLIAE			T	1	T	Ì	T	Ī	Ī
PHICAC ECOL!	MCRC PROTEIN					T	T	T		Ī	
PRICRD AGETVC	REDUCTASE OPERON PROTEIN D				T	1	T	T	Ī		
PATON ECOLI	MALATE DEHYDAOGENASE	ESCHENCHIA COLI				1		T	Ī		T
PAIDH METFE	MALATE DEHYDROGENASE		131.161	T	1	T		T	T		I
TO ST	MALATE DEHYDROGENASE		464.493	644.711	992-1019	T					
Pior Ecol	MDL PROTEIN		18.15	Т		Ī					
PAIDOH ECOLI	BIOSYNTHESIS FRUITIN MUXOR		17.								
PAGECI STAEP	METHICILLIN MESIS MEG PROTEIN NELL	3133			T	Ī			Ī		
			110.405	10,773	Ī	Ī	Ī	Ī		Ī	
PKIECK STAEP	METHICILLIN RESISTANCE MECK! PROTEIN				Ì	T	T	T			
			***		1	T	T	T	Ī	Ī	
PMEMB METCA	PHEMB METCA METHANE MONDOXYGENASE COMPONENT A	METHYLOCOCCUS CAPSULATUS			1	Ť	1	T		Ī	
PALENCE METTR	METHAME MONOOXYGENASE COMPONENT A				1	1		1			
PAGEND ECOL	SHCHC SYNTHA		191-101		1	1	1	1		Ī	
PACERA STRL!	PROBABLE HG TRANSPORT PROTEIN	CES LIVIDANS	139-160		1	1		Ī	I		
PLEIL BACSA	NEACURIC REDUCTASE				1	1		1		Ī	
PACERA STANU	MERCUNIC REDUCTASE			925.766	Ì		1	1			
PAREAR STAAU	MERCURIC RESISTANCE OPERON REG PROTEIN	AUREUS			Ì		1	1			
PAGETB ECOLI	CYSTATHIONING GALOLA-SYNTHASE		36-383		1	1		1			
PAGIC ECOLI	CYSTATHIONINE BETA-LYASE		65.3%		1		1				
PASETC SALTY	CHSTATHIONINE BETA-LYASE	німолом	2.29				1	1			
PAGE ECOLI	METHIONINE SYNTHASE		441.412					1	Ī		
PLIETH ECOL.	METHIONINE SY		371-398	642-676			1				
PASS CCOLL	TRANSCRIPTION		185-212								
PIGA ECOL	GAL ACTOSIDE-BINDING PROTEIN		62-19	312-310							
PAINC BACSU	EPTOM SITE DE		5.53 65.53					1			
PMIOC ECOLI	MIOC PROTEIN		67:170		1	1					
Phill CHLTR	KD MEMBRAN	CHLAMYDIA TRACHOMIATIS	61-13		1	1	1			T	
PMIP LEGMI	CTER MEMBRA			30.156		T	Ī	Ī			
TARSI ENTRY	CANA ADENING NAMED HATTIRANSPRASS	ENISACIONES PARCALIS	5		T			Ī			
Phil.S1 STANU	INA ADENINE		-	20-154			T		l		
PARLS2 COTTA	KNA ADERIME		3		Ī		Ī	Ī			
PMC SE BACSA	BOND ADENINE NAME IN LINEAR PROPERTY		=	120-154			Ī				
THE STORY	BUA ADENINE	NIAE	=	130-134	Ī						
PART STREAM	ANA ADENINE		4.81	120-154							
PAR.SC BACFA	UNA ADENINE		[9-4]								
PACKAGE METC	HETITANE MONC	CAPSULATUS	2.5			1	1				
PADAB ECOL	JOLYBD COFAC		92.30		1	1	1				
PACIBA THIFE	MOBA PROTEIN			9/2-162		Ī		1			
PMCMC_TRIFE	PHONG THIFE MODE PROTEIN		200		1	T	1	1			
PMOBD THUFE	MOBID PROTEIN	TRIOBACILLUS PERCUCAIDANS	7			T	T	T			
PAOS ECOLI	MOB PROTEIN				Ì	T	1				
PMOEA ECOLI	MOLYBOOPTERIN BIOSYNTHESIS MOEA PROTEIN	ESCHERICHIA COLI	243-270		T	T	T	T			
PMOP CLOPA	MOLYBDENIAL					Ī	Ī				
PMOP2 CLOPA	MOLYBDENUM-P	CLOSINGOM TASTECACATION	100	734 144		Ī	Ī	T			
PHOXY PANDE	GETHANOL UT	GILANS		10.00	367.30		T	Ì			
PAPEU SYPY	BILLIN BIOSYNTHESIS PROTEIN MOLEU	STANCHOCCOS ST	200	76.74		Ţ	Ì				
PACEV SYRPY	BILIN BIOSTNINESIS PROTEIN MEET	SECTION COL.	1717		Ī		Ī				
NO. C.	MARKA PROJECT	PACELLIS STREETH IS	8	247.241	Ī	T	Ī	Ì			
200	AND SHAPE DETERMINING PROTEIN MAEB	BACILLUS CEREUS	[[6-2]]								
PAGEC BACSU	PACIFIC BACSU ROD SHAPE DETERMINING PROTEIN MOLE		63-112								
PROUG KLEP	PACKE KLEPH CHAPERONE PROTEIN MOKE PRECURSOR	KLEBSTELLA PNEUMONIAL	161-332	П			1				
PACKE KLEPA	HOURC PROTEIN PRECURSOR			452-489	392-622			1			

PCGENE 1671786	P4071	Proharyatic Sequences	П	П		17		П	1 1	П	\prod
ELL NAME PROTEIN	NITH A PARTY OF CASE OF PARTY ASSOCIATION OF THE PARTY OF	ORGANISM ELEBEREL A BUELLADAIA B	7	1	48.42	4 1 1 1 1	7	A A A A A A A A A A A A A A A A A A A	V V	7 7 7	1
PHAKE KLEPY MOKI			193-220		T	l	Ť	T	T	Ī	
PHREA STRUY FIBRE	Ø	STREPTOCOCCUS PYOGENES	7-46	П		1 1		П	Н		
PHOTO STRSU MOR	MURAMIDASÉ-RÉLÉASED PROTEIN PRÉCURSOR	UIS	П		163-291	431-448 15	\$67.534	\$18-622 7	173.800	058-1015	
PHISBA ECOLI PROB	PROB ATP-BINDING TRANSPORT PROTEIN MSBA		2 2	2							
PHSKA STAEP ERYT	ERYTHROMYCIN RESISTANCE PROTEIN	EPIDERAIDIS	12.21	8.3			1		1		
PMSY'S ECOCI ACID	ACIDIC PROTEIN MSYB	ESCHENCIA COU	B)	13.14		†	Ť	1		Ī	
TATA ELUCI MOD	IPICATION METRASE ECON	SCHEMOTIN COL	т	N. C. P. L.	1	\dagger	Ì	1	1	Ţ	
PATAB ENGE MODE	MODIFICATION METHODS ACC		10.46	1	\dagger	\dagger	Ì	1			Ī
PUTAL BEEFF MOD	FICATION RETUYLATERE	IDERAIDIS	Ţ,	100.116	T	\mid		T	Ī	Ī	
PATE HELAU MODI	MITH HERALI MODIFICATION METHYLASE HGIBI		Т		T	t	T	T	T	Ī	
PMTB2 BACAM MOD	FICATION METHYLASE BANGII		35.62		t		Ì	T	T		Ī
PATEL BACAR MODI	ISICATION METHYLASE BANIII		186.2	T	T		Ì	T	Ī		
PMTBA BACAR MODI	IFICATION METHYLASE BANI		Г	383-409		t		-	Ī	T	
PHTBB BACSU MODI	IFICATION ACTUALASE BSUBI		Τ	467-496				l	l		
PMTBF BACSU MODI	PMTBF BACSU MODIFICATION METHYLASE BSUFI		Г			f	İ		Ī		
PMTCI CITTR MODI	FICATION NETHYLASE OF NEI		ě	20.55	252-279						
PMTCI_NEJCAU MODI	FICATION METHYLASE HGICI	TIACUS	130-147			\mid	T	İ	İ		
PMTC2 HERAU MODI	IFICATION METHYLASE HGICII	HEIDETOSIPHON AUTONATIACUS	110-182								
PMTEI ECOL! MOD!	FICATION METHYLASE ECON			145-172							
PMTEI HERAU MODI	FICATION METHYLASE HOLE!	URANTIACUS	281.308								
PMTE2 ECOLI MODI	MODIFICATION METHYLASE ECORU		3						I		
PAITES ECOLI MODII	FICATION METHYLASE ECORY		33-100								
PMTEC ENTCL MODE	MODIFICATION METHYLASE ECAL			П	П	П			П		
PMTF1 FLACK MODE	MODIFICATION METHYLASS FOX!	ITES		379-306	337-366	398-425 59	333-646				
PMTF1 FUSNU MODI	FICATION METHYLASE PRUDI	2	ş	Ì	1			1			
FALLS HARLA MODIL	MODIFICATION METHICASE NOAPS	HAEMOTHICUS UALLINAKUM	6		1	Ì	1	1	1	1	
PATHY METT MODULATION MET	MODULE AT THE PART OF THE LATER OF	MOROBANCICIES	707	27.50	†	\dagger	1	1	1	1	
PMTKI KLEPN MODII	MODIFICATION METHYLASE KPNI	Т	Т		t	\dagger	İ		T	Ī	
PINTLD STRWO MANY	VITOL-1-PHOSPHATE S-DEHYDAGGENASE	IS MUTANS	Т	124.231	349-176		T	T	T	Ī	
PHTMI MORSP MODII	MODIFICATION METHYLASE MISPI		Γ	20.4		İ	T	T			
PMTN3_NEILA MODIL	FICATION METHYLASS MLAIN	CA	П	183-210			r	T	Ī	Ī	
PMTP2 PROVU MODIS	MODIFICATION METHYLASE PVU II		304-335						ĺ		
	MEMBRANE.ASSOCIATED ATPASE	LDARIUS	9-67								
	MODIFICATION METHYLASE PSTI	JARTII	26.76								
7	TATPIOPHAN-SPECIFIC TRANSPORT PROTEIN	ESCHENCHIA COLI	Т	┑		1					
			561-61		600-643	1	1	†	1	1	
PMTS9 STAND	MODIFICATION METHYLASE SAUSS	S ATREUS	75	T	t	t	†		1	Ī	
	MANDIFICATION METHYLASE SCRFI.A		T	187.214	\dagger	t	T	Ť	1	Ī	T
PMTSB LACLC MODII	TLASE SCRITO	ACTIS	13-61	T	l	T	ļ	\dagger	T	Ī	
PMTSI SPISQ CPG D	ASE		118-230	156-290				l		l	T
PMTSM SERMA MODIL	MODIFICATION METHYLASE SMAI	45	91-119					l			
PMTT1 THETH MODE	MODIFICATION METHYLASE TTIGODS	AQUATICUS	\$ P								
PMTVI VIBSS MODI	MODIFICATION METITYLASE VSPI		13-66	_							
PMUKB ECOLI (MUKB PROTEIN	PROTEIN		120-381	1014-1048	1216-1252					П	
PAULI ERWAM MANU	R COLEA MEMBRANE LIFOTACIEIN FREE	ERWINIA AMYLOVOIA	× .		†	1	1	1			
THUL MUMO TO SE	A COLEA PERMINANG LINOTROLEGIA FAEC		ž.		-	1	1	1		_	-
PACE PROPERTY	M COLEA MEMBRONE LINOTALIEN PREL		Т		-	†	1				-
PACIFIC BASSO UST	DON'S E		Т	200	1	1	1		1		
PARTY ECOLI UDP-A	MUNNAC-PENTAPEPTIDE SYNTHETASE		60.73	\dagger	†	t	1	1	1	1	
PMURZ ECOLI ENOY	ENOYLPYRUVATE TRANSFERASE		392-419		T	t	T	\dagger	T	Ī	
1 .1	TRANSFERASE		392-419	T	T	t	t	t	T	Ī	T
PAUTA STRCM METH	L-COA MUTASE BETA-SYBUNIT	NENSIS	1.58	T	t	t	t	t	T	Ī	T
					l	1	1		1	1	

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	7.1.00	ORGANISM	I.	4		2					
	LILE CACHE CONTINUE ON THE CONTINUE ALPHA SUBUNIT	PROPIONIBACTERUM PREUDENREICHIII	368.378	1			ľ	1			
	A SECULL AND WINE OF VEOSYLASE	SALMONELLA TYPHIMURUM	373.180	1			1		\dagger	t	
ינום זערוג	THE PROPERTY OF THE PROPERTY O	STREPTOMYCES CINNAMONENSIS	481-508			1				T	
STATE STATE	STATES STATES AND ASSESSED TO SERVICE PROTECTION MATERIAL	ESCHERICITA COLI	2					-	+	t	l
מעור בנסכו	DAY MISTA OF BEARING MICH.	SALMONELLA TYPHINIUM	\$0.114			1	1	1	\dagger	\dagger	1
1016	TOTAL STATE	VIBRIO CHOLERAE	134-169			1				t	
TOTAL VIBER	THOUSEN MOTE BEATE BOOTEN ACITY	ESCHERICHIA COLI	119-153						1		
AUTS ECOLI	UNA MISMA ICH AETAN	STREPTORIYCES AMBOFACIENS	60-87				1		1	1	İ
MY 15,	MUTT STAM INCLINE PROJECT	PRELIDOMONAS ACEVALONII	341-368		٦				1	1	
LIVAA PSEKTV	COENZYME A NEDUCIASE	ETREPOCICION DATES	5-129	149-182	190-217	240-301					
4X_STRPY	NI-RELATED PROTEIN PRECURSOR	SINET CONCLUS TO SECURITION OF	100-152								
AYCO STRCI	MYCOLYSIN PRECURSOR	STREPTONYCES CACAUI								l	
AVEC VERSI	PALYEC YEARD INTECTION PRECURSOR	YEASINIA ENTEROCOLITICA				Ī				Ī	
4	MICOTINATE MUCLEOTIDE PYROPHOSPHOAYLASE	SALMONELLA TYPHIMUNUM	X	1						T	
	TANADA BECKE ATOR NADE	SALMONELLA TYPHINIUMURI	111.260							T	ļ
- V	LEANING TOWNS TO SECURITY OF THE PARTY OF TH	ESCHERICHIA COLI	115-102							1	
AUD ECOL	MACO ECOLI INACO PROTEINA	CLOSTRIDIUS PERFRINGENS	41.13	990-1017						1	
ACH CLOPE	HALURONOGLUL	February Col 1	19:153						-		
PNACK ECOLI	NAGR PROTEIN	ESCREPTION COC.	3	216.310	922.088						
ANY CLOSE	STALLDASE PRECL	CLOSTIUDIOM SEPTICUM		Т							
VANA CLOSO	PHANN CLOSO ISIALIDASE PRECURSOR	CLOSTRUDIUM SORDELLII	5						İ	Ī	
VY IAN UNALES	AL IDASE	SALMONELLA TYPHINUMUNI	716-042						ľ	T	
200	ALL CALLES A NOT INC.		16-130							Ì	
Y EN IN			386-420								
MAKO ECOLI	MESPIRATURY PIL		76.10)							1	Ì
HARL ECOLI	REGULATOR PRO	Cache Court Court	155.180								
PNAM ECOLI	REGULATOR PROT	ESCREDICTION COL	110.343	140.114	431.458	\$65.538			l		
PHAILX ECOLI		ESCHEMUNIA COLI									
MINA AVON	BETA-11->2)GLUCAN EXPORT PROTEIN &	MHIZOBIUM MELILUTI								Ī	
VIEW STRUK	NEOMYCON RESIS	STREPTOMYCES CYANOGENUS	100						t	Ī	
VECTA FCOL	ACYLINEURALIMATE CYTION WITHANSFERASE	ESCHENCHIA COLI	787	2						T	١
MEA ECOL	NA ADSORPTION	ESCHENICHIA COLI	1000						T	Ī	
NAME OF COLUMN	NA ABSORPTION	ESCHENICHIA COLI							ľ		
NEAC ECOL	Ne ADSOND TION	ESCHERICHIA COLI							Ī		
PNFSI ENTCL	NAD(P)H NITROREDUCTASE	ENTEROBACTER CLUACA!	2 20						T		
MHAA ECOLI	4A(+)/H(+) ANT IP	ESCHENCIA COLI	191116								
MILE ECOL	AK+YAK+) ANTIP	ESCRENCHIA COCI									
PINIAB PSECL	NITICLE HYDRATASE SUBUNIT BETA	PSEUDOMORAS CHUORORATIIS	10.14								
NOW TEN	HIGH HIGH HITRIE HYDRATASE SUBUNIT BETA	MODOCOCCUS INFORMACIANOUS									
HIFA AZOBR	NIF.SPECIFIC REGULATORY PROTEIN	AZOSPINILLUM BRASILENSE									
PNIFA BRAJA	NIF-SPECIFIC REGULATORY PROTEIN	BRAD TRUIL CBION JAPONICON		105.501	137.75						
NIFA HERSE	NIF.SPECIFIC REC	HERDASHALLUM SERON TOLAN							ļ		
NITA NILLE	NIF.SPECIFIC NEC	RHIZOBIUM LECUMINUSAKURI									
PNIFA RHIME	NIF SPECIFIC RECULATORY PROTEIN	CHIZOGIUM MELILOII							Ì		
PHIFA RIPOCA	_	AHODOBACTER CAPSULATUS	187-Duz						T	Ī	
NIFR AZOVI	NIFB PROTEIN	AZOTOBACTER VINELANDII	A01-761						İ	Ī	
PATER KLEPN	NIFB PROTEIN	KLEBSIELLA PNEUMONIAE							1	I	
PAIRD ANASP	NITROG MOLYBD	ANABAENA SP	374-401						T		
PATED AZORE	1	AZOSPINILLUM BRASILENSE	111-404						T		
ON HERO	NITROG MOLYBO	PLECTONEMA BORYANUN	117-414								
PATE OF THE PERSON	-	THIODACILLUS FEAROOXIDANS	363-410								
Sales Cally	BIORYNTHESIS	CLOSTAIDIUM PASTEUTUANUM	359-386								ł
AND THE	MTROCKNASE	FRANKIA SP	1995							1	-
100	WITE COPINASE IRON PROTEIN	PLECTONEMA BORYANDA	267-294		-						
17001	KITTOO MOLYBD-IRON PROTEIN	AZOSPINILLUM BRASILENSE	430457							Ī	
1100 200	NETROG MOLYBD-IKON PROTEIN	BRADYRHIZOBIUM JAPONICUM	43.510								
PARTE NO. ASP	NITROG MOLYBO-INON PROTEIN	BILADYIUIZOBIUM SP	476.503						1	-	
PHIFK CLOPA	NITROG MOLYBI	CLOSTNDIUM PASTEURIANUM	2.2					1			
PNIFK THIFE		THIOBACILLUS FERROOXIDANS	675.98								
									•		

PCLINE	11674.13844	Problements Conserved		-		-	-	-		
FILE MANIE	PROTEIN		AREALA	AREA 1	AREAL	AREA	AREA & AREA &	A 6 AREA	AREAI	ARCA 9
PHIFN BRUDA	BIOSYNTHESIS PROTEIN NIFN	BIUM IAPONICUM	П						Ι	
PNIFS ANASP	NIFS PROTEIN		112-139							
PMFS LACDE	INIFS PROTEIN HOMOUNG	CKI	\$0.16							
FNIFT AZOVI	NIFT PROTEIN	t Vinel ANDII	A-33							
PRIFU ANASL	NIFU PROTEIN		6.0				-			
PNIFU ANASP	NITO PROTEIN	ANADAENA SP	146:178	1		1	1	-		
PNIED KLEPH	MIPU PROTEIN		66.60	200, 925		+	1	-		
PANIE POOL	CALL TAGLES NAME TRECORSOR		Т	Т	130-45)	+	1			
MINE ECOL	AND THOUSEN AIME		53			\dagger	+	1		
			Ī,	7/1-62			$\frac{1}{1}$			
THE COLUMN	INIAC PADIEIN		M(2:212	1	1		$\frac{1}{1}$			
PNIKS PSEST	PRECURSO		Т	┪	╗			-		
VIIS LACLA	III7 KD MEMBKANE ASSOCIATED PROTEIN			_	663-697	216-920				
PNISC LACIA	MISIN BIOSTNEHESIS PROTEIN MISC		٦	7						
NIST CACLA	NISIN TRANSPORT PROTEIN NIST		П	╗	426.470					
INIVA CLOPA	KOMOCI I KATE STATINASE, ALPRA SUBURIT	CLOSTUDIUM PASTEURANUM	_	╗	_			-		
PRIVO CLOPA	SOMOCITICATE STATINASE, OMEGA SUBUNIT		1	<u>.</u>	Ì	31.310	1			
יישיר ביים	CAN TRUE IN MACHINES			96-69	335-362	1	1			
PROOF BRASS	ODULATION PROTEIN C	M SP	3.30	1	1					
PRODUCE RELIE	OUULATION PROTEIN L		210-313	1						
PRODE NIIL	NODOLATION PROTEIN C		7	1		+	-		_	
אינור אינורא	GOULATION PROTEIN	OSARUNI	= = = = = = = = = = = = = = = = = = = =							
TYOO TO	ACCULATION PROJECT		9.60	1	1			+		
NODG KHOME	VODULATION PROTEIN G		<u> </u>							
PNODO INTINES	COULATION PROTEIN G		5.5							
PNODC AHILY	GOOD ATION PROTEIN L	7	36-53							
PNODO AZOBR	CODULATION PROTEIN O		7	П			-			
PNODI KHILT	ADDULATION PROFEIN T		╗	П	430-454					
PNOD1 PHILY	WOOULATION PROFEIN T	IMIZOBIUM LEGUMINOSARUNI	╗	416-443	1					
MODU KHIJA	COULATION PROTEIN U		┪		1					
A004	COULTION FROIEIN V	BRADTRILLEUBIUM JATONICUMI	7	739-766		1				
A PORT	COUCH LONG FROITING		171-139	+	1	+				
PNOUS KLING	COULATION PROTEIN NOLA	III	21.6	\dagger	†	+	1		1	
PNOSD PSEST	KOSD PROTEIN PRECURSOR		1		1	†	+	+		
PNOSR PSEST	ROTEIN NOSA		13.154	\mid	\dagger	$\frac{1}{1}$	1			
PNOS PREAF	REDUCTASE PRICINSOL	N.A	167.704		<u> </u>			-		
PNOSZ PSEST	MIRCHES CONTRIBUTE I AND PRICCESSOR		143.591			:		<u> </u>		-
	BACILLOLYSIN PRECURSOR	JEFACIENS	113-147 21	217.244			-			
PNPAE BACPO	BACILLOLYSIN PRECURSOR	KA	П	187-226	_					
FRME BACSU	BACILLOLYSIN PRECURSOR		ş	307.334						
	WALK-USIQUINGNE CALLANEEUCTASS 21 KD CHAI		-	i		i	i			
LINE STATE	ANALIS ELECTRIC SECTION BELIEVE AND	SECTION AND AND AND AND AND AND AND AND AND AN			-	<u> </u>	+	1		
PNVA ECOL	CYTOCHROME CSS2 PRECURSOR		110.166	İ	t		+			
PNYG ECOL	NAJO PROTEIN		13:111	\dagger	1	$\frac{1}{1}$	+	+	\prod	
PHALL AHONH	ALIPHATIC MITULASE	ODOCIROUS	96:50	\dagger	\dagger	+	1	+	1	
PHSA LACLA	NISIN RESISTANCE PROTEIN		t	15.162	\dagger		 		1	
PHICA ANASP	THA-BINDING PROTEIN VFI		Ť		T		1	<u> </u> -		
PHICA SYAPT	CLOBAL NITROGEN REGULATOR	SYNECHOCOCCUS SP	14.91	\dagger	F	+	+			I
PHTCA SYRY)	GLOBAL HITROGEN REGULATOR	YNECHOCYSTIS SP	67.94		-	l	ļ			
PHYTHE VIE L	MITROGEN REGULATION PROTEIN NTRB	TBRIO ALGINOLYTICUS	£ 23	\mid	t	-	+			-
PMRC PROVI	NITROGEN REGULATION PROTEIN NR	ROTEUS VALGARIS	115-412			-		-		Ī
PATRC NILVE	NITROGEN ASSIMILATION REGULATORY PROTEIN IN	HIZOBIUM MELILOTI	451-476							
PRUZE SYRF	PRUZE SYNEY NACH-PLASICQUINGNE OXIDOREDUCTASE CHAIN IS	YNECHOCOCCUS SP	10-107				Ц			
CANA JAMA	NAME ASTOCINOSE OXIDORED POR SECURIOR SECRETARION SENTECTION SE	WECHOCOCIIS OF	27.34	1	+	1	+			
				1	1	$\left \right $		-		
							•			

П	1071/7614	Penharyatis Sequences	Т	AREAL	AREAJ	ABGA	AREA 3	ABEA	AREAT	ABEAI	3
	PROTEIN	CONTROL SELECTION OF THE CONTROL OF	163-190			1					
PNUJC SYNY3	PROB NADK-UBIG	SVAECHOCYSTIS SP	169-190								
PHUKC SYNY3	PROB NADM UBIO	CYNECHOCYSTIS SP	46-40								
ž	NADH-PLASTOQUI	FCNERICINA COLI	168-402								
2	NADH DEHYDROGENASE I CHAIN	F CCISE LICITA COLI	30.57	496-52)							
	NADIS DESTURIOR NASE I CITATION	E STUBBLICHIA COLI	919-266					1			
MON ECO!	NADH DEHYDROGENASE I CITAIN N	ECCIFFICITY COLI	17:11	134.164	156.153						
ECOT.	MUCLEOTIDE PERMIEASE	ESCUEDINA COLI	11.62								
ECOLI	IUSA PROTEIN	Cache Street Court	13.65	10.97							
ECOLI	NUTICIZATION SUBSTANCE PROTEIN B		14.14								
17023	TRANSCRIPTION ANTITERMINATION PROTEIN MUS										
41164.4	TRANSCRIPTION ANTITERNINATION PROTEIN MUS		27.10			Ī					
1	A AVIOLOGICA AND A P. DINGE HYDROLASE		23.20								
TOTAL PARTY		PLAVOBACTERIUM SP	123-250								
	PANICAL MARINES	BACILLUS CEREUS	101-111								
POIGG BACCE	OCIGO LACACOSTIANA	ACHODA PIERICAL TUNE FACILIES	172-202								
ACA 16	OCTOPINE - DENDING	TOTAL STATE OF THE PARTY OF THE	139.156								
POLICI AZOVI	1.OXOGR. UTAILATE	ACCIONAL IER VINCEASSIII	15	000.000							L
PODO! BACSU	1-DXOCLUTARATE DEHYDROGENASE EI CONDONE	BACILLUS SUITTLES									
200		ESCHEIUCHIA COL!									L
	NACE INCOME	BACILLUS SUBTILIS	30.5								
	TO THE PARTY OF TH	PSEUDOMONAS PUTIDA	223-254								
ODOB PSEN	7-0X0X01	ESCRIBILITIA COLI	624.651								
200	PYRUVA IE DEILY	APOTOGACTER VINELANINI	\$18.545								
202	HIYDROLIFOAN	ESCUENCIA COL	1771	117-144							
200	MHYDROLIPOAM	ENCHANGE OF A DATE BUILDING ITS	200.111								
A BACST	VALUVATE DEMY	BALILLUS SI EAROTHERANCE	211.301						L		
POOPA BACSU	VALVATE DEHYDROGENASE EI COMPO	BACILLUS SUBTILLS	9						L		L
PODPE BACST	YRUVATE DEHY	BACILLUS STEAKOTHERNIOPHILUS									
2	YELIVATE DEHYDROGENASE EL COMPO	BACILLUS SUBTILIS	0								L
1 PU 8	SKDCYSTERE	CHLANYDIA TILACHONIATIS	3								
	WITTER ACELINA	KEISSERIA GONDRUI IDEAE	8								ļ
	CHITE LIEVING AND PROTEIN PLA PRECUISOR	MEISSERUA MENINGITIDIS	350-386								
TONA PERME	TOTALE SPECIAL AND PROTEIN PLA PRECUASOR	NEISSERIA MENINCITIDIS	333.380								1
100	ATTEN APPLIANT PROTEIN P IS PRECURSOR	NEISSERJA GONORNIOEAE	163.90								
SCHOOL NEWS	ATTER LANGE ANY SECTION PIR PRECUESOR	NEISSEN A MENINGITIDIS	63.90								
	CONTRACTOR AND DESCRIPTION OF PRESCRIPTION	NEISSERIA CONORCHOEAE	61-90								1
Salar Media	NAMES AND AND PROPERTY PIR PRECUISOR	NEISSEAJA MENINGITIDIS	63-90								
N. LIME	COLENATION OF PROPERTY PIR PRECINCOL	NEISSERIA MENINGITIDIS	99.69								
SAIB) PEINE	COLER MEMBER	NEISSERIA MENINCITIDIS	14-51	63.90							
POPER MEINE		INSISSERIA LACTAMICA	1	L							
	OUTER MEMORA	NEISSERIA SICCA	5.0	6).80							
	OUI EA MENIBRA	A PTINGRACILLUS PLEUROPNEUNONIAE	114-131	L							
אלטאן אלוור	OUTER MENIBUA	LA ENDOUGH OF INSTITENZAS	134-184	101.10	341-368						
PONPI HAEIN	OUTER MEMBIRA	LA EL LOSTITITION DE LE LA EL LE LA EL LA	16-31	220-234	136-155		L			L	
PONITI HAEIN	OUTER MEMBAA	DESCRIPTA CONDEDITORAE	7.7				L	L			
PORUS NIJEO	XITER MEMBER	PERMITTER OFFICE ATTRETTS	61.80								L
PONIE STANU	N KD OUTER ME	STATES OF THE ST	100-138	121.12	11).349	155.192	301.328	351-385	L	L	
1 TEX	A OUTER MEMBRANE PROTEIN ALPHA PRECURSOR	INERCACIONA MANCIEMA		3							L
DONE FOOL	DUTER MEMBRANE PROTEIN C PRECURSOR	ESCHERCIA COLI	1					L			L
POATPC NEIGO	OUTER MEMBRA	NEISSELLA COMONORAE								L	L
POACH SALTI	г	SALMONELLA TYPHI			ļ				ļ		ŀ
Ö	CULTIN MISMINIANI PROTISIN F PRECURSOR	ESCHERICHIA COLI	2							ļ	ţ
SSET PAPER	OMPH PROTEIN	PHOTOBACTENUM SP						ļ		1	
0	PROTEKSE VII P	ESCHEALCHRA COLI	3					1	\downarrow		ļ
	OPACITY PROTE	NEISSENIA CONORUIOEAE	=			ļ		1	\downarrow		
S S	OPACITY PROTE	NEISSERIA GONORBHOEAE	8								\downarrow
NOPAL MEICO	OPACITY PROTE	HEISSENIA GONORAHOEAE	71-12						1		ļ
SKID		NEISSERJA GONGUCIOEAE					\downarrow		ļ		ļ
DOIN IVEOR		NEISSEALA CONORAHORAE					1	ļ	ļ	ļ	
	1										

PCCINE	1007-178-4	Proharyedic Sequences								
FILE NAME	PROTEIN	ORGANISAI	17380	AREAZ	7757	AREA	<u> </u>	AREA AREA!	1 AREA 8	AREAS
POPAK NEIGO	OPACITY PROTEIN OPASS	NEISSERIA CONORTHOEAE	-103		1	1		-		
POPDA ECOLI	OLICOPEPTIDASE A	ESCHENCIIIA COLI	2							
POPDA SALTY	DLIGOPEPTIDAS	SALMONELLA TYPHINURIUM	2						1	
POPDE PSEAE	TRANSCILLPTION	PSEUDOMONAS AERŪGINOSA	<u>2</u>				1	1		
POPPA ECOLI	OLICOPEPTIDE-B	ESCHENCHIA COLI	~ Ç							
POPPB SALTY	OCICOPEPTIDE P	SALMONELLA TYPHILIUMURI	4							
	OPACITY RELATED PROTEIN POPMI	NEISSERUA MENINGITIDIS				Ì	1	1	1	
S NEW	OPACITY-RELAT	NEISSERIA MENINGITIDIS				1	\dagger			
POSNIC ECOL!	OSMOTICALLY B	ESCHEATCHIA COLI	7		171	166 165				Ī
NOSYA BONED	OUTER SUIPACE PROTEIN A PRECUASOR	BURGELIA BURGUOLIERI	3	1	57.1		İ			
POSPB BOXEU	OUTER SURFACE	BURGETIA BURGOOK EU	Č.	8,770			1			Ī
POTCE BACSU	DRINTHINE CAU	BACILLUS SUBTILLIS	1					1		
POTCC PSEAE	OWN THE CASE	PSEUDOMONAS AEKUUINUSA	*				1		1	
POTCC PSERU	ORNITHINE CARBAMOYL FILANSFERASE	PSEUDOMONAS PUTIDA	-				1	1		
POUTB BACSU	SPORE CUTCROWTH FACTOR B	BACILLUS SUBTILLS	228-222				1			
POUTO EXWCA	LEADER PEPTIDASE	EXWINIA CARGTOVORA	9.310				1			
PPICK STUDA	IN KD PROTEIN IN PLWA 1 REGION	STREPTOCOCCUS PARASANGUIS	13:149]
PPISK STRSA	IN KB PROTEIN IN SSAB TREGION	STREPTOCOCCUS SANGUIS	2	₹ 2]
יייי נאמני	PI.TYPE PROTEINASE PRECURSOR	Lacrococcus Lacris	107-155	- 1	023-1130	0521-622	1466-1496	1625-1655		ightharpoonup
PPZ6 MYCHOL	PROTEIN P29	MYCOPLASMA HYORHINIS	ž	- Į	202-246					
1	PII. TYPE PROTEINASE PRECURSOR	LACTOCOCCUS LACTIS	3.	_[1073-1130	1223-1250	967 937	1675.1680		
7.5 CC	PII.TYPE PROTEINASE PRECURSOR	[LACTOBACILLUS PARACASEI	107-155	904.941	103. 103	1223-1250	1466-1496	1621-1655		
	PJO PROTEIN	ESCHERICHIA COLI	59-03							
ı	PROTEIN PA	NCKETTSIA NCKETTSII	626	(a)-sed						
PP3 MYCHR	PROTEIN PJ7 PRECURSOR	MYCOPLASMA HYORHINIS	11.13							
	PHILTIPE PROTEINASE PRECURSOR	LACTOCOCCUS LACTIS	167.155	056-106	0011-1/01	0821-[22]	1223-1230 1446-1496 1628-1655	628-1655		
	43 KD PROTEIN	PSEUDOMONAS CHLORORAPHIS	316-315				_			
PPS4 ENTEC		ENTEROCOCCUS PAECIUM	\$1.03	141-209			_	_		
PP60 LISGA	PACTEIN P46 PRECURSON	LISTENA GRAY!	9	101-142	300.334	2 72				
PP60 LISTN	PROTEIN P60 PRECURSOR	LISTENIA IMMOCUA	67.04	102-143			1	-		
PP60 LISTV	PROTEIN PSO PRECURSOR	LISTEILA IVANOVII	2	2						
PP0 LISMO	PROTEIN PSO PRECURSOR	LISTERIA MONOCTIONENES		101, 414	77.	\$17,791		+	1	T
7760 LISSE	PROTEIN PROTUCCURSON	LISTENA SECTIOEN		17.61	104.491			+		Ī
1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	3	MACOUNT ACCOUNTS	364.30		11.617		\dagger	+		I
100	A PART COUNTY OF	BACH LIKE EIGHT IS					T	+		
TABA BACSO	ALC STRUMASE	BACILLOS CIRCOS	100				İ	-		
TABLE BACSU	- AMINO 4 DEGA	ESCULECCE SUCCESSION OF THE POST OF THE PO	. 4				1	+	-	Ţ
TABLE ELOC	PACTERIAL	CTREPTONIYCES CRISELIS	23.78				T	-	 	
AT A TANK	PENCH I'M ACYLASE PRECIDEOR	ARTHUROBACTER VISCOSUS	136.19	197:161	571.606	640.674				
PPAC RACE	PENICEL IN ACY	BACILLUS SPHAERICUS	233-259				-			
PPAC STRAN	AC PROTEIN PR	STREPTOCOCCUS MUTANS	146.276	201-465	331.565	376-610	1075-1102	1139-1166 1381-1434	1434	
PPAIL BACSU	LEGULATORY	BACALUS SUBTILIS	101-137	L						
PAID BACSU	REGULATORY PROTEIN PAI 1	BACILLUS SUBTILIS	145-172							
PANE ECOU	FINGRIAL PROTEIN PAPE	ESCIENCHIA COLI	69-21	186-123						
PANE ECOLI	MINOR FINDRALA	ESCHERICHIA COLI	16.31							
PANG ECOLI	PINGSUAL PROTEIN PAPG PRECURSOR	ESCHENCHIA COLI	262-316							
PPARA AGRIU	PAKA PROTEIN	ACROBACTERUM TUMEFACIENS	19-09						_ :: 	
PPARS ECOLI	TITAL CINEAL	ESCHENICHIA COLI	117.154	349-313						1.1
PANE ECOLI	TOPOISONGLASE	ESCHENCHIA COLI	444-471	326-353				-		1
PAUE SALTY	TOPOISOMELASE IV SUBUNIT B	SALMONELLA TYPHIMURIUM	2447	536-553		п			_	
PPA BACA	PROTECTIVE ANTIGEN PRECURSOR	BACILLUS ANTIRACIS	11.53	135-152	196-315	\$19-515	P19-059			
PPBP1 ECDLI	PEMICILLIN-BINDING PROTEIN 3	ESCHENCIA COLI	95-133	176-205	101-241			I		
PPBP2 NEICO	PENICILLIN-BINDING PROTEIN 2	NEISSERIA GONORAHOEAE	97.73							
PBP2 NEIME	PENICILLIN-BINDING PROTEIN 2	NEISSEILA MENINGITIDIS	2				1		1	
	PENCILLIN-BINDING PROTEIN 28	STALF TOCOCCUS PREUMORIAE			20.4.2	200	1	1		
PPBP) ECOLI	PEMICILLIN-BINDING PROJECT) PRECURACE	ESCRENCHIA COLI	107-277	370-300			1	1	-]

PCGENE	107177814	Probaryatic Sequences	П			40.00	4.00.4	40646	40149	14.4	. 7.40
FILENAME	PROTEIN	ORGANISM					т	Т	1	Т	
PPBP4 BACSU	PENICILL IN-BINDI		134.363			-		T	Ī		
PRBM ECOL	PENICEL IN BIND		145.172			t	-	T			
PPBPA ECOLI	PENCILLINGUAD		Ï	263.200	-						
NAME ECO.		STEERSTOCOCCIS BAR (BLOCIA)		104-735		-					
7 3 10 L	PERSONAL PROPERTY.	STAPHYL OCOCCUS AUREUS	76-106	176-203 120	263-324 50	\$02.529					
TO STAND	CACI AIGNAERAS	PSETIDOMONAS PUTIDA	115.142 2	226-253			_				
PEC I TOWAY	DECTATE I VACE III PRECIUESOR		110-137								
PPEL CRACA	PECTABLI VASE A PRECURSOR	ERWINIA CAROTOVORA	110-137								
POET B EBWCA	205111388 2547 1847 196 417 1848 1848	ERWINIA CAROTOVORA	10:13								
ADEL CERWICA	PECTATE LYASE C PRECURSOR		ĭ				1	Ī			
NAME OF STREET	PECTATE LYASE E PRECURSOR	ERWINIA CHRYSANTHENII	40.67	109-243				1			
PPEIDENCA	PERIPLASMIC PECTATE LYASE PRECURSOR		287-557		-						
26127 4 1344	PFRIPLASMIC PECTATE LYASE PRECURSOR	YERSINIA PSEUDOTUBERCULOSIS	439-489								
PPELX FINCA	PUTATIVE PECTATE LYASE X PRECURSOR	ERWINIA CAROTOVORA	812-881								
HOMEN X ENWINE	PPELY ENWINE EXORDLYGALACTURONATE LYASE PAECURSOR	ERWINIA CHRYSANTIENI	466-493	-				1	1		
Despired to	AMINOACYT. MISTIDINE DIPEPTIDASE	ESCIENCIA COLI	364.314			_					
DESCRIPTION OF STREET	X.Bech Dipeptina	ESCHENICHIA COLI	121-152								
TOPE A SECOND	PERTACTIN PERCIT SOR	BOADETELLA BRONCHISEPTICA	617-644				-				
PPERT BORDA	PERTACTOR PRECURSOR	BORDETELLA PARAPERTUSSIS	618-655								
PPERT ROSPE	PERTACTIV PRECINSOR		616-643								
PACK COACE	т-	CORYNEBACTERUM GLUTMICUM	111.00								
PCK FCOL	PHOSPHOG: YCE	ESCHENICHIA COLI	912-981								
PACK LIFTER	PHOSPHOG! YOUR	METHANOBACTERSUM BRYANTS	16-61								
POR THERE	т	THENUAUS AQUATICUS	333-249								
A WCA	FNDO-POLYGAL	ERWINIA CAROTOVORA	117.291								
PPOTE SALTY	CHITTER MENDRA	SALMONELLA TYPHUMUNI	16-99						1		
PHAI FIED	C-PHYCOCYANIN	FREMYELLA DIPLOSIPHON	21-41						7		
PPHAS FREDI	C-PHYCOCYAMIN	FREMYELLA DIPLOSIPHON	21-48				1		1		
PPHAN PSEOU	POLY() HYDROXYALK ANDATE) POLYMEJASE I	PSEUDOMONAS OLEOVORANS	2	1		1			7		
PPHAB ANACY	LLOPHYCOCYA	ANABAENA CYLINDRICA	•	T		1	1				
PPHAB ANAV	LLOPHYCOCYA	ANABAENA VAIDABILIS		1			\dagger	1	1		
PPHAB FREDI	ALLOPHYCOCYANIN BETA CHAIN	PREMITELLA DIPLUSIFICA		T	†	t	T		T		
PPHAB MASIL	ALLOPHYCOCYANIN BETA CHAIN	MASTIGOCLADUS LAMINUSUS		1	Ì	\dagger	T	Ī	T		
PHAS SYNT	PPHAB SYNNA ALLOPHYCOCYANIN BETA CHAIN	STARCHOCOCCUS ST	91	T	\dagger	\dagger	T	Ī	T		
PHIAC SYMP	ALLOPHYCOCTANIN ALPHA-B CIALIN	TEREVOET A PURI ORIGINA	350	T	t	t	T	T	Ī		
PPIAG FIED	ALIOMITCUCTANIA GAMMA CHAIR	SEGMENT A DISTORDANCE	9	T	1	T	T	Ī			
1000	A CONTRACTOR I AND A CONTRACTOR AND A CO	ALCALIGENES EUTROPHUS	52-25	İ							
TANKS VINE	CAHYCOCYAND	SYNECHOCYSTIS SP	\$.				<u> </u>				L
PHCR SYDE	C.PHYCOCYANIN	SYNECHOCOCCUS SP	21-55								
PPICB SYNT	C.PHYCOCYANIN	SYNECHOCOCCUS 3P	11-35								
PPHCB_SYNY!	C.PHYCOCYANIN	SYNECHOCYSTIS SP	<u> </u>		1						
PPIEA ECOCI	CHONISMATE M	ESCHERICHIA COLI	٦	7		1					
PPHEA ERWH	E CHONSWATE MUTASE	ERWINIA HEMBICOLA	٦	7	252-2116	1					
PMEA PSESP	PREMOC 2-MONDOXYGENASE	PSELIDOMONAS SP	_	20.5	437-464						
PPIEB MASLA	PHYCOERYTHOLO	MASTIGOCLADUS LAMINOSUS	₹			1	1				
PPIEB PSESP	CATECHOL 1,2-DIOXYGENASE	PSEUDOMONAS SP	<u>~</u>				1				
PPHEC SYNP	LINKER POLYPE	SYNECHOCOCCUS SP	21.15								1
PPHEP ECC. 1	PHENYLALANDIE-SPECIFIC PERMEASE	ESCHEALCHIA COLI	<u> </u>		-		1	1		1	-
PHIBI CLOSA	PEREDITY SINGE (PE	CLOSTILIDIUM PASTEUNIANUNI	Ş			1		1	1		
PHILL BACK	SPHINGOMPTELIN	BACILLUS CEREUS	2.36								
PPHEL BACKE	S PHUNGOMYEL IN	BACILLUS CEREUS	9								
PPIG.3 BACCE	SHEROOMYELD	BACILLUS CEREUS	1		l	1	1	1			
PPHIC BACCE	PHOSPHOLD ASE	GACILLUS CENEUS	A 15	34.346	İ	1	\dagger		Ī		
PHEC CLOS	PHOSPHOLIPASE	CLUSTINDIAM BITEAMEN LANS		140.100	1	1	1		Ī		
PPH.C CLOPE	7	CLOS I MOVEM TEN AND CARS	1			1					

PCGENE	1107217014	Prokaryothe Sequences								Γ
FILLPAME	LROILIN	ORGANISAL	J	AREA1 AREA1		AREA AREAS AREAS		ABEA? AB	IV IVIEV	AREAS
PPAC LISMO	PHOSPHOLIPASE		67-174				1		+	
PPIC PSEAE	HEMOL YTIC PHO	\ \	71/40	1	 		1		1	Ī
PPIC STAND	PHOSPHOLIPASE	SAUREUS	17.		+		1	1	1	T
삐	PHOSPHOLIPASE								1	1
- 1	SPHINGOMYELINASE C PRECURSOR	LEPTOSPILA INTERCOGANS	7	270-26	+	1	1	+	+	1
PPHIND ECOL.	PHIND PROTEIN	ESCHEMICKIA COLI	976-047	1		1	1		\dagger	T
L L	PIIME PROTEIN	ESCHERICHIA COCI		1	+	1	İ	+	\dagger	Ī
PPINM ECOLI	PHINM PROTEIN	ESCHENCINA COCI	86.5				1	+	+	Ī
THIS CHAR	OUTER PREMISEA		T	T	Т	1	Ť	\dagger	+	T
PPIOE ECOLI	OUTER MENBACHE PORE PROJEIN E PRECURSOR		Ī	104-10	7,077	1	1		1	T
PPHOE KLEOX	OUTER MEMBER		1				1		1	1
PHOE KLEY	OCTER MEMBRA		┪	6			1	\dagger		1
PPHOE SALTY	OUTER MEMBRA	INIURUM	╗	120-347						
PPHOP BACSU	ALK PHOS SYAT		115-219				_			
PPHOQ ECOLI	SENSOR PROTEIN		144-278	_		1				
PPHOO SALTY	VIRULENCE SEN	HATURIUM	9	_	-			-		
PPHON BACSU	ALK PHOS SYNT	8	19.145 337	327-425				-		
PPHOTA ECOLI	PHOTOREPAIR PI		63.90 207	207.241	-			-	l	
L	A.PHYCOCYAND	SYNECHOCOCCUS SP	10-02	_					ŀ	
PPHIRA SYMPZ	R-PHYCOCYANIN		10-01	-				l		
PPHSO ECOU	OLYCOCEN PHOS		157.184 488	418-515			 	-	l	Ī
	MALTODEXTRUM PHOSPHORYLASE	ESCHERICHIA COLI	11:10							
PPILA NEIGO	PROB SIGNAL RECOGNITION PARTICLE PROTEIN	NEISSENA GONORRHOEAE	39.6					-		
PPILB PSEAE	FINGRIAL ASSENDLY PROTEIN PILB	PSEUDONIONAS AERUGINOSA	09-91	_	_					
PPILC PSEAE	PILC PROTEIN	VS.	143-170					-	ŀ	
PPILD NEICO	LEADER PEPTIDASE		110-137	_				-		
PILO PSEAE	FINDRIAL ASSEMILY PROTEIN PILO PRECURSOR		Г	939-669				-	-	
PPILS PSEAE	SENSOR PROTEIN PILS		9-46					-	L	
i	PI PROTEIN							-		
PPIV MORBO	PILIN GENE INVERTING PROTEIN (Н	152-182		1			_	
	PILIN CENE INVENTING PROTEIN	NATA	152-182							
PLC BACCE	PHOSPHODIESTERASE PRECURSOR		317-245	+						
PILC BACTU	PHOSPHODIESTERASE PRECURSOR		216-245							
PLC LISKO	PHOSPHODIESTERASE PRECURSOR	LISTERIA MONOCYTOCENES	116-205			1		1		1
200	ALTE KANSPERASE		201	$\frac{1}{1}$	+		1	+	†	
יייייייייייייייייייייייייייייייייייייי	PECTUAL CARE		21 21 12	+	 		1	$\frac{1}{1}$	1	
PACE ECO	PECTIN CTASE		76.77	1		1	†		\dagger	T
TUNE LOS	PECTAGESTERASE PRECINSOR	4731Eh13	60.13				Ì		\dagger	T
PPLICY ECOL	PHOSPHOGL YCE		\$2.116					t	t	Ī
PPAGY ZYNOM	PHOSPHOGL YCE	11.15	Г	10110		ļ	t	t	\dagger	T
PPNP ECOLI	POLYRIBONUC NUCLEOTIDYLTRANSE		360-394	_					t	Ī
PFNIK SALTY	PASK: PROJEIN	JA!	174-205			;	-	:	!	i
PPODK DACSY	PYRUVATEORTI		11:16						-	
POOU PSESY	OUTER MEMBRA		11.13		_					
PPORO PSEAE	PORIN O PRECU			╗					Н	
PPORT PSEAL		RUGINOSA	П	260-217 169-196	و			_	Н	
POTO ECOL	DENDING PROTEIN PRECURSOR	ESCUERICHIA CO.I	200	1	+	†	1			
									1	
POXE EC			Т							
DY B	ALKALING PHOSPHATASE III PRECURSOR		I	97-160						-
200		BACILLOS SUBILLIS	Т	136-36)		1		+	1	
TO SECURE	ALKALINE PROCESSATIAN PARTITIONS	TIEONIE	707-667		+	1	1	1	1	1
POPUL STANE	PROLYT ENDOPERING AS PRECIMEN		13.100	1	+	1	1	+	+	
PPCF FLAME	PROUYL ENDOPE	FLAVOBACTÉRIUM MENINGOSEPTICUM	138-199 254	156-283	-		t	\dagger	†	T
PPCK ECOLI	PHOSPHOENOLP		Т			1	I	$\frac{1}{1}$	t	T
									1]

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	PROTEIN	CLOSTADIUM PENTUNGENS		Π						
1			49.76							
PPPSA ECOLI	PHOSPHOENOLY I	TER CALCOACETICUS	40-34				-			
אכונץ	TALL SHIPS DESKINGENT PROTER OF PRECURSOR		191.191			1				
PPECA ANAVA	PROTECTION DESCRIPTION OF THE PROPERTY OF THE	PHILUM	11:11				 			
TALA INCAL	TO THE STATE OF THE PARTY OF TH		134-192	166-393		-				
PARC ECOL	I ALLEST CONTROL AND	AUREUS	27.18	152-179	264-347					
	PLASMIU RECOMB		41.15	102-181	110.361	166-393				
٦I.	PLASMID RECOMB	2	17.71	391-316						
٠ĺ	PLASKID RECOMBINATION ENGINE		3-40						1	
	INEGULATORY PROTEIN		22	201.745						
	PLASMID RECOMBINATION ENZYNE		Т	Т	270.00	-			L	
PRE STRAG	PLASMID RECONGINATION ENZYME	2	J		,			-		
CA151 - 15140	I ISTERIOLY SIN REGISTATORY PROTEIN	TOCENES	- 1	13:50			1			
2	7 14 14 14 14 14 14 14 14 14 14 14 14 14	ESCHERICHIA COU	218-245				-			
אמע בכסר	_		183-433				-			
PPILIM BACSU		1 12	9	282.319		-				
PRIN BUCA							_	-		
PPRIM CLOAD	DNA PRIMASE	UI TLILUM					-	-		
7 17 171 000	DNA PRIMASE	LACTOCOCCUS LACTIS	169.296	I	7					
	-	RICKETTSIA PROWAZEKII	10.37	145-286	477-504	526-593				
A MICA	-	MICANS	30-37							
PRUS DESDE	DSMANE PROTE		119.344				_			
PPRLB ACHLY	BETA-LYTIC META	ACMOMOBACIENTINOS				-		_	L	
PPRIB LYSEN	BETA-LYTIC MET	2	7					-		
07171	THE METALLOPA	LISTERIA MONOCYTOGENES	٦	273:310		1				
2011	т	LISTERIA MONOCYTOGENES	111-145							
LIST COMP	TOTAL PROPERTY.		306-336				-			
PPROA SERUMA	CAMMA GLUIA	STABLE OFFICE ATIBETIS	57.20							
PPROA STANU	ROTEIN A MEC		7.					 -		
PPROB SERMA	GLUTAMATE S-KINASE						_		L	
PPROB_STRAG	PROTEINB	TREFICUACIOS AUXILIANOS	,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,				<u> </u>	-	_	
PPROC PSEAE	PYRAOLINE-5-C	SEUDOMONAS AERUGINOSA								
PROH BACSU	PYRROLINE-S-CARBOXYLATE REDUCTASE HOMOL B	ACILLUS SUBTILIS	77.00				 			
PROP ECOLI	PROLINEGETAL	SCHENCHIA COLI	400-48				 			
PPROV ECOLI	PERPHENAL M	SCHENICHIA COLI	24:34				1			
PPROV SALTY	PER PRENAL M	SALMONELLA TYPHIMURUUM								
PRESE FOLL	PARE PROTEIN	ESCHERCHIA COLI	70-197				+			
100	ANTICODON RUCLEASE	ESCHEMICHIA COLI	31.100				1			
TO STATE OF	MISTOR CARA	ESCHENCHIA COLI	278-30\$						-	
	SECURE CANAT PROTEIN PRICE PRECURSOR	BACILLUS SUBTILUS	18-25	48-184						
PPRSA BALSO	TRUIEIN EALON	STREPT OMYCES CRISEUS	\$-110 \$-110							
PPRTA STRUK	TOTEASE A PACT	CHAPTER CONTRACTOR	103-130							
PPATC_ERWCH	ECKETED PROT	KAN AND AND AND AND AND AND AND AND AND A	244.313					-	L	
PPRTC PORGI	COLLAGENASE PRECURSOR	COUNTY CONTRACTOR	100			-			-	L
PPRID ERWCE	H PROTEASES SECRETION PROTEIN PRID	ERWINIA CHATSANITEMI		3,6 9,6	76.74			-	ļ	L
FFETE NACINO	EXTRACELL ULA	THE STATE OF THE S			100					
PIRTE EXWCI		EKWINIA CITATSANTI LEMI			2			-	-	ļ
PPRTF ERWCH	FROTEASES SECRETION PROTECN PRIF	ERWINIA CHILYSANTHEMI	210-210						-	ļ
PRIN LACA	A PROTEASE MATURATION PROTEIN PRECURSOR	LACTOCOCCUS LACTIS	10	¥ (1.5)			1	1		1
PPRTM LACLE	PROTEASE MATE	LACTOCOCCUS LACTIS	Ç.	70-103	21.21					
PRETIL LACE	PROTEASE MATURATION PROTEIN PRECURSOR	LACTOBACILLUS PARACASEI	16-103		اً					
AND 44 C. D. A.	CYTEACE LINA	SIGNATIA MARCISCINS	194.11	178-A117	101.TH					j
THE STREET	44 81 8 13 8 14 14 14 14 14 14 14 14 14 14 14 14 14	KINKATIA MARCISCINS	<u> </u>	2	1007-104					
THE STANK	CALLACTURE CONTRACTOR	COUNTA CHRYSANTHEMI	114.34)				-	L	L	_
PPRTX ERVICH	SECRETED PROTE	ENGLANCOCKIE EL DNGATUS NAFOEL	120-147		-		-	_	L	L
755 SY	CHLOROPHYLL	PONECIACION CO	90.09	136-356					L	L
PPSAA SYND	CIGLOROPHYLLA	STREETING COCCUS ST	130.00						L	Ļ
PPSAA SYNWU	CHONOPHYLL	STRECHOLOCUS VOLCANOS		136.143	118.168				ŀ	L
PPSAA STAYS	CHLOROPHYLL A	STRECTOCTS IS ST	342.31						L	L
PPSAN YEAP	CHAPERONI: PRO	TENSINIA TESTIS								L
PPSAD SYNM	Т	STREAM BEATE	1					-		L
PPSAE YERJE	PSAE PROTEIN P	TENSINAFESTIS								

Colorada Colorada	PCGENE 1107117114		Proharyobe Requences	П	17		, , , ,	* * * * * * * * * * * * * * * * * * * *			
	HOITH	Security barrens	ORGANISM ANACYCTIC MINIT ANG	Т	1		4			9	a de
	I ABILIE INCOME	OFFICE A	Bechie Frink Cot 1		-				T		
	TAKE SIECE PE	MANAGE CITATINA PREFITE CON	WOLKELL A SECONDINE	1				<u> </u>	ĺ		
	MOCENIATE RIVE	LAC PROTEIN PALCINE COR	FCTHERICINA FOLL	2.5	_						
	HINSHEITEANU	FIASE	MACILLUS SUNTILIS	39.52		<u> </u>					
	NO SHIDTLANS	FLASE	ESCHERCIBA COLI	Г	1.426						
	PHOMPOTANS	ERASE	SALMONELLA TYPHINICAUM	Ť	977-						
	PHOSPHOTRANS	EKASE	STAPHYLOCOCCUS CARNOSUS	П							
INCOMINGE FOR THE FIRE THE FORTER FOR THE FORTER	MIOSPHOTEANS	ERASE	STREPTOCOCCUS SALIVARIUS		1.332	-				1	
IntegrinGravate Law Envirol LACTORACLIA CAME 1918-94	PHOSPHOTICANS	FRASE ENZYME II	ERWINIA CHAYSANTILIM	127.154	-		-				
		ENSE ENZYME II	DACILLUS SUBTILES	610.667	-		-	1			
Interpretation Inte		ERASE ENZYME II	LACTOBACILLUS CASE!								
		erase enzyke ii	LACTOCOCCUS LACTIS	┪	9.5		$\frac{1}{1}$				
	PPT3L STAAU PHOSPHOTRANSFE	ENASE EN2YSIE II	STAPHYLOCOCCUS ALMEUS	┪	SE SE	-	-				
MICHAELE REPORTE STATEMENT COLD AND STATEMENT COLD AND STATEMENT CARLOGUES 174-15	PPT2M_ECOLI PHOSPHOTIANSFE	ERASE ENZYNE II	ESCHERICHIA COLI	445-419		-	-				
INCOMING TANASE ALLO SECTION OF A STATE OF	PPT:N STACA PHOSPHOTRANSFE	ERASE ENZYAGE II	STAPHYLOCOCCUS CARNOSUS	3							
INGENIOTALMSTEASE FOR PAIGNESS 19145 191	PP13N ECOLI N.ACETYLGLUCOS	SANTNE-PERMEASE	ESCHENCHIA COLI	310-68	+	$\frac{1}{1}$	+	1			
INCORPORTABLE NOTION SALEMENT NOTION STATEMENT NOTION	_ [ERASE ENZYME II	STREPTOCOCCUS NICTANS	120-000						Ī	
INGENIOTARIST RATE FOLDER 19.55	╗	ERASE FPR PROTEIN	SALMONELLA TYPHIMUMIUM	107-134	+		-	1]	Ī	
MIGNIOCANDER PROTEIN PROFESS MASSIGLA PRELATORIA 11-45		ERASE PACTOR III	LACTOBACILLUS CASEI	000		1					
MOTOCALULE PROTEIN PART MATERIAL PRELIMONIAL	Т	PROJEIN MPR	EXCREMENTAL COLUMNICATIONS		-		+				
PROTECTED 17-251	BALLA PRILATE AND IE	LESCHEN UPP	KI BROTH I A PARTAIONIAE	11-65		+					ĺ
PULL CLANASE	TROSPINO AND THE PROPERTY OF T	10000	PECTATE COLI	Γ	1.251		-				
LEGIE PETIDASE KLEBSIELLA PNEUMONIAE 194318	PART A DI RAW BIN LIN ANA CE		KI FRSIEL LA AFROGENES	Г		-					
LAGIST PETTIONSE KLEBSIELLA PREUNONIAE 17-201	TOUR A WILES POLLOLANASE		X ERGEL A PARTAONIAE	104.918	-		-				
VECTOR VECTOR VELOSIELLA PREUNINAE 10-41 10-21 10-	FACE SEPTION		KI PRIEL A PKE MONIAE	171.205	-	-		ļ			
UPTAKE PROTEIN PRECURSOR PRECURSOR PRECURSOR	HIN C BRECHECK		KI PRIFLIA PHELMIONIAE	10.07		+	-				
AMIDOPHOSPHOLOGYTTANNSFPEC BACELLUS SUBTILS 194411 14415 144411 14415 14411 14415 14411 14415 14	PTAKE PROTEIN	PRECIMENT	PSEUDOMONAS PUTIDA	Г	Γ	Г					
PHOSPHODUROSYALANINE-GLYCING LIGASE BACHLLUS SUBTILIS 149-114	AMIDOPHOSPHO	IBOSYLTHANSF PAEC	BACILLUS SUBTILIS	Т	Т	Т					
PORTATION SERVINE PACTICUS SUBTILIS 19-194	PHOSPHORUBOSY	AMINE GLYCINE LIGASE	BACILLUS SUBTILIS	346-376		Н					
STATUTE CARBANOULT TANISTE ALS ACCOLL 15 STUTILES STUTI	FORWALTRANSFE	MASE.	BACILLUS SUBTILIS	149-176		_					
SACHASE BACILLUS SUBTILIS 11-19	FOUNTTRANSFE	LASE :	ESCHENICHIA COLI	3.5	1	-	$\frac{1}{1}$				
ACCOLOGATE BACILLUS SUBTILIS 11-114	PPURA BACSU SYNTHASE!		BACILLUS SUBTILIS	S I	1]			
ACCRETATION COLUMENTS RETATION COLUMENTS ACCRETA	PPURS BACSU CYCLO-LIGASE		BACILLUS SUBTILIS								
ADENT, DISCICIANTE LYASE BACILLUS SUBTILIS SE-150	PPUNG ECOLI AIR CARBOXYLAS	3	ESCHENCHIA COLL	20110		+	-				
ADDITION OF THE PROPERTY CONTRIBUTION	PPURY BACSU SARCAL STATINE	A35	BACHLUS SUBTILITS	Т	1363	+	-				
ACCAT PLANSFORMYLASS I ACCATURS SUBTILLS 19-35 ACCAT TRANSFORMYLASS I EXPERIORIA 219-284 ACCAT TRANSFORMYLASS 1 10-24 219-284 ACCAT TRANSFORMYLASS 1 10-24 210-24 SYMTHASS 1 10-24 20-24 LINKER POLYPETION CPCGI ANABARIA SP 11-14 LINKER POLYPETION CPCGI ANABARIA SP 18-116 LINKER POLYPETION CPCGI ANABARIA SP 18-116 LINKER POLYPETION CPCGI ANABARIA SP 18-116 LINKER POLYPETION CPCGI ANABARIA SP 18-116 LINKER POLYPETION CPCGI ANABARIA SP 19-116 LINKER POLYPETION CPCGI ANABARIA SP 19-118 LINKER POLYPETION CPCGI ANABARIA SP 19-118 LINKER POLYPETION CPCGI ANABARIA SP 10-113 LINKER POLYPETION CPCGI 10-113 ANABARIA SP 1 10-112 </td <td>SPINE BACSO ADENTICOSOCCIA</td> <td>715 LIASE</td> <td>FYCHERICHIA COLI</td> <td>L</td> <td>77.7</td> <td>+</td> <td></td> <td></td> <td></td> <td></td> <td></td>	SPINE BACSO ADENTICOSOCCIA	715 LIASE	FYCHERICHIA COLI	L	77.7	+					
AICAN TRANSFOLMTAISE ESCHERICHIA TYPHINDUNA 218-348	PPURE BACSU AICAR TRANSFOR	AYLASE	BACILLUS SUBTILIS	Γ	1,000						
ACAT TRANSFOLMTLASE	AICAR TRANSFOR	MYLASE	ESCHENICHIA COLI	239-268							
INTER FOLTPETIDE CPCG ANABARIA SP 18-115	AICAR TRAMSFOI	MYLASE	SALMONELLA TYPHIMURUM	218-267							
JANUAR POLYPETIDE CPCG AVABARIA SP 19-111	SYNTHASE II		DACILLUS SUBTILIS	609-616		+					
INVER. POLYPETIDE CPCG AAASTAGOCLADUS LANINOSUS 18+116	CINKER POLYPEP	TIDE CPCGI	ANABAENA SP	£::		-					
ANABARNA STATES ANABARNA STATES ANABARNA STATES ANABARNA STATES ANABARNA STATES ANABARNA STATES S	LINKEK POLYPE	TIDE CPCGI	MASTIGOCLADUS LAMINOSUS	911.6		-	+				
INVER POLYPETIDE CPC21	TUNKER POLYPE	TIDE CPCG1	ANABAENA SP	\$ =	$\frac{1}{1}$	+	-				
Inverse Pol-Type Tipe Eccol AAABAENA SP 11 RO LINKER POLYPETIDE AAABAENA SP 12 RO LINKER POLYPETIDE AAABAENA SP 13 RO LINKER POLYPETIDE REMYELLA DIPLOSIPHON 104-13 14 RO LINKER POLYPETIDE REMYELLA DIPLOSIPHON 124-40 15 RO LINKER POLYPETIDE REMYELLA DIPLOSIPHON 124-40 15 RO LINKER POLYPETIDE REMYELLA DIPLOSIPHON 124-40 15 RO LINKER POLYPETIDE REMYELLA DIPLOSIPHON 124-40 15 RO LINKER POLYPETIDE REMYELLA DIPLOSIPHON 124-40 15 RO LINKER POLYPETIDE REMAYINA MARKÉZENS 124-40 15 RO LINKER POLYPETIDE REMAYINA MARKÉZENS 124-40 15 RO LINKER POLYPETIDE REMAYINA MARKÉZENS 124-40 15 RO LINKER POLYPETIDE REMAYINA MARKÉZENS 124-40 15 RO LINKER POLYPETIDE REMAYINA MARKÉZENS 124-40 15 RO LINKER POLYPETIDE REMAYINA MARKÉZENS 124-40 15 RO LINKER POLYPETIDE REMAYINA MARKÉZENS 124-40 15 RO LINKER POLYPETIDE REMAYINA MARKÉZENS 124-40 15 RO LINKER POLYPETIDE REMAYINA MARKÉZENS 124-40 15 RO LINKER POLYPETIDE REMAYINA MARKÉZENS 124-40 15 RO LINKER POLYPETIDE REMAYINA MARKÉZENS 124-40 15 RO LINKER POLYPETIDE REMAYINA MARKÉZENS 124-40 15 RO LINKER POLYPETIDE REMAYINA MARKÉZENS 124-40 15 RO LINKER POLYPETIDE 15 RO LINKER POLYPETIDE 115-14	PPYG2 MASLA LINKER POLYPEPI	TIDE CPCG2	MASTIGOCLADUS LAMINOSUS	*	$\frac{1}{1}$	$\frac{1}{1}$	$\frac{1}{1}$				
LINER POLYPETIDE CHCG6 ANABARIA SF 13.1 R. LINERE BOLYPETIDE ANABARIA SP 13.4 R. LINER POLYPETIDE FRENTELLA DIPLOSIPHON 13.40 13.5 R. LINER POLYPETIDE FRENTELLA DIPLOSIPHON 13.40 13.44 13.5 R. LINER POLYPETIDE FRENTELLA DIPLOSIPHON 13.40 13.44	PPYG3 MASLA LINKER POLYPEP	TIDE CPCG3	MASTIGOCLABUS LANIMOSUS	21:12		1					
13.1 KD LINKER POLYPETIDE	LINKER FOLYPE	TIDE CIPCO	ANABAZNA SF		+			1			1
	32.1 KD LINKER	OLYPEPTIDE	ANABAENA SP	2		-	-				-
11 & C. LINKER POLYPETIDE FRENYELLA DIPLOSIPION 17-40 17.7 I.G. LINKER POLYPETIDE FRENYELLA DIPLOSIPION 10-143 10.1 INKER POLYPETIDE FRENYELLA DIPLOSIPION 10-143 10.1 INKER POLYPETIDE FRENYELLA DIPLOSIPION 10-143 10.1 I.S. 143 10-143 10-143	27.9 KD LINKER	OLYPEPTIDE	FREMYELLA DIPLOSIPHON	261-401		-					
11.5 KD LINER POLYPETIDE FRENTELLA DIPLOSIFION 10-10	11.6 KD LINKER P	OL YPE FIDE	FREMYELLA DIPLOSIPHON	35	+	+					
NO EXOLUNES NO. TRETTORE 1.0.0 ANAINTATE CARBANOTITAVISTERASE SERUATIA MANCECENS 10-10 ANAINTATE CARBANOTITAVISTERASE SERUATIA MANCECENS 10-91 DINYDROCKOTATE DEHYDROCENASE 1 EXCERICINA COL.	37.5 KD LINKER	OCYPEPTIDE	FREMYELLA DIPLOSIPHON	_		1					
ANTARE CABAMOTI TRANSFERASE SELLATARE CABAMOTI TRANSFERASE SERLATAR CABAMOTI TRANSFERASE SERLATAR MACESCERS SONTOR GOOD TABLE SECRETACINA COL	NO. 8 KD LINKER	OLYPEPTIDE	FREMYELLA DIPLOSIPHON	T	2	+	\downarrow				
DINYDROOROTATE DEHYDROCENASE : ESCHENICHIA COLL	PPYRB BACSU ASPARTATE CALL	BAHOTLI RAKSPERASE	RACIECTOS SOB ILLIS		$\frac{1}{1}$	\downarrow	\downarrow				
DINTERCORDINALE DENTIFICACIONALE COMPANIONI	PYTE SEUK ASPARIATE CAR	HANDTEI KANSTEKASE	SECURATION MANUESCENS	100	+	1	+				
	PPYRD ECOCI IDINTDRODUCION	TE DEMTURCALENASE	EXMENUMATION		-	$\left\{ \right.$	$\left \right $				

	Prohomotic Sequences			A A A A A A A A A A A A A A A A A A A	т	V S VAUV	V D VARY	V AND A		
ROTLES	ORCANISM		98	4 2 3 3 3 3	т-	1	ī	\mathbf{T}	г	
PPYAD SALTY DENYDROGROTATE DEHYDROGENASE	SALMONELLA ITPHINIUMIUM	3,4,103	133.148		T					
TP SYNTHASE	I				t	T	l			l
	٦				t	T				
		314.343			T	T				
		31.40	13.233	ļ	Ī			l		
PRINK CLOPA 14.1 KD PROTEIN IN RUBREDOXIN OPERON	CLOST MOTOM PAST EURIANOS.			<u> </u>			T			
KACC MOTER	CTREATOCOCCIO PARTICIONI IIS	152.189		-						
ASPARTATE RACE	STREET COCCOS INCOMENCES	132.162								
PRACK BACSU PROBABLE AMINO ACID RACEMASE	BACILLUS SUBILLIS	10.116		-						
ALPHA-GALACTO	ESCUENCIA COLI	141.174		İ	l	Ī	-			L
AAS FIDAD SE INVER		95,	10(.33)	T	Ī	Ī		Ţ		
PRISC ECOLI MINOSE TRANSPORT SYSTEM COMPONENT		91.		Ì		T				
NIBOKINASE	ESCHEDCHIA COLI				T	T	T			
UBITOL (RBT) OPE	KLEDSIELLA AEROGENES				T	T		Ī		
PACSA ECOLI BIOSYNTHESIS ACTIVATION PROTEIN A	ESCHENCHIA COLI	100	,		Ì	T	T	Ī	Ī	
PRESA ENWAM BIOSYNTICESIS ACTIVATION PROTEIN A	ERWINIA AMYLOVORA				T		T	Ì		
BIOSYNTHESIS AC	ERWINIA STEWALTII	2 2			†	T	T	T		
PROSA ILLEAE BIOSYNTHESIS ACTIVATION PROTETN A	KLEBSIELLA AEROGENES	6	791 971		T	T	T	Ī		
PRESS ECOLI CAPSULE SYNTHESIS & COMPONENT	ESCHENICHIA COLI	1	24.		1	Ť	T	1		
PRECILEGEN RECAPROTEIN	LEGIONELLA PNEUDIOPITILA	017-707			Ť	T	T	T		
PRECA ACIDA RECAPROTEIN	ACHOLEPLASMA LAIDLAWII	DIC-CO.	777.		1	1	T	T		
PRECA AGRITU RECA PROTEIN	AGROBACTERIUM TUMEFACIENS	B	13:-13	MC-187	1	1	T			
PRECA ANAVA RECA PROTECH	ANABAEM VAUABILIS	1725-349			Ť	1	1	T	l	
PRICA ACKIPY RECAPACITION	AQUIFEX PYROPHILUS	0¥-50			1		1	1		
PERCA BACKE RECA MOTEIN	BACTERONDES PARGICIS	108-135			1	1	1	1	l	
PRICE BACSU RECEPROTEIN	BACILLUS SUBTILIS	267-394					1			
PRECA BRUAN RECA PROTEIN	BRUCELLA ABORTUS	2	35:136	780-307	1	1	Ť			
PRECA BURCE RECAPROTEIN	BURKHOLDENA CEPACIA	23:109		†	1	1	1	T		
PRECA ERWCA RECA PROTEIN	ERWINIA CAROTOVORA				Ī	Ī	T	T		
PRECA LACOE RECA PROTEIN	LACTORACILLUS DELBRUECKII				T		İ	1		
PRECA LACHE NECA PROTEIN	LACTORACIONE RELACTION	135,162	112.269	211.315	I	Ī	T			L
PRECA LACLA NECA PROTEIN	LACTOCCOCCOS CACTOS	266-303								L
PRECA METCL RECAPROTEIN	METAN GRACH LUS FLAGELLA TUN	276-303	Ĺ		Ī					
PRECA METRI MECA PROTEIN	MYCOPI ASMA PULMONIS	10-31								
PRECA MYCPU MECA PROTEIN	MYCOBACTERUM TUBERCULOSIS	749-176								
PARCA MYCTU NECA PROTEIN	METAGERIA CONORDIOEAE	263:310	L							
PRECA MEICO MECA PROTEIN	PROTEUS MIRABILIS	283-310								
PRECA PROME MECA PROTEIN	PSEIDOMONAS AERUGINOSA	343:309								
PRECA PEAS NECK FOURTH	INIZOBIUM LECUMINOSARUM	8	131-131	260-307						
THE CANADA TO SECOND STATES	INIZOBIUM LECUMINOSARUM	110-146	268-295							
PACCA MALLY ACCA SECTION	MIIZOBIUM MELILOTI	119:146	\$62-192							
SECTA DIVINE NECES PROTEIN	NHODOBACTER SPHAEROIDES	119:146								
PECA MICH RECABILITION	STREPTOCOCCUS PNEUMONIAE	134-161	193-127					1		
SPECA SYMPS RECAPROTED	SYNECHOCOCCUS SP	134-151								
PRECA VIECA PROTEIN	VIBRIO CHOLERAE	290-319			Ì	1	1			
PRECE BACSU RECEPROTEIN	BACILLUS SUBTILIS	4.31	78-205		1	1			ا	
-	ESCHERICITA COLI	83.109	147-174							
THE PROPERTY	FROTEUS MIRABILIS	16-113								1
PRECE PSEN RECEPACITION	PSEUDOMÓNAS PUTIDA	111		=		1				1
	SALMONELLA TYPHIMURIUM	147.174			1	1	1			
EXONUCLEASE R	ESCHENICHIA COLI	52.79		╗	T					
Τ_	BACILLUS SUMTILIS	2	₹ 2	192-347	380.330	144-331	T	Ī	l	
DNA HELICASE A	ESCHENCHIA COLI	461-493	1	1	Ī	Ī	T	Ī		1
PRELA ECOLI GTP PYROPHOSPHOKINASE		13.16	81-16		T	T	T	Ī		
PREMA BACSU REPLICATION AND MAINTENANCE PROTEIN	ERN BACILLUS SUBTILIS				Ī		1			
TALLER BLACK CLASS CONTROL AND THE PROPERTY OF THE PARTY		20:22				•				

PCGINE	107417844	Probaryolic Sequences	П		7 7407		4574 4 48544	, var	ABEAS	AREA 9
FILE NAME	PROTEIN	ORGANISM		700	2000	ı	т			
PRENUA STAEP	REPLICATION AN	STAPHYLOCOCCUS ENDERWINDS		- -	-	-	-			
PREPS ECOLI	REPLICATION PROTEIN REPA	BACH THE CHETH IS	F	-	-	H				
PREPA BACSU	MEPA PROJECT	PSCHENCHIA COLI	11:10	226-255		H				
PARTA ELON	BEM ICATION PROTEIN	NEISSERIA CONORUNIOEAE	П	131.172		-	1			
PREPRIACH.	REPLICATION PR	LACTOBACILLUS PLANTARUM	= 2		1	\dagger		1		
PREPM STAAU	REPLICATION IN	STAPHYLOCOCCUS AUREUS		†	+	\dagger	1	1	-	
PREPN STAAU		STAPHYLOCOCCUS AUREUS	10.46	\dagger	+	+	-			L
PREPR STRAG	REPR PROTEIN	STREPTOCOCCUS AUGLACIANE	431.461	1	1	+		+		
PREPS STUPY		SI RETICUCIOS FIQUENCIS	T	015.16		\dagger		 -		
PREPX STANU	REP PROTEIN	STATE OF COURSE OF STATE OF ST	1		+	\dagger		-		
PREPY ECOLI		CLOATEIDIEM PERFENCIENS	L	297.334 34	343.375	\mid	-			
TEN CLONE	31	ECOSTACION COL	Т	Т		-				
100	REP PELICASE	I ACTORACII I IS PI ANTARUM	Т	260-287	╁	\mid				
TATE OF THE PERSON AND		CLOSTNDIUM PERFUNCENS	68.102	131-115						
יייייי איניייי	PERSONANSE PERSONANDER CARE CARE FACTOR 2	BACILLUS SUBTILLS	34.62		-	H				
1071 PACSO	PERTINE CUANT	ESCHERICHIA COLI	1 6111-918	163.204		L				
	PERTURE CHAIN BELLEASE FACTOR 2	SALMONELLA TYPHINGRUPA	Γ	63-204		H				
100111	PEPTIDE CHAIN RELEASE FACTOR >	ESCHENCHIA COU		443-473	_				-	
PREATE FOOL	I LOALACTOSYLTRANSFERASE	ESCHERICHIA COLI	199-226			+	-		4	
PETAD FOOL	BIOSYNTHESIS PROTEIN MAG	ESCHENCHIA COLI	12			1				
PETAL ECOLI	1.2-CLUCOSYLTKANSFERASE	ESCHENCINA COLI				1			1	
PERSONAL SALEY		SALMONELLA TYPHIMUNUM		145-172 23	136-263	1				
PEFAK SALTY		SALMONEUL A TYPHIMUMUM	335-369							
PRIVAL RCOL		ESCHENICHIA COLI	166-393			1	1	1		
PRIVAL SALTY		SALMONELLA TYPHIMURIUM	326-360			1	-			
PAFA ECOL		ESCHERICHIA COLI	1			+		1	+	\downarrow
PRFAS ECOL		ESCHERICHIA COU	1	10.240	+	+	1			\downarrow
PRIVAY ECOL!		ESCICENCIA COLI			1	$\frac{1}{1}$	1	<u> </u>	1	1
PNYAZ ECOLI		ESCHENCIAL COLI	9			+		1	-	
PRUBB SALTY	DTDP-GLUCOSE 4.4-DEHYDRATASE (SALMONELLA ITPHINIONIONI	10000	t	+	\dagger	<u> </u>	 -		L
PRUBM SALTY	MANNOSE-1-PHOSPHATE GUANYLYLTIANSPERA	EALMONEULA LIPRINIUMIUMI	۳	\$16.313	+	\dagger	-		-	
PMFBS SALTI	PARATOSE SYNTHASE	CORP. A MODIL A PLAN	140.3%			+				
PINES VIBAN	PRECURSOR YOU PERCUC ANGUISACTIN	PACIFICIAL COLL	13.110			t	-	<u> </u> -	-	L
PILLY ECOL	PEPTIDE CHAIN	PATE 1 1 C THE BOARD	T	190-262	110-143	l	-			
PROIS BACTO	PUBLICATION OF SHEET STE	ESCHENICHIA COLI	٦	1	-	ŀ				
4 12 641144	NAMANIA OK IN	SALMONELLA TYPHINURIUM	175-202							
PERMAN FCOL	L. EHANDOSE OF	ESCHERICHIA COLI	10-41							
PEHAS ECOL	L. MALANOSE OF	ESCHENCHIA COU	153-179							
PRUITE RHILV		MHZOBIUM LEGUMINOSARUM	206-233			1		-	4	
PINE ECOL	INNA HELICASE BUT BARADA	ESCHENICIUA COLI	7			+			4	-
PRING BONBU	TRANS TERM FACTOR IUNO	BORRELIA BURGDOMERI		37. JES	1	1	1			_
PRICE BACSU	1	BACILLUS SUBTILIS	23. 100			1	1			_
MUSA ECOL	RHSA PROTEIN	ESCHERUCHIA COLI	967-694		_			1		
PRHSB ECOLI	Г	ESCHERICHIA COLI	┑	┪		1			-	
PRHSC ECOCI	1	ESCIENCIIIA COLI	7	-	1056-1083	+	-			
Pulso Ecol	MASO PROTEIN	ESCHENCHIA COLI	671.712	1001-100	-	1				4
PAUSE ECOL	MASE PROTEIN	ESCHENICHIA COLI	345-372		-	1	1			
PRINCE ECOL	•	ESCHENCHIA COLI	63:137	1	1	1		1		
FRES ECOL	ALBONUCLEOSIDE-DIPHOSPHATE REDUCTASE	ESCHEALCHIA COLI	167.194		-	+				_
PLISA PHOLE	г	PHOTOBACTERIUM LEIOGNATIII	Ş	=======================================		1	-			4
PLUSB BACKSU	REDOFT AVIN S	BACILLUS SUBTILIS	=	1		1	$\frac{1}{1}$			_
PRISB PHOLE	S KLINYLY S	PHOTOBACTERUM LEIGGNATH	Τ	111	\dagger	†	$\frac{1}{1}$	-		\downarrow
PRLIO STRAT	\Box	STREPTOMITES ANTIBIOLICUS		3	\dagger	\dagger	+	+	+	\downarrow
PILL 12 SYNY I	405 REBOSONIAL PROFFIALIZ	SYMELHOL TATIS ST	1,7		1	1	$\frac{1}{1}$			

П	107117814	Probarystic Sequences	ABEAL	1920	7 7387	7	ABGAS	AREAL	VALV	1737	2414
THEMANE	PROTEIN STORES	THE EXOTOGA MANUTINA		п		1	1	†	Ī	1	
PRI IS THE KA	SOS RIBOSOMAL N	BACILLUS STEAROTHERMOPHIN.US	ŝ			1	1	1			
Ş	SOS MUSICIONAL PROTEIN EIN	MICROCOCCUS LUTEUS	Ş			1		1			
	NO MEDICACAL PROFESSION	INTEOPLASMA CAPRICOLUM	21:02			1	1	1	Ī		
<u> </u>	NO KUROSONIAL PROTEIN LIS	BACILLUS LICHENIFORNIS	7		1			T	Ī	T	
3	NO MUNICIPAL PROTECT IS	BACILLUS STEAROTHERAIOPHILUS	-		1	1		1	Ī		
	GOT BERGERAL PROTEIN LIS	BACILLUS SUBTILIS	93-122					1		Ī	
10 CUR YE	GOT BIRDSONIAL PROTEIN LIS	CIRAMYDIA FRACIONIATIS	10.00			Ţ		Ī			
	SOS REDOCCIONEL PROTEIN LIS	ESCHERICHIA COLI				1		T			
	GE BIBOSOMAL	LACTOCOCCUS LACTIS	?				T				
	MA BIBOCORIAL	MIETHANOCOCCUS VANNILLII	2 2			1		T	Ī	T	
٧ ١	No King School and Park School and School an	MYCOPLASMA CAPRICOLUM	63.135								
Л	NO KIBUSCHALL TROITING IN	BACILLUS STEAROTHI RNIOPHII UN	11.58				1	1			
		CIG ANYDIA TRACIONIATIS)1·16								
PR 19 CR.18	NOS MINOSCARAL PROJECTIVA	HALOARCIA A MARISHMATICI	10.107					1			
	VO RUBOSCIAL PROFILIS ES	ALVEORIASSIA CAPRIFORM VI	61.19								
-1	MOS KIIIDANAAN FRONTSA LII	FECHERICIIIA COLI	2 2								
-		HALDARCULA MARISMORTI !	101-120								
_		METHANOCOCCUS VAXNIFLII	14:33		Ì	7					
7	PROBABLE 303 KINGSOUNCE TO SECOND SEC	PROTEUS VUI GARIS	150.194								
THE PROPERTY.	NO MINOSONAL PROTEIN !	SULFOLOBUS SOLFATARICUS	17.5	184-211							
L	TAS BINOSONIAL BROTEIN L'YO	ESCHERICHIA COU	7-				\int				
	See Productive Pentervito	AIYCOPLASAIA FERMENTANS	14.41								
THE BUTCH	NO PRIOCESSES PROPERTY 131	BACILLUS SURTILIS	6:18								
PRLZI RACSU	The BIDGONAL PROTEIN 13	ESCHENCHIA COLI	20-55								
ı.	NOT THE PROPERTY OF THE PERSON AND ADDRESS OF THE PERSON AND THE P	INETHANOCOCCUS VANNIELII	20.57								
	THE PROPERTY IN	MYCOPLASMA CAPRICOLUM	2.50 2.50								
	LOS EIBOSONIAL	HALOARCULA MARUSAIORTUI	2								
FTV	LOS BURDSONAL	METHANOCOCCUS VANNIELII	8.18								
MICEO	SOS RUBOSONIAL P	NIICROCOCCUS LUTEUS									
H.TH.	SOS RIBOSOMAL	CHILAMYDIA TRACHONIA IIIS	8 3								
FRL19 ECOLI	SOS RIDOSONAL P	PESCHENCINA COCI	200								
PRL 29 MYCCA	SOS MIBOSOMAL	ATTOCKASHA CACAMONICALINA	3								
Ş	SOS MIBOSOMAL I	ANY COST A CAPRICOL UM	144.198								
PL . LIYCCA	SOS RIBOSOMAL PROJECT LA	THERMUS ADUATICUS	50								
PRLY THEIM		BACILLUS STEANOTHERAIOFIFILUS	79.106								
	SOS BINOSOMAL PROTEIN LA	ESCHERICHIA COLI	19.48								
POLY LIETVA	SOS RIBOSOMAL PROTEIN LA	METHAMOCOCCUS VANNIELII	š.			-					
	SOS RIBOSOMAL PROTEIN LP	BACILLUS STEAROTHERMOPHILUS									
PRL 9 FOLI	SOS RIBOSOMAL PROTEIN LO	ESCHERICIIIA COLI		į	:	<u> </u>	ļ				
PRI AD HALCU	ACTIVIC KINDSOMAL PROTEIN TO HUMOLOG	HALOBACTURIUM CUTIRUIRUM								L	
PRIAB HALHA		HALOBACTERUM MALOBION		161,184					L		
PILAS HALMA	ACIDIC REGIONAL PROTEIN IN HOMOLOG	HALDARCULA MAUSMURI UI	194.321		l				L	L	
PALAO METVA	ACIDIC RIBOSOMAL PROTEIN PO HOMOLUU	METROCOCCOCCOS VOCACECIII	10.84								L
PILA HALEU	RIBOSOWAL PROTEIN'A'	INCOMINE CONCINCTION	1	1		1		L			L
FRIA HALIIA		TITL CARPY A MARICANIA FILL	2		! !-						
PRI.A IIALMA	SOS RINOSOMAL PROTEIN 1.12	TOTAL CONTROL OF THE CANADIST II									<u> </u>
FRLA METVA	RIBOSOMAL PRO	METRACOCCO PARTIES	2	100				L			L
PILA MICEU		EALIGNET A TYPHINGERIAL	36-360	L	-		L				
¥.	4) KD KELAXATI	STAPHYL OCOCCUS AUREUS	5	102-132	117.75	266-300		L			
PALX: STAND	RLX PROTEIN	SALMONELLA TYPHINIURIUM	19:53								
PILIX2 SAFETY	A POTENTIA	STAPHYLOCOCCUS AUREUS	36	162.133	261-295						
	ST X PROTEIN	STAPHYLOCOCCUS AUREUS	3.30	146-216							
01 10 10	SOS RUBOSOMAL PROTEIN LX	SULFOLOBUS SOLFATARICUS	33-63								1
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PUGENE	1197017809	Sequences	1	П	10.00	7 7 3 9 7	7 7397	7 7 4 4 7	6.7487		40640
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אמע בכסו	MURCHUS III		413.440	621-662	T	ľ		Ì			Γ
PRINT BUCK	RIBONICH PASE PROTEIN CONFONENT	כמרא	211.5								
PRINCE BACK!	I RONING FASE		98-186								
PRINS ECOL	REGULATORY PROTEIN RNS	ESCHENICHIA COLI	091-911				1	Ì			
PRN BACC	UBONUCLEASE	BACILLUS CIRCULANS	<u>8</u>	1		1			1		
PIN BACIN	UBONUCLEASE	BACILLUS INTERAEDIUS	31-72		1			1			
PRP28 BACTK	RMA POLYMERASE SIGMA-18 FACTOR PRECURSOR	BACILLUS THUMMGIENSIS	2								
PRESS CITTER	RNA POLYKERASE SIGMA-32 FACTOR				1			1		Î	
PRP15 BACTX	RNA POLYMERASE SIGNIA-35 FACTOR PRECURSOR		╗	8				1	1	1	
PROSE ALCEU	RNA POLYMERASE SIGMA-S4 FACTOR		239-266								
A20CA 220CA	RNA POLYMERASE SIGMA-54 FACTOR	AZORHIZOBIUM CAULINODANS	174.308	П							
Paper haffell	ANA POLYNOR	BACILLUS SUBTILIS	1791	12.124	274-308	196-423					
200	BINA BOL YAFBACE CICMA-SAFACTOR I	APONICUM	97.134								
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TAUS PLEFF	27 17 17 17 17 17 17 17 17 17 17 17 17 17	PLOCAL PARTIE ATTIC	155.185		Ī						
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PIUSH SALTY	PROBABLE SIGMA(S4) MODULATION PROTEIN	KIUM	3	1		73, 55,	111				
PR 70 BUCA			T	┱	T	Т				I	
PRO TO CHETR		ICONIATIS			Ī		1		Ī		
PRP 70 ECOL	INA POLYNŒRASE SIGMA-70 FACTOR		2	1		1				Ī	
PRPTO PSEAE	KNA POLYMERASE SIGMA-70 FACTOR	PSEUDONIONAS AERUGINOSA	╗								
PRO NOR	•	NCKETTSIA PROWAZEKII	┪	¥6.33		Ī					
PRPED MYXXA	RUA POLYMERAS	NYXOCOCCUS XANTHUS	T	110.10	39.16						
PRINCE SYNDY	BILIN BIOSYNTH	SYNECHOCOCCUS SP	180-207	1							
PROOF BACSU	DNA-DIRECTED R		9								
PRPOA ECOLI	A DIRECTED RNA POLYMERASE ALPHA CHAIN		ž								
		SALAIONELLA TYPHIMURUM									
PRPOA HALHA	ONA-DIRECTED R	N5.	<u>§</u>								
PRIPOR HALMO	A-DIRECTED RNA		29.270	╗				1			
PRPOA METTH	DNA-DIRECTED R	AUTOTROPHIC	210-245	Т	Z.666						
PRPOA SULAC	DNA-DIRECTED!	SULFOLOBUS ACIDOCAL.DARIUS	7	28	693.720						
PRPOA THECE	DNA-DIRECTED!		20. E		1	Ī					
PILYOB ECOL!	DNA-DIRECTED	ESCHENCHIA COLI	Т	101 - 103							
PRINGS MYCLE	DWA-DIRECTED R	MYCOBACTERIUM LEPRAE	П	1							
PRPOS SALTY	A-DIRECTED ANA	SALMONELLA TYPHINURIUM	90.0		101:101						
PRPOB SULAC	A-DIRECTED MA POLYMENASE SUBURIT B	SOLFOLUBUS ACIDOCALUARIOS	,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,		T						
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12 A A A A	MA-DIAECTED		T	MI.934	123.1217	T					
	NA-DIRECTED	HAI ONACTERIUM HA! ONUM!	Т		Ī						
	MANUAL DISCORDING	HALOCOCCUS MOREHUAE		7.14	207-114						
	MA.DIRECTED	METHANOBACTERUM THERMOAUTOTROPHICU		Т	127.154						
	AND PETER BAN	MYCOBACTERUM LEPRAE	273.300	L	816-116	131:1158					
CONT. LOCAL	NA.DIRECTED	-	Г	Т							
200	NA DIRECTED	•	г	13.214	 						
	CHA-DIRECTED BNA POLYMERASE SUBUNIT A.	THEAMOCOCCUS CELER	5.2								
	NA DIRECTED	NOSTOC COMMUNE		403-449	539-566						_
	NA POLYNORA	ESCHENCHIA COLI	Т	ī	F						-
201	NA POLYNGRA	ESCHEACHEA COLI	281.308								
1000	NA-DIRECTED	HALOBACTERUM HALOBIUM	811.6								
PENSA ACKTU	NA POLYNERA	AGROBACTENUM TURIEFACIENS	310-347	197-427							
PAUSA ANASP	RNA POLYMERASE SIGMA-A FACTOR	ANABAENA SP	11.105								
PRPSA CLOAD	RHA POLYMERA	CLOSTRUDIUM ACETOBUTY LICUM	1-39								
PRPSA STRAU	RNA POLYMERASE SIGMA FACTOR RPODY	STREPTOMYCES AUREOFACIENS	200.05								
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FRESS ANASP	PROTEIN			П							l
PRISB ANASP	NA BOT WAS BASE	ANABALAA 37	Ī	ī	-		l				
PIUSB BACSU	NA POLITICION	DACHT HE STRAIL IS		169-196	300-230					Н	
	NA POLYNIERAS	MILITA	Ţ	Т		ľ					
FRPSB MYXX	RNA POLYNERAS	454	121-92			ľ				+	
PRPSB STIAU	ANA POLYMERASE SIGMA-BIACTION		51-15							$\frac{1}{1}$	I
PIUSC ANASY	KNA POLITICIOS	TILIS	672-261				1		-	-	Т
TAN BALL	BLA BOLVARENASE SIGNALE PACTOR PRECURSOR					1	1			+	Τ
PRESE BAC	NA POLYNIERAS	OBUTYCICUM		8	1	+	1	+	1	1	T
1000	NA POLYNORAS	13	٦	- -	1	+			 	+	T
PERCE BACKE	NA POLYNCRAS		2		1	1				 	
PAPES NACKU	NA POLYMENS		7	2.5	1					+	
1078 73486	ENA POL VIVERAS	ORNIS	=======================================							+	ĺ
Pa Peter BACS	ENA POL YMERASE SIGNIA-11 FACTOR		_			+	1			1	
PER BACK	NA MIL YMERAS		٦	200		1	1		+	+	-
1	NA POLYNGRAS	AUREUS	9-46			1			1	+	
COLLA CALCO	NA POLYNGIAS		131.273	1		1	1		1	+	Ī
PERCY BACTE	POSSIBLE RNA PO	BACILLUS THURINGIENSIS	\$		1	1				+	Ī
LICON BOOK	195 RIBOSOMAL P	ESCHENICHIA COLI	Š			1	1			+	I
PACE NACEL	INS RIBOSOMAL P	BACILLUS SUBTILIS	Ĩ	1		1	1			+	Ī
BACKII	105 BUBOSONAL P	BACILLUS SUBTILIS	2	1		1				1	I
120	TO BIRDSON D	VANNIELII	┪				1			-	I
1 7 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	TALENCO ALL			П		1	1			+	1
	168 BIRDSOLAT PROTEIN ST	PROVIDENCIA SP	39-66	265-292	349.376	1			1	1	1
PART PART	THE PROPERTY OF THE PROPERTY ST		91-125	112.217		1				1	۱
100	NO BINGSONAL PROTEIN \$21	ERMOPHILUS	1.26							+	١
Care 1 Care	TOUR PROCESS AND PROTEIN ST.		91-125			1			1	+	١
A 15.00	TO BIRDSOMAL PROTEIN 33	ACHOLEPLASMA LAIDLAWII	╗							+	١
PRS1 MYCCA	JOS RIBOSOMAL PROTEIN \$3	MYCOPLASMA CAPMCOLUM	J	134-163					+	$\frac{1}{1}$	
PRS4 ECOLI	THE RIBOSOMAL PROTEIN SA	ESCHENCHIA COL!	ě							+	
PRSS HALMA	305 RIBOSOMAL PROTEIN \$5	HALOARCULA MARISMORTUI	è	7		\dagger			-	+	l
PASS MYCCA	TOS RIBOSOMAL PROTEIN SS	MYCOPLASMA LAFACOLONI			T	T	Ī			-	ı
PRS6 THETH	305 AUBOSOMAL PROTEIN SE	APPROVIDE VANNELLI	99			T			-	H	
PAST METVA	10S TUBOSOMAL PROTEIN 37	INVODACTERINAL PREAF	9								
PRS) MYCE	105 IUBOSCHAL TROISIN & 1	MICROCOCCUS LUTEUS	103-130							Н	
	TOS BESOGGILAS, PROTEIN SE	MYCOPLASMA CAPRICOLUM	1:3							-	ı
	SERBITO IKE	ESCHENCHIA COLI	10-107							-	l
PRINT POOL	RNA-DIRECTED D	ESCHENICIÓN COLI	П						+	+	
PSACS BACK	A LEVANSUCAASE PRECURSOR	BACILLUS AMYLOLIQUEFACIENS	٦			1		1	+	1	l
PSACE BACS!	EVANSUCILASE	BACILLUS SUBTILIS	_			1		1	+	+	ı
PSACB STRUMU I	LEVANSUCAASE PRECURSOR	STREPTOCOCCUS MUTANS		Т		1			1	$\frac{1}{1}$	
PSACO BACL	SACO REGULATORY FACTOR	BACILLUS LICHENIFORMIS	,	316						+	Ì
PSACT BACSI	ACPA OPERONA	BACILLUS SUBTILITS	Т							-	
PSAGP STIUY	STREPTOCOCCAL ACID GLYCOPROTEIN	STRETTOCOCCOS PTOCEMES	10,137			T				-	
PSAOX BACS	AACOSDIE OXID	C. Develop in Digenitrant	1773			T					l
PSAS: CLOB	SPORE PROTECT	BACH CIA CEREIIC	1							-	l
PSASO BACCE	SPORE PROJECT CAMPANITY	BACH FIX STEAROTHERAIDFILLS	3								
PSASC BACS	STATE TRUE EIN COMMAN TO	SCHEDICHIA COLL	35.1	137.364	335-515	622-656 7	778-812	831-865 915	915-942		ĺ
2362		ESCHENCHIA COLI	23:15	334-397	Ī					Ľ	
	+	ESCHELUCIDA COLI	2	436-470	553-580					L	ŀ
TO WELL	SEP PROTEIN	BACILLUS SUBTILIS	28:55								
100	CSA PEPTIDASE PRECURSOR	STREPTOCOCCUS PYOGENES		784-811	011-10						
PSCRB KLEYK	SUCROSE 4 PHOS	KLEBSIELLA PNEUNINE	174-201	П					-	+	
PSCR5 LACLA	SUCROSE 4 PI 105	LACTOCOCCUS LACTIS	11.313	34-363	195.422				+	+	i
PSCRD STRAU	U SUCROSE-FRIOSPITATE HYDROLASE	STREPTOCOCCUS MUTANS	135.162					1	+	+	
PECRE SALTH	H IFRUCTOKINASE	SALMONELLA THOMPSON	97.124						1	$\frac{1}{1}$	ļ

PCGENE	10721784	Preharyeite Sequences	п	П	\boldsymbol{T}	П	П		П	
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	PROCEOUS SECTIONS		Т	240-267	T	T	I	$\frac{1}{1}$	ļ	
AL IVA ALLA	I CROSE PORIN	ž	Τ	Т	340-267	T	-	$ar{I}$	-	
PARTA BACSU	PREPROTEIN TRANSLOCASE SECA SUBUNIT	BACILLUS SUBTILIS	Γ	2		Ī	-	F	-	
PSECA ECOL!	PREPROTEIN TRANSLOCASE SECA SUBUNIT		-	137-661		П	H	Н		
PSECB ECOLI	PROTEIN-EXPORT PROTEIN SECB							1		
PSECO ECULI	PROTEIN-EXPORT MEMBRANE PROTEIN SECO	ESCHENCHIA COLI	1	2		Ī	+	+		1
PSECT ECOLI	PROTEIN EXPORT MEMBRANE PROTEIN SECT	ESCHENCHIA COLI		T	1		1	+	1	-
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N 125	ACCOUNTS OF CHANGE OF CONTRACT		Т	117.719	T	T	\dagger	\dagger		-
PERA BACSU	D. I. PHOSPHOOL YOUR ATE DEHYDROGENASE	BACILLUS SUBTILIS	Т	147.174	Ì		-	\mid	-	
PERAN ECOL	S-FIMBRIAL PROTEIN SUBLINIT PRECURSOR	ESCIENCHIA COLI	T				-	 		
PSESA ECOL	SLKTAR FERMEN		~	İ	T			-		
PSFUA SERVA	A INON-TRANSPORT SPUA PROTEIN PRECURSOR	SERVATIA MARCESCENS	19:97	T	Ī	Ī		l	L	
PSIRUI ECOLI	SHUFFLON PRO		234.262		Ī			\mid		
PSHUZ ECOU	SHUFFLON PROTEIN A.		234.362							
PSHUS ECOLI	SIN/FILON PROTEIN B		290-262						_	
PSHU4 ECOL!	SIKATLON PROTEIN B'	ESCHERICHIA COLI	234.262					-	_	
	SINFFLON PROTEIN C		Г	402-439			\mid	-	_	
	SHUFFLON PROTEIN C		134-362							
PSHU7 ECOLI	SMIFILON PROTEIN D	ESCHERICHIA COLI	193							
PEINE BACK	SINE PROTEIN		9.10	43-80				ŀ		
	SINR PROTEIN		П			П				
PSLAP ACEKI	CELL SUNVACE	Ü,		382-309	113-481	421-154	\$17-544 [56]	1991 1991	641-685 726-753	1
			2		1	1		1		
	SAU PROTEIN	ESCHERICHIA COLI	7				1	+		
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	SO SOLVOYSON			1	1	1	1	1	1	1
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PSCOM PROFIE	SUPEROXIDE DIS			İ	Ì	Ī				
PSONTE ECOLI	SONG PROTEIN!		Г	70-07	273.300				-	
	SOPB PROTEIN	ESCHENICHIA COLI	151.279							
PSOXA ECOLI		ESCHENCHIA COLI	[6-6]							
PSPOI BACSU	STAGE 6 SPORULATION PROTEIN J	BACILLUS SUBTILIS		Ì	Ì	Ì		1		
PSYZA GACINE	STAGE II SPORULATION PROTEIN AA			1	1		+	+	1	1
PEPIN NACI	STAGE IS SPORTLY ATION PROTEIN AB			T		Ī	\dagger	1	1	
PSP2B BACME	STAGE II SPORUI	BACILLUS MEGATERIUM	15.5				-	ł		
PSP1D BACSU	STAGE II SPORU		134.161	T	T	Ī		H		ļ
PSP2G BACTK	POSSIBLE ASPAR	ENSIS	4.36	11:14	Ì		-	-		-
PSP1J DACSU	STAGE II SPORULATION PROTEIN I			463-500			Н			
PSP10 BACSU	STAGE III SPORI			\$2.16						_
PSP31 RACGU			44.75]					_
PST4A DACSU	STAGE IV SPOR	DACILLUS SUBTILIS	29-180	1			1	-		
2540	STAGE IV SPOR		99 66	1	Ì		1			
PSP4G BACSU	STAGE IV SPORULATION PROTEIN AB	BACILLUS SUBTILIS			1	Ī	1	+		
PSEAN BACSO	ANTIGEN I	OWNE	814.518	1	1	Ī		$\frac{1}{1}$		
PSPAR BACSU	SUBTILIN BIOSYNTHESIS 117 KD PROTECH		902-181	T				ł		
PSPAC BACSU	SUBTILIN BIOSYNTHESIS PROTEIN SPAC.		11:31	T	T	T	\dagger	\dagger	\downarrow	+
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TALVISPOSAJE SYGGELLA SOPNE 11-18 200-227 TALVISPOSAJE ESCHENICIA COLI 718-744 TALVISPOSAJE TALVISPOSAJE TALVISPOSAJE 178-744 STORI PROBADIL TALVISPOSAJE SACILLUS TRUTRINGIENSIS 111-304 119-446 STORI PROBADIL TRANSPOSAJE SACILLUS TRUTRINGIENSIS 131-304 119-446 TALVISPOSAJE SACILLUS TRUTRINGIENSIS 131-304 119-446 STAPPATO COCCUS AUBLUS 1	100		ESCHEDUCHIA COLI	16:15								
TRANSPOSASE ESCHELICHIA COLI 129-154	TLAS SHOSO		SHIGELLA SONNE!	11-15	200-227	131.23						
PUTATIVE TAANSFOOAASE	PLAT ECOL	1	ESCHENICHIA COLI	729-756								
13019 PROBABLE TAANSPOSASE BACILLUS THURNOENSIS 211-308 151110 1511-308 1511-3	TRAS MYETL	PUTATIVE TANN	MYCOBACTEMUM TUBERCULOSIS	129-186							Ì	
	TILVE BYCTE	S231B PROBABL	BACULUS THURINGENSIS									
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	SIALASE PRECURSOR SIGNAL REPRESSOR PROTEIN SE TIONAL REPRESSOR PROTEIN NI-NEINYL TANNSFERASE WITHOUT ALPINA CHAIN WITHASE ALPINA CHAIN WITHASE ALPINA CHAIN	AND PRICALES AND	137-154 113-14 113-14 113-14 113-16 100-103 1102-114 1102-1	111-853	1130-1371				
The state The	N N NEITALÄSE PRECURSOR ASE IPTIONAL AEPRESSOR PROTEIN THITISSE ALPIA CHAIN YMTHASE ALPIA CHAIN YMTHASE ALPIA CHAIN YMTHASE ALPIA CHAIN	AUGINOSA SECENTIIA		111453 111453 111453	130-1377				
1001 110	N N NEIALASE PRECURSOR ASSE PATIONAL REPRESSOR PROTEIN PATIONE ALPIN CHAIN YNTHASE ALPIN CHAIN YNTHASE ALPIN CHAIN YNTHASE ALPIN CHAIN	NILEMALE.			136-137				
	N NEITONAL AEPRESSOR PROTEIN FITONAL AEPRESSOR PROTEIN FITTING THAT CHANNE ELASE THITISSE ALPIA CHAIN VATHASE ALPIA CHAIN VATHASE ALPIA CHAIN	SILVA JAS			136-137				
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	N MEIALASE PRECURSON ASS PRICORAL REPRESSOR PROTEIN FINITALIANT TRANSFERASE FINITALIASE ALPIA CHAIN VATHASE ALPHA CHAIN VATHASE ALPHA CHAIN	NILES JOS			136-195 136-1377 136-1377				
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THE ECOL TRY	MEINAL REPRESSOR PROTEIN FILIONAL	NILLES JOS			156-1495 150-1377 150-1377				
	METALASE PRECURSON ASSE PRIORAL REPRESSOR PROTEIN FINITALISM ANSTERASE E-NI-NETHYL RANSFERASE F-NI-NETHYL RANSFERASE TWITISM ALPHA CHAIN VATHASE ALPHA CHAIN VATHASE ALPHA CHAIN	NILEMAN S			185-195 135-1377 130-1377				
180 1501 1504 1	MEINAL REPRESSOR PROTEIN ASE PETONAL REPRESSOR PROTEIN STATISTITYL TRANSFERASE ENILYMATERIASE TWITISSE ALTHA CHAIN VATURE ALTHA CHAIN VATURE ALTHA CHAIN	STEERING STE			165.195 136.137 130.137				
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THEY ECOL THE PROPERTY OF THE	PTIONAL REPRESSOR MOTERN STATEMENT TRANSFERASE ENI-NETHYL TRANSFERASE TWITISSE ALPHA CHAIN VATHASE ALPHA CHAIN VATHASE ALPHA CHAIN	STEERING STE	2288 2 228		135-137				
	S-FAIETHYLTANSFEASE E-NI-SETHYLTANSFEASE TYTHIASE ALPHA CHAIN TYTHASE ALPHA CHAIN TYTHASE ALPHA CHAIN	NILIAS JAS			1350-1377				
THE FEGEL THE PROPERTY OF THE FEGEL	S. P. RETHY, TANSFEASE E. NI. S. R. M. T. M. S. E. M. S. F. M. S. F. M. S. F. M. S. F. M. S. F. M. S. F. M. S. F. M. S. F. M. S. F. M. S. F. M. S. F. M. S. F. M. S. F. M. S. F. M. S. F. M. M. S. F. M.	S S S S S S S S S S S S S S S S S S S		\$\$3.914 \$\$3.914	135-137				
FINE ECOL 15%	S-FRETHY, TRANSFERASE E-NI-NETHY, TRANSFERASE TWITIASE ALPIA CHAIN TWITIASE ALPIA CHAIN TWITIASE ALPIA CHAIN TWITIASE ALPIA CHAIN	S S S S S S S S S S S S S S S S S S S		837.914 817.914	135-137				
	S-PAETHYLTANSTERSSE ENISTENTET CONTRIBUTE THINSE APIN CHAIN YMINAE ALPIA CHAIN YMINAE ALPIA CHAIN	S S S S S S S S S S S S S S S S S S S		\$13.914 \$13.014	1350-1377				
FILL ECOL 11A FILL ECOL 11A FILL ECOL 11A FILL ECOL 11A FILL ECOL 11A	S. FARETHYL TRANSFERASE TWITISSE ALPIA CHAIN	S S S S S S S S S S S S S S S S S S S		197.014	1130-1131				
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200 00000000000000000000000000000000000			176-103				-		
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PTAUS BACSU TRY		A CTORESTORNAL M.	81.5				-		
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PINE LACCA TRY	MIKASE BETA CHAIN		7		$\frac{1}{2}$				
TING LACLA IAN	TRYPTOPHAN SYNTHASE BETA CHAIN		,	+		+		1	
PTRPO VIOFA 11RY	NTHASE BETA CHAIN 1.		39:67				1		
PIRC BLEIA IND	ROL PHOSPHATE SYNTHASE	LACTOFERMENTUM	229-256			1	1		ŀ
PTRIC RCOLL IND	INDOLE 3 GLYCEROL PHOSPHATE SYNTHASE		203-232			+	1		
PINC LACLA IND	INDOLE J. OLYCEROL PHOSPHATE SYNTHASE		100				+		
PTAPE VIBBA IND	OL PHOSPHATE SYNTHASE		╗					1	
PTRPD ACICA AN	HOSPHORIDOSYLTRANSFERASE	ricus	113-150 160-194				1		
WALLEY PAILAR	ANTIGAMILATE PHOSPHICANOSYLTHANSPERASE	NOSA	205-232						
THE PARTY OF LIFE			103-232						
TIETO TOCA CONTRACTOR OF THE PERSON OF THE P		ricus	3:20						
LINE VIEW			350	-					
		MOCELLUM	165-236				L		
TICE CLOIM ANIMANIEM			143.191						
	TANK MANAGEMENT OF THE PROPERTY OF THE PROPERT	I INTOKURA BEFIERA	43:130			<u> </u>			
			19.166						
PIRFE RITME AN	THIMANILATE STRITIASE		816 191	-					
PTEUE SALTY AND	ANTHUANILATE SYNTHASE COMPONENT I		11.11.11		1				
PTILVE SULSO AND	STRUMNILATE SYNTHASE COMPONENT I					1			
FIRPE, VINPA ANY	THEANILATE SYNTHASE COMPONENT IS		Ī	1			_		
FIRE ACK'A AR		ETICUS	£						
PIRE AZINIA AN	ANTITATION OF STREET STREET	VSILENSE	6.3			-			
FYER SCOUL	ANTIIRANILATE SYNTHASE COMPONENT II		5.33						4
PTENG LACE AN	ANTHUAMILATE SYNTHASE COMPONENT II		4-31						-
PTENG PSEAR AN	ANTIGAMILATE SYNTHASE COMPONENT II		12.39						
PTAPE SALTY AN	ATTIRAMILATE SYNTHASE COMPONENT II	SALMONELLA TYPIIIMURIUM	1.3[
THE SECTION	ANTHUAMILATE SYNTHASE COMPONENT II		9-43						
AV YOUR DAILY	ANTHUANILATE SYNTHASE COMPONENT U		5.33						
PILO PSEAL PUT	PUTATIVE TRANSCIUPTIONAL REGULATOR	UKINOSA	147-174			1			
PTISE ECOL TR	TRAS PROTEIN	ESCHENICHIA COLI	61.5	$\frac{1}{1}$		1			
Ł	ESISTANCE PROTEIN PRECURSOR		164.221						

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THETTE	PROTEIN	CREATING A TVPHIM BUILD		VINO PORO	מאנט אסאס	क्राब रुपार		7	V VXV	4
12 12	PERSON PERCURSOR	STREPTOMYCES ORISEUS	10-107		ŀ		l	t	l	Ī
MSR STRAZ	NWA WETHYL		2							
PTSST STAND	TOXIC SHOCK S	AUREUS	29-63 102-	102-129						
PTSX ECOLI	CHANNEL-FORM		235-252	$\frac{1}{1}$	\downarrow		1	1		
PTTK ECOLI	HYPOTIGETICAL 24 3 KD PROTEIN	ESCHENCHIA COLI	17.01	107.114	+		\dagger	\dagger	†	T
PIVA BACRE	TVENTININE SY		-	\$61 1019-105	120		İ	l	\dagger	T
PIVE PREPE	ANTIGEN TYF!	ENJE	П	1					T	
PTYX BACSU	POSSIBLE PREPAENATE DEHYDROGENASE		244-271 312-342	342						
ITYLA ECOLI	CHORISMATE	ESCHENICHIA COLI	379-370							
PTYLL ECOLI	TRANSCRIPTIONAL REGULATORY PROTEIN TYRK	ESCHENCHIA COLI	411.510							
PTYSY LACCA	THYMIDYLATE SYNTHASE	LACTOBACILLUS CASEI	139-173	-			1	1	1	1
איז	LACTOCOCCUS LACTIS	25-108	1	1		1	+	1	T	
PTYSY STAND	THYMIDYLATE SYNTHASE	STAPHYLOCOCCUS AUREUS	316.303	 - -	\downarrow		1	1	\dagger	Ī
24 12 20 11 11	SENSON FACILITY OF DESCRIPTION OF THE PROPERTY	CALMONE LA TYPHIMARINA	274.101 316.141		-		ľ	l	t	Ī
PURANC SALTY	UNDIC PROTEIN		Т	-	-			l		Ī
PUPP ECOLI	URACIL PHOSPHONBOSYLTANSFERASE	ESCHENICHIA COLI	10.57							
PURAN ECOLI	UNACIL PERMITASE		350-384							
PUREI HELPY	UREASE ALPHA SUBUNIT	HELICOBACTER PYLONI	15.42					1	1	
PURE! PROM!	UREASE ALPW		12.99	$\frac{1}{1}$	-		1	1		Ī
PURE PROVO	CARACTER ALPINA SCHOOL	i validira	T	481.413			İ	\dagger	T	Ī
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PUREK PROM	UNEASE ACCES		57.84		L			l	T	
PUREF KLEAE	UNEASE ACCESSORY PROTEIN UNET PRECURSOR	INES	Γ	П						
PUSAS LACLA	SECRETED 45 KD PROTEIN PRECUISOR	\$ LACTIS		150-223 276-303						
PUSHA ECOLI	P-SUGAR HYDROLASE PRECURSOR		56-43		4					
PUSHA SALTY	SILENT PROTEIN USHA(0) PRECURSOR	SALMONECLA TTPHINGUIGM	30-47	071.000	1	1	1	1	1	
1000 A	EXCIPATION DE SOUCHE A		т	646 614.718	177.040		1	T	1	Ī
PUVEA PARDE	EXCINICLEASE ADC SUBUNIT A	ICANS	т	Т	Т		T	t	T	
PUWIC BACSU	EXCINICLEASE ABC SUBUNIT C	•	_	538						
PUVAC ECOLI	EXCINICLEASE AND SUBUNIT C		37-64 333-362	295						
PUVRD ECOLI	WELICASE II	ESCHENCHIA COLI	286.307		-					
PVANC FINISA	PUANA ENTRE IVANCOMYCIN RESISTANCE PROTEIN VANC	ENTEROCOCCUS GALLINARUM	11.2	1				1	t	
PVID4 ACRTS	VIRBA PROTEIN PRECURSOR	AGRODACTERIÚM TUNIEFACIENS	131-172	L						
PVIBA ACRTS	VIRDE PROTEIN 1.	AGROBACTERIUM TUNIEFACIENS	190-227							
PVIDE AGRTS	VIRTIE PROTEIN	AGROBACTERIOM TUNIEFACIENS	200	1				1		
PVIDA ACITY	VIRIO FROIEIN		177-04				1	1	1	
PUIDY ACRES	┰	ACROBACTERIOA TIRKEFACIENS	T		+		İ	1	1	Ī
PURK ACRTS	1		Τ	316	-			\dagger	Ì	Ī
PVICE AGRICA	VIRCI PROTEIN	UNIEFACIENS	L		_		T	T	T	
PVICE AGRTS		AGRODACTERIUM TUNIEFACIENS	101-10				T	l	İ	
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PVID) AGRIA	VIRDS PROTEIN		_		 -				Ī	_
FVIRA AGNIS	WIDE HOST ICAN		П					H		
PVIRA ACL	WIDE HOST ICAN		П	П					H	
PVIRA ACK	WIDE HOST RAN	MEFACIENS								
PVINB SHIPE	VIRB TRANSCRI	SHIGELLA FLEXNER	1	07-134 187-214	233-391					
PVIEW YEAR	VINCENCE NE	TERSINA ENTEROCOLITICA	2 3		+		Ì	1		Ì
PVIRE AGR 16	LIMITED HOST RANGE OF HIS VILLA PROTERY		125.53	1	\downarrow		1	†	†	T
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FILEPANE	PROTEIN	ORGANISM	4.	N N	4	रकाक रकाक		1	Т		
MSC ECOL!	ASC PROTEIN	ESCHENCIAL COLI		Ì	1	T	t	T	T	T	Ī
PVLPA MYCHOR	VALIANT SURFACE ANTIGEN A PRECURSOR	MYCUPLASMA HYDMINIS		T	t	T	\dagger	T	T	Ť	T
PVN103 8000G	PVN(0) BOILDE OUTER NEWBIANE LIPOPROTEIN I PRECURSOR	BOXXXXI A TENSOI		T	T	T	T	T	T	T	T
PVMO2 BURNE	COLER MENBRANE LITTOPHOLEIN / PACCASON	PORCEST A HERMSII	130-351			T					T
SHECK SCHOOL	OUTER MEMBEANE LIPOPROTEIN 24 PRECURSOR	BORNELIA HERMSII	3:15								
PVASS BORKE	COLITER MENIDRANE LIPOPROTEIN 25 PRECURSOR	BOADELIA HERMSII									
PVNFA AZOVI	PUNTA AZOVI MIROGEN FIXATION PROTEIN VNFA	AZOTOBACTER VINELANDII	131-161	\$16.345							
PVNFK AZOCH	HITROGENASE VANADIUM-IRON PROTEIN	AZOTOBACTER CHROOCOCCUM MCD I	٦				1	1	1		Ĭ
PVNTK A20VI	MITTOGENASE VANADIUM.IRON PROTEIN	AZOTOBACTER VINELANDII	╗	25.5	1	1	1		1	1	
PVEDI SALCH	63 KD VIRULENCE PROTEIN	SALMONELLA CHOLERAE-SUIS	Š	1	1		1		1	1	
PAN: SALBU	63 KD VIRULENCE PROTEIN	SALMONELLA DUBLIN	\$11-538			1					
PVSDE SALDU	VIRULENCE PRO	SALMONELLA DUBLIN	3-36								
DVBIV BIVV	EYTOLYSIN SECI	VIBRIO VIENTICUS	\$								
PWAPA STRUM	WALL ASSOCIAT	STREPTOCOCCUS MUTANS		313.386							
PWRBA ECOLI	TAP REPRESSOR	ESCHENCHIA COLI] 911-60								
PX191 ECOL	K POLYPEPTIDE	ESCHENICHTA COLI	16.19		H						
PX103 FCOL	IX POLYPEPTIDE	ESCHERICHIA COLI	104-131					1			
SXISS ECOL	X POLYPEPTIDE	ESCHENCHIA COLI	24.13								
PXISA ANASP	EXCISASE A	ANABAENA SP	г	1 911-68	135.162	-	-				
	POSSIBLE INTEGRASEAECOMBINASE XPRB	ESCHENCHIA COLI	261-295								
PINT A STAIN	YMOSE ISOMER	STAPHYLOCOCCUS XYLOSUS	100								
PYYOR KIEAF	KYTUT OSE KINA	IXLEBSIELLA AEROCENES	8.29		l						
1000	YVI I DEFENDATE	LACTOBACILLUS PENTÓSUS	52-79	211-238	260-287						
NA K KAYA	XY IN OSE KINASE	STAPHYLOCOCCUS XYLOSUS	Γ	Т	Г	246-273		Ī	Γ		
2000	VALUE BEPRES	BACILLUS SUBTILIS	5	L	Т	T	ľ	ľ	ĺ		
A CALLED	XVI OKE BEPREKKINE	LACTOBACILLUS PENTOSUS	L		l	l		İ			
NA P CYAYY	XY OSE REPRESSOR	STAPHYLOCOCCUS XYLOSUS	\$ 62	101-158	101-215	221-255	174.301				
PYYL Z PSEPU	FLECTRON TRANSFER COMPONENT	PSEUDOMONAS PUTIDA	21:38	104-131					ľ		
AN CALSA	PYWA CALSA PUTATIVE ENDO I 4 BETA-XYLANASE	CALDOCELLUM SACCHAROLYTICUM	198-225								
PXYNA BACCI	O. 1 4-BETA-XYLANASE PRECURSOR	BACILLUS CIRCULANS	2.2								
PYYNA BACSS	NDO-I 4-BETA-	BACILLUS SP	13,200								
PXYNA BACSU E	NDO-1,4-BETA-3	BACILLUS SUBTILIS	П								
PXYNA CALSA	NDO-1,4-BETA-	CALDOCELLUM SACCHAROLYTICUM	59	226-256							
PXYNA PSEFL	NDO-1.4 BETA.	PSEUDOMONAS FLUORESCENS	13-11								
PXYNB BACPU	DETA-XYLOSIDASE	BACILLUS PUMILUS	459-486								
PXYMI CALSA	HETA-XYLOSIDASE	CALDOCELLUM SACCIJARULYTICUM	£0.474	7	7						
PXYNB PSEFL	ENDO-1,4-DETA-3	PSEUDOMONAS FLUORESCENS	2		2.74	ž Ž	1	1	1		
PXYNC PSEFL	ALPHA-L-ARABINOFURANOSIDASS C PRINCURSOR	PSEUDOMONAS FLUORESCENS			1	1	1	1	1	1	
PXYNC STRLE	ENDO-1,4-DI:TA-XYLANASE C PRECURSOR,	STRUCTOM TOLS CIVIDANS	7.7	Ī	1	1	1	1	1	1	
Y I K HALMO	HATOTREELOAL 14.9 AD PROJECT	CONTRACTOR OF ALIG	10.1	Ī		Ť	1	Ì	Ī	Ī	T
TANK ALLE	וואשט גווהגועיין	METHANDRIE VIDACTER SAUTIII	121.162	177.218	T	T	T	Ī	T	T	T
PVAAC FCOL!	RYPOTHETICAL 34 & KD PROTEIN	ESCHERICHIA COLI	171-298		T	T		Ī	Ī		
PYAKC PSEPL	HYPOTHETICAL 33 9 KD PROTEIN	PSEUDOMONAS FLUORESCENS	174-301								
PYANN ECOL	PYAAM ECOLI HYPOTHETICAL 19 I KD PROTEIN	ESCHERICHIA COLI	45.72								
PYAN ECOLI	HYPOTHETICAL	ESCHERICHIA COLI	352.379								
PYAAQ ECOLI	IIYPOTHETICAL	ESCREMENTA COLI	155-162			Η					
PYABC ECOL!	HYPOTIETICAL	ESCHENCINA COLI	131-158								
PYABO ECOLI	HYPOTHETICAL	ESCHŒNICHIA COLI	037-950	627.654							-
PYABN ECOLI	HYPOTHETICAL	ESCHENCHIA COLI	421-455		-: :-						
PYACS PSEAK	HYPOTHETICAL	PSEUDOMONAS AERUGINOSA	48-35	130-177							_
PYADZ CLY IB	HYDTIETICAL	CLOS FILIDIUM ACETOBUT YLICUM	2.109	П		٦					
PYADS CLOND	IYPOTHETICAL	CLOSTAIDIUM ACETORUTYLICUM	2	8	20.23	1					
PYADS CLOND	IYPOTILETICAL	CLOSTRIBIUM ACETORUINLICUM	Ş	- 1		1					
PYADA YEREN	NVASIN PLECU	TERSINA ENTERCOUNTA		100	116.311	Ì	1		1		
PYADA TERUS	NVASIN PRECU	YERSINIA FOEULALI UREN, ULADA	77.40	247.50	1	1	1	1	1	1]

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EULE MAME	PROTEIN		\exists		V TVJEV	PYZEV	\$ 7287	AREAS	7 VZNV	TVINV	AREA
PYADC ECOLI	HYPOTHETICAL PROTEIN	ESCHENCIRIA COLI	╗	<u>=</u>	1						
PYACA RICKI		RICKETTSIA RICKETTSII	107-134								
PYAHB ECOU	PYAND ECOL! INPOTHETICAL 29 4 KD PROTEIN	ESCHENCHIA COLI	121-248			_					
PYAFD_ECOL!	HYPOTHETICAL 29 I KD PROTÉIN		=								
PYAFE ECOLI	HYPOTHETICAL 23 0 KD PROTEIN		123-150								
PYAIB ESCIE			÷								
PYAMI SALTY	PUTATIVE AMID	SALMONELLA TYPIIINUARINI	8								
LAVII SYNY	IYIQIIBE IICAL	SYNECTIOCYSTIS SI*	Т	T							
PYAT AIYOLE	IYPO PROTEIN P	LETRAE	Т	2	100						
PYATA BACFI	HYPOL ATP.BINE				1	1					
PYATS MYCGA			7								
PYATU MYCGA	HYPOTHETICAL PROTEIN	7		.1.00							
PYAVS XANCV	HYPOTHETICAL SO KD AVIAULENCE PROTEIN	WIPESTRIS		199.226							
PYBAH ECOL!	HYPOTHETICAL 14 S KD PROTEIN		49.79								
PYBBA ECOLI	PYBBA_ECOLI HYPOTHETICAL ABC TRANSPORTER		6-69								
PYBED ECOLI	HYPOTHETICAL # 8 KD PROTEIN	ESCHENCHIA COLI	51-62		_						
PYBID ECOLI	HYPOTHETICAL 14 I KD PROTEIN		97.134		-						
PYCAE ECOL!	HYPOTHETICAL 24 S KD PROTEIN	ESCHENCHIA COLI	14-61								
PYCBA ECOLI	HYPOTIETICAL PROTEIN	ESCHENCHIA COL!	18-65		ľ						
PYCEL BACUN	PYCBL BACUN HYPOTHETICAL 15 J KD PROTEIN	FORNIS	99-100								
PYCEA BACLA	HYPOTHETICAL PROTETY		1. 201-114								
PVCFC_ECOUL	HYPOTHETICAL 23 F KD PROTEIN		57.79								
PYCHR ALCEU	HYPOTIETICAL PROTEIN	ROPHUS	7								
PYCIB ECOLI	HYPOTHETICAL 20 I KD PROTEIN		3								
WELL ECOL	IS A KID PROTEIN		Ī	34.66	ľ						
	HYPOTIGHICAL PROFES			Ī	l	Ī	Ī				T
1001	HVPOTRIETICAL ALLED PROTRIN		17.75	T	T		Ī	Ī			
PYCES SYNEY	HYPOTIGETICAL 29 3 KD PROTEIN		- N	l		Ī	Ī				Ī
PYCP) SYNY)	HYPOTHETICAL 28 0 KD PROTEIN		Г	130-134	T						Γ
т	-		277-304		r	Ī	Ī				
PYCPG MASLA		AMINOSUS	<u>*</u>	Ī							
PYCPY PSEA			į								
PYCE BACTE	PYCKL BACTIK HYPOTHETICAL 19 I KD PROTEIN	CIENSIS	П	133-160							
PYCSS ECOU	HYPOTHETICAL PROTEIN PRECURSOR										
PYCWS BACSU	HYPOTHETICAL PROTEIN										
PYDIM HERAU	HYPOTHETICAL	URANTIACUS			П	П					
PYDBA ECOLI	HYPOTHETICAL		П	117.144	163-216 2	137-167	205-339	458-485	676-717	136-1163	1499.1530
PYDED ECOLI	HYPOTHETICAL		П	П							
PYDD8 ECOL	HYPOTHETICAL 16 7 KD PROTEIN	ESCIPLICION COLI	909-000		726.753	1					
1000	ATTO DE LICAL		Т	Т	100	1					
ANER CON	UVPOTUETICAL :		41.79		1	T	Ī				1
ANDEL ECOL	I VENTARTICAL			Ī		Ī	T				
PYDEK ECOLI	KYPOTHETICAL		8	34.55	\$65.503	T	Ī				
PYDN'N BORBU	HYPOTHETICAL	ONFEN	Т	Т					ľ		
PYDO! SULSO		cus		100	İ	T			Ţ		Ī
PYDOS SULSO	PYDOJ SULSO HYPOTHETICAL 169 KD PROTEIN /		T			Ī	Ī				
PYEBA ECOLI	HYPOTHETICAL		93.120		T	T		Ī			T
	HYPOTHETICAL	ESCHELUCHIA COLI	20.33			T	Ī	Ī	Ī		Ī
		ESCHENCHIA COLI	57.70	Ī	È		Ī				-
PYEEF ECCL	HYPO 49 8 KD TRANSPORT PROTEIN	ESCHENICHIA COLI	147.174	-	F			Ī	Γ	Ī	T
PYEGA ECOL	HYPOTHETICAL		145-172			Ī			Ī		F
אינות נכמה	HYPOTHETICAL 36 9 KD PROTEIN		69.106	20.510							T
PYEMB ECOLI	HYPOTHETICAL			\$01-545					Γ		T
PYEITO ECOLI	HYPOTHETICAL		96-123								
_[-1		٥								
PYCHI ECOLI	IIYPOTHETICAL 138 1 KD PROTEIN	ESCHERICHIA COLI	15.70	102-129					Γ		

PCGENE	1107517314	Prokaryotte Sequences		* * 4 % *				7 . 44.	* * * * * * * * * * * * * * * * * * * *		1
THE NAME	KILIOR	ORGANISA	45.7	_	1		1	Т		T	Ţ
PYENS ECOLI	WYONG TICAL .	Country Countr	977	T	İ	\dagger	T	l		1	Τ
PTEK ECOL	TYPOTHETICAL)	ESCHEMIN COLI		Ť	t	t	1			1	T
PYEIF ECOLI	HYPOTHETICAL PROTEIN	ESCHENCHIA COLI		1	Ì	T	1		 	1	T
PYED ECOU	TYPOTHETICAL 4	ESCHEKICHIA COLI		1	1	1	T			1	T
PYELA ECOLI	INTOTHETICAL A	ESCHENICHIA COLI		1	\dagger	†	†	1	1	+	T
PYLIF ECOL!	YPOTHETICAL	ESCHE/UCHIA COCI		1	1	†	1			1	T
FYFIO FCOLI	HYPOTHETICAL 91 2 KD PROTEIN	ESCHENCHIA COLI	1	1	1	1	1	1		1	T
FY1110, 1 COL.1	HYPOTHETICAL 40 6 KD PROTEIN	ESCHERICHIA COLI	707	1	1	+	t	1	1	1	T
PYFU2 NACST	IYPOTHENCAL X	BACILLUS STEAROTHERAIGHILUS	2 2	1		\dagger	T			\downarrow	T
PYFXX BRAJA	HYPOTHETICAL P	BRADYKHIZOBIUN JAPONICUM			1		1		-	\downarrow	T
PYGAP BACKE	HYPOTHETICAL 3	BACILLUS MEGATENUM	200	1	1	+	1			1	T
PYCFD ECOLI	HYPOTHETICAL 2	ESCHENICHIA COLI	214-241			1		-	-	-	٦
PVCCB FCOL	HYPOTHETICAL 1	ESCHENGIIA COLI	225-252							_	
1023 2223	VAPOTICAL I	F SCHENICHIA COLI	209-336						_	_	Γ
3	1000	PANTICATED AT A LICENSE	1997			-	T			L	Γ
LACIS BACTO	HTTO I WILLIAM AND TROPER	SEEMONOWA CHILDA	161.70				Ī			ļ	Ī
NGS PSEC	HYPOTICETICAL	Perimeter Political		1	T	l	İ		-	-	T
PYGIF ECOLI	HYPOTHETICAL	ESCRENCIAL COLI		1	\dagger			l		+	T
PYGL4 BACST	HYPOTHETICAL 1	BACELUS STEAROTHERMOMILUS	2		Ì	1		1		1	T
PYCL SACST	HYPOTHETICAL PI	BACILLUS STEAROTHERAIOPHILUS	113:200			1				4	٦
PYCLN BACCE	INPOTHETICAL I	DACILLUS CEREUS	19:134	1						4	1
PYGRD BACSU	PPOTIETICAL P	BACKLUS SUBTILIS	20-47							_	
PYCRE BACKU	PPOTIETICALI	BACILLUS SUBTILIS	111.11								
PVCAP BACKU	PPOTIETICAL 1	BACKLUS SUBTILIS	\$21.96								
010 0 0000	VECTOR	CLOSTRUDIUM ACETOBUTYLICUM	166.210							L	Γ
1010	VECTORICAL	STREPTOCOCCUS MUTANS	r	10.00	135-262					L	Γ
	VECTOR	ESCHERICHIA COLI	T	Г						L	Γ
200	National Asset Services	ESCHERICHIA COLI	25.55	Ī						L	Γ
THE STATE OF THE	WOTHETICAL	ESCHENICHIA COLL	Γ	20:165		l		-		H	Γ
PYIMO FCOL!	ROBABLE ABC	ESCHERICHIA COLI	176-103			<u> </u>	ľ	-	_	L	Γ
PYNIBG PSEPU	PROBABLE ABC TRANSPORTER	PSEUDOMONAS PUTIDA		106-135	141.618					L	Π
PYIMG THUFE	ROBABLE ABC	THIOBACILLUS FERROOXIDANS	113-140								П
PYIDE ECOLI	YPOTIETICAL	ESCHERICHIA COL!	267.297							_	
PYHEM DACSU	*YPOTHETICAL	BACILLUS SUBTICIS	£ 20				1			-	
PYHET ANASP	IYPOTHETICAL P	AMABAENA SP	11.00		1	1				-	٦
PYIGHA ECOLI	IYPOTHETICAL I	ESCHERICITIA COLI	26.15							\dashv	
PYHIG ECOL!	IYPOTHETICAL I	ESCIIERICIIIA COLI	-								
PYMIN ECOL!	IYPOTHETICAL I	ESCHENCHIA COLI	10:01		1			-			
PWII LACLA	IYPOTHETICAL	LACTOCOCCUS LACTIS	167.194							_	
PYHIJ LACLA	HYPOTHETICAL 38 9 KD PROTEIN	LACTOCOCCUS LACTIS	ž	2 2		1					
PYHIS LACLA	HYPOTHETICAL	LACTOCOCCUS LACTIS	2	1			1			_	Ì
PYIII	IYPOTHETICAL)	LACTOCOCCUS LACTIS	2	2	<u> </u>		Ì	_		4	
PYIII STANI	HYPOHIE HEAL	ALMITIC	11-67								
ryin'n viocii	IYPOTHE HICAL!	VIBRIO CHOLERAE	36.1%							_	
PYING METER	AYPOTHETICAL 1	METHANOTHERMUS FERVIDUS	200		1	1				4	
PYHSI CLOAB	PYPOTHETICAL 1	CLOSTADIUM ACETOBUTYLICUM	Ş							4	٦
FYHSA CLOAB	HYPOTHETICAL 2	CLOSTAIDIUM ACETOBUTYLICUM	£	ī	į		Ì			4	1
PYHEC CLOAN	IYMITII;IITAI, A	CLOST MINION ACI; TONOT YI, IT IN	23-32	1	2					4	
PYIIVI LACITE	INTERNITION OF	LACTORACILLUS IIIII.VETICUS	93.120	137.154							
PYHYA PSESN	IIYPOTIIETICAL !	[PSEUDOMONAS SP	217-266							-	П
YIII MALIN	HYPOTHETICAL 3	HALOBACTERUM HALOBIUM	245272				Ī	_			
PYIS MYCHU	I SHIR HYPOTHET	MYCOBACTERIUM TUBERCULOSIS	1946								3
PYI43 PSEAY	IIYPOTHETICAL (PSEUDOMONAS AMYLODEKAMOSA	97.6	П							
PY148 ME TY	ISMI HYPOTHETI	METHANOBREVIBACTER SMITHII	3.100	154-184	111.165						
PY153 HALMA	HIYPOTHETICAL!	KALOBACTENUM HALOBIUM	3								
PYIDS ECOLI	HYPOTHETICAL !	ESCHENCKIA COLI	203-239		1	1	1	$\frac{1}{1}$		4	٦
PYIDD ECOLI	HYPOTHETICAL	ESCHEUCHIA COLI	2		1	1		1		4	7
PYIBE ECOLI		ESCHENCHIA COLI				1			_	4	7

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PCGENE	107217814	Proharyatie Sequences	П	I-1	H	• 1	H	1 1	
ELENAME			AREAL AREAL AREAL	-т	ABEA &	AREAS	AREA AREA?	EAL AREAL	48.64
PYIBO ECOL			70-97			1	1		
PYICC ECOU	11	ESCHENICHIA COLI	4)-170		1	1			4
PYICE ECOL!	HYPOTHETICAL 31 I KD PROTEIN		32.139						
PYICH ECOL!	HYPOTHETICAL 62 3 KD PROTEIN		401-13		1				
PYICI ECOLI	HYPOTHETICAL 48 I KD PROTEIN		133-149						
	HYPOTHETICAL IS 2 KD PROTEIN	ESCHENICHIA COLI	76-103						
	HYPOTHETICAL 49 9 KD PROTEIN		320-347		1	1	1		
	HYPOTHETICAL 13 8 KD PROTEIN		7			1			
	HYPOTHETICAL 38 9 KD PROTEIN		102-204	377.304	1	1			
	HYPOTHETICAL IS IND PROTEIN	ESCHENCHIA COLI	<u>2</u>			1			-
	HYPOTHETICAL 63 I KD PROTEIN	-	*						-
PYIDE ECOLI	HYPOTHETICAL		63.97						
	HYPOTHETICAL 4	ESCHENCHIA COLI	221-24						
PVIEC ECOLI	IYPOTHETICAL	ESCHENCHIA COLI	20.51 270-797			l	-	-	
NUMBER STATE	AVPOTITE TICAL	4 THE KI	Γ		l	İ			-
1000	V 14 21 14 11 1		14.190			l	l		
100000	THE PERSON AND PROPERTY.		101 101		l	Ì		1	
	HYPOTHERICAL 48 V NO PROTEIN	ESCALACINA COLI	175:(A)			T			+
	HYPOTHETICAL 24 7 KD PROTEIN		91-19						
	HYPOTHETICAL IS OND PROTEIN		┑		1	1			
	HYPOTHETICAL SIS KD PROTEIN		301-242 380-407		1		-		
PYIFC_ECOL!	•		115-202						
	HYPOTHETICAL 140 KD PROTEIN		36-15		_		-	-	
			120-154			r	-		L
	HYPOTHETICAL S4 7 KD PROTEDI		201.234				-		
	LIVERTICAL 28 I KD PROTED		67.94				-		-
1000		GECHERICHIA COL	31.78			t	$\frac{1}{2}$		+
	LOCALISTICAL STORY DESCRIPTION	Secure and a Coll	13.140		İ	t			-
יייייייייייייייייייייייייייייייייייייי	ATTO THE HOLD AND THOUGHT	ESCHEDICH & POLY	201.15		t	t	l	1	+
	ATTOTICAL ALA NO PROTEIN		30.44			1		1	1
300	2 :	Escretoria con			1	+			
Luin Econ	HYPOTHERICAL SAIL NO PROTEIN		90(-2)7			1	1		1
	HYPUTHETICAL 19.1 KD PRUTEIN	ENCALMINA COLI	461-711			1			$\frac{1}{1}$
	HYPOTHETICAL 65 4 KD PROTEIN		16.4		1	1		1	
	HAYOTHE REAL DE 9 KD PROTEIN		201-12	477-75	Ì	1	1		
	HTFU: NE INCAL BILB AD PROLEIN	ENTRACTION COL	200.710		1	1	$\frac{1}{1}$		1
MINO ECOL	HYPOTHETICAL 33.1 RU PROTEIN				1	1			
	HTPUHEIICAL JI.V KU PROJEM				1				
	HYPOTHETICAL 23.5 KD PROTEIN	ESCIENCIAIA COLI	9:36		1	1			
	HYPOTHETICAL IS 9 KU PROTEIN					1			-
PYILE COL			(8.77		1	1			
PYIID ECOLI			24:71			†		1	-
VIIIC ECOLI		ESCALING CUCI	19-197		1	1	1		$\left \right $
	REPORTED AL 18 J. NO PROJEIN		(07:07		1	1			
	HYPOTHETICAL 11 2 KD PROTEIN		26.53			1		-	
	HYPOTHETICAL 12 I KD PROTEIN]	╗						
	HYPOTHETICAL 46 6 KD PROTEIN		110-137 419-446				_	_	
PYINE LISMO	HYPOTHETICAL 26.8 KD PROTEIN	TOGENES	7.34						
PYISI SHISO			62:19						
PY1SI STACO	ISTIO HYPOTHETICAL 43.6 KD PROTEIN	OFLICOLOR	135-152						
PYIS) SINSO		NNEI	8.50						
PYISP DACE	HYPOTHETICAL 42.1 KD PROTEIN		313.339	•		l		_	L
PYJAG ECOLI			51.78				-	_	-
	HYPOTHETICAL 20 4 KD PROTEIN	ESCHENICHIA COLI	18-122			ľ	-		
	HYPOTIGETICAL 78.5 KD PROTEDI		93.120			l	-		-
	HYPOTHETICAL 9.7 KD PROTEIN		10-37				-	-	
	HYPOTHETICAL 16.7 KD PROTEIN		112-149				-	-	-
	HYPOTHETICAL IS 7 KD PROTEIN						-		L
PYICC ECOLI	HYPOTHETICAL 60 1 KD PROTEIN (ESCHENICHIA COLI	18-65 414-441	265-151			L		

2007-1-10 100-1-10 10 10 10 10 10 10 10 10 10 10 10 10 1	Pratacyotie Sequences		7	7	т	Т	ì	ī	ı	
	ORGANISM	1511	1438	V	4	2	4	AND LAND	1	1
	ESCHENCHIA COLI	244		1	1	1	1	1	1	
CO FEDEL HYPOTHETICAL 19 2 KD PROTEIN	ESCHERICHBA COLI	12.22		1		1	1	1	†	I
HYPOTHETICAL 35	ESCHEALCHIA COLI	91.118					1	1	1	I
HYPOTHETICAL 53	ESCHENCHIA COLI	242-269		1	1	1		+	1	
	ESCHENICHIA COLI	366-396			1	1	1	1	1	
HYPOTHETICAL A	ESCHENICHIA COLI	30-54			1		1		1	Ĭ
	ESCITE ALCHIA COLI	13:29	451-485			1	1	-	1	
	ESCHERICHEA COLI	103-134						+	1	
HYPOTHETICAL II	ESCHERICHUA COLI	15-69	11-139				1		1	
HYPOTHETICAL 40	BACILLUS FORMUS	321-355							1	
HYPOTHETICAL PR	LACTOBACILLUS ACIDOPHILUS	47.74								
AND THE TICAL IS	LACTOBACETUS ACEDOPHILUS	13-43								
	LACTOBACILLUS ACIDOPHILUS	47.74								
NO PURTICAL SA	SULFOLOBUS SOLFATANCUS	23-50								
HYPOTHETICAL	PSEUDOMONAS PUTIDA	116-213	114-341							
_	YEASINIA ENTEROCOLITICA	184-221								
HYPOTHETICAL !	ANABAENA VANIABILIS	172-199								
AYPOTHETICAL 29	LACTOCOCCUS LACTIS	15.70								
PYME2 BACSU HYPOTHETICAL 15 3 KD PROTEIN	BACILLUS SUBTILIS	53.79	П			٦			1	
IG2 MYCCE HYPOTHETICAL 114 4 KD PROTEIN PRECURSOR	MYCOPLASMA GENITALIUM	56-13	29-10	20.443	1001-186	1		┧	1	Ì
GA CLOPE HYPOTHETICAL PROTEIN	CLOSTRIDIUM PERFUNCENS	139-166				1	1		1	
PYNGS CLOPE HYPOTHETICAL 31 3 KD PROTEIN	CLOSTIUDIUM PENFIUNCENS	╗	5.9	≅				+	1	
III METTL HYPOTHETICAL PROTEIN	METHANOCOCCUS THERMOLITHOTROFINCUS					1		_	1	
OF PARDE HYPOTHETICAL \$3 KD PROTEIN	PARACOCCUS DENITRUFICANS	52-86						1	1	
TI ANASP HYPOTHETICAL 28 I KD PROTEIN	ANABAENA SP	171-198							1	
TS ANASP HYPOTHETICAL PROTEIN	ANABAENA SP	17.165					1	1	1	
HD ECOLI HYPOTHETICAL 21 4 KD PROTEIN	ESCHERICHIA COLI	273				1	1	+	1	
PYONG ECOLI HYPOTHETICAL 43 3 KD PROTEIN	ESCHENICHIA COLI	104-17				Ī			†	
IA ECOLI HYPOTHETICAL ISOKOPROTEN	ESCHENCHIA COL:				1	Ì	T		T	
PYOJE ECOLI HYPOTHETICAL 91.5 KD PROTEIN	ESCHEROCIA COLI					T	1	+	T	
ST ECOLI MYTOTHERICAL V. FLO PROTEIN	SCHENCIA COLI	143:193			T		T	\mid	T	
HTTO INC. I	PECHEDICALA COLI	94-121				ľ	Ī		T	l
SYCHOLO BUCKE INVESTIGATION PROTEIN IN ORDER STEERON	PHOTOBACTERUM SP	32.59				Γ				
	YEASINIA ENTEROCOLITICA	63.108					Ī			
PH YEAPS IPROTEIN-TYROSINE PHOSPHATASE YOPH	YERSINIA PSEUDOTUBERCULOSIS	63.105								
PH YEALN OUTER MEMBRANE PROTEIN YOPH	YEASINIA ENTEROCOLITICA	23.50	(6-99	133.262						
PYOPH YEARS OUTER MEMBRANE PROTEIN YORN 'S	YERSIMIA PSEUDOTUBERCULOSIS	23.50	6.9	233-762			Ī	+	Ť	
PO VEREN YORG PROTEIN PRECURSOR	VERSINIA ENTEROCOLITICA	9					1	1	1	
RA HAEIN HYPOTHETICAL 31 SKD PROTEIN	KAEMOPKILUS INFLUENZAB	147:174			1	Ţ	1	\dagger	1	
PYORA LISMO HYPOTHETICAL 23.6 KD PROTEIN ;	LISTELIA MONOCYTOGENES	27-27			1	1	1	\dagger	1	
IYPOTHETICAL 14	PTROCUCLOS WOESES	017:591			1	1	Ì	1	1	
PYONG HAEIN HYPOTHETICAL IN IND PROTEIN	HAEMOPHICUS INFLUENTALE	19-00				Ī	1	\dagger	Ť	
AC HAER HYPOTHETICAL IN A KU PRUTEIN	ILLENOPULI DE INFLUENZA F	47.75	81:58				1	+	T	l
PYORE HARIN BRUTAULIN	TO A ELECTRICATION OF THE TRANSPORT	100,336			Ī	Ī	Ī	+	T	
PYON HAEIN 18 I KO PROTEIN	INTERCOPULITY INTUITIES AND				T	Ī	T	\dagger	T	l
NATO RELICAL	MACMORNI 114 TARE LIENZAR	416.450	611.323		Ī	Ī	T		T	l
THE HARIN (9) 4 KD PKOLEIN	BACH LISCHALL IS	148.175			T		\dagger	\dagger	T	
STORY BACKO BACKOTHE ICAL PROTEIN	PYROCOCCUS WOESE!	(6-90					Ì	\dagger	Ī	-
AND THE PROTECTION IN PROTEIN	LISTEIUA MONOCYTOGENES	27.54	L						Ī	1
THE CYALL MYPOTHETICAL IS NO PROTEIN	STAPHYLOCOCCUS AUREUS	1.91	110-137					-	ľ	
PYPES BALLED HYPOTHETICAL 22 S KD PROTEIN	BACILLUS SUBTILIS	27.84	L						Γ	
HYPOTHETICAL	STAPHYLOCOCCUS AUREUS	29-70								
HYPOTHETICAL	STAPHYLOCOCCUS AUNEUS	34:10								
PYP2B STAAU HYPOTHETICAL 21.0 KD PROTEIN	STAPHYLOCOCCUS AUREUS	2	47.20	87-62		1		+	1	
EVEST STABLE HYPOTHETICAL 21.7 KD PROTEIN	STAPHYLOCOCCUS AUXEUS		2							

PCGENE 18921784		Postsonsiis Comments						ŀ			ſ
FILE MAME PROTEIN			ARCAL	AREA 2	ARFA 3	ARFAI	ABTAG	OV YVANY	A 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4		1
PYPT AGRT4 HYPOTHETICAL	ITICAL PROTEIN 1	EXS	Г	1	1	T	I	Т	Т	Т	1
PYPA3_LEGPN HYPOTHE	TICAL PROTEIN		94-135	Ī	T		T	-	ļ	+	T
PYPAS ENTRA HYPOTHETICAL	STICAL 13 KD PROTEIN	sytis.				I		-	-		Τ
PYPA BACAN HYPOTHETICAL	TICAL 21 6 KD PROTEIN	Cis	13-47	115-162				-	-	\mid	T
PYCI ECOLI HYPOTIES	TICAL 27 6 KD PROTEIN		=======================================				H				Τ
SYSTEM SALSO MYPOLITERICAL	TICAL 27.3 KD PROTEIN	2	- T		1					L	
PYBUI CYCET GUENTERICAL	TICAL IS THE PROJECT		2			1					
т-		STRECAUCION SP	Ī	T		1	1				
PYPIS CLOPE HOROTHE	TICAL IA & KIN PROTEIN		I		6):(4)	1				-	
PVELY CLOSE HISTORIANICAL	TICAL IS AN ENGLAND			Т			1				
A PER PER LA PER	TITAL SE AND BEATER			703.250	303-340	1	1				
PVPB BACKII INMOTINETICAL	TICAL DESCRIPTION OF A SECOND	PACTURE AND ACTUAL OF THE PACTURE OF	77.77	1						4	
TOTAL PROPERTY OF THE PARTY OF	TICAL BEOTERS		379-336	1				-			
PVPES PLEBO LINCOLLEGICAL	TICAL IN THE BEOTHER		22.73	1		1	1				
┱	TICAL IN THE PROTEIN		Ť				1				
-	TICAL TO LED MOTERA	1	Ì	6							
PVBVT VETTE HVBOTABLICAL	PICAL INTERPORTED	Т	2	1	1	+					П
TOTAL PRESENT STATE OF THE STAT		Т	7		1						
TOTAL BACKET HANDTHEFT	- -	SELECTION THE WIND CONTROL OF	1	380-430	1	1	Ì				
PVB71 METTE LIVEOTICETICAL		T				1					
		Ť	T	308-133			1		$\frac{1}{1}$		
PVP25 METTE HVBOTHET	TICAL OF IND PROPERTY.	7		201-74			1	1	-		
PVP? NETTE LIVESTREET A	TICAL BY SO DECITED	MCTIVANOSACIENCIM INERNACIONALICIONAL	Ŧ	7	101-101	1	1				
TOTAL PROPERTY OF THE PARTY OF	TOTAL TO A P.D. BENEFIT	┪			1						
TOTAL PROPERTY OF THE PARTY OF		741976	12:10a			1					
PARE COMP. COMP.	TICAL AS A PERSONNEL		200		1	1		-			
THE CALL AT THE PARTY	PICAL AND PROPERTY		49.70		1	1					
PYRES SALTY HYPOTHETICAL	TICAL 41 0 KD PROTEIN		2		1		1	+			
PYRS SALTY HYPOTHETICAL	TICAL 30 4 KD PROTEIN			Ì	1		1				1
PYRE SALTY HYPOTHETICAL		SALMONELLA TYPHIMITALIM		1	t		1	1		+	1
PYRG3 LACLA HYPOTHES	IICAL PROTEIN		140-167	T	†		1	+	1	$\frac{1}{1}$	1
PYRLI METVA HYPOTHETICAL P	FICAL PROTEIN		Ť	29.156	t	\dagger	\dagger	1	1	1	Ţ
PYRP2 METVA HYPOTHET	IICAL II.6 KD PROTEIN		T		t	\dagger	\dagger			+	Ţ
PYREY SULAC HYPOTHETICAL	TICAL II S KD PROTEIN		3.31		t		†			+	T
PYNE SULAC HYPOTIETICAL	IICAL I SKD PROTEIN	CALDAMUS	15:1	T	t	I	t	-		1	T
PYRIP BACSU HYPOTHETICAL 25	IICAL 25.3 KD PROTEÍN		5.5		l	l		+			T
PYRTS BACSU HYPOTHES	IICAL II.4 KD PROTEIN		3.30	18:47			\mid	-	-	+	T
PYSCB YEAEN HYPOTHEI	FICAL YSC OPERON PROTEIN BY	1	90-121				\mid		-	+	T
PYSCC YEARN YSC OPERO	YSC OPERON PROTEIN C PRECUNSOR			165-399				-		+	T
PYSCU YEKEN YSC OPERO	DA PROTEIN D	YEASINIA ENTEROCOLITICA	242-269	-				L	-		T
SVECIL VEBBE IVER OBERN	VAC OBBESTU BENEFIT IS		2					-			Γ
	Non-Day and	20-32	1	+	1					Γ	
	ON PROTEIN !	VERSINA PREIDOTINENCIA DEIA	2, 40	†	1	1		-		H	П
1	ON LIPOPROTEIN J PRECISSOR.			1	1	1					
	YSC OPERON LIPOPROTEIN I PRECURSOR I		00-136	t	1	1	+	1	4		٦
PYSCL YEREN YSC OPER	DNPROTEINL		1717	T	\dagger	†	1	1	1	1	1
PYSCL YEARS YSC OPERON PRO	DNPROTEIN	OSIS	19:17	ţ	\dagger	\dagger	+		1	1	٦
PYSMA SERMA HYPOTHET				t	t	+	Ť	+	1	+	7
PYSO2 DES M HYPOTHETICAL 2		VALENS	69-100	t	+	†	+	+	$\frac{1}{1}$	7	٦
PYSOJ DESAM HYPOTHETICAL			1 2	t	+	\dagger	\dagger	+	$\frac{1}{1}$	+	Ŧ
PYSPI LEPP JINFOTHER			Τ	2.5	\dagger	\dagger	\dagger	1	+	1	Ī
PYSKI WYCAY HYPOTHETICAL!		Omes	35.99	Ŀ	300.327	\dagger	Ť	+	1	+	T
PYSY) BACSU HYPOTHE			11.99			\mid	f	-	1	+	Τ
PYSYN METER HYPOTHETICAL	FICAL PROTEIN	lous.	\$01-84			H	H	\mid	-	+	T
PTIJE SIENE INTRUINE	- I	STREPTOMYCES FRADIAE	142-312						L	+	Т
											1

					-		L	
181-131-4	Prokaryetic Sequences	7			47 7724	, , , , ,		4 5 F.A. 8
I	MATAC	AREAL AREAL	AND A	10000	AND AND AND		7	1
FILERAME ZROILIN		344.371 1779.306	7		_	_	-	
EVENTY RAPERITINATION OF THE ASSESSMENT OF THE PROPERTY	BACGLUS SUBTILLIS	Ť					-	
	LEPTOSPICA BIFLEXA	14-113			-		1	
3	II ACTIONNICIIS LACTIS	16-112	:		-			
PYTIN LACLA HYPOTHETICAL 13 J AU PROTEIN		77.6	-					
SOURCE BACKLI LOVEDTHETICAL 20 KD PROTEIN	BACILLUS SUBTILIS				1			
17 11 10 11 11	SPIROPLASMA CITIU	102:149	_					
אווערוויער	PACTI 1:00:00:00	17.64 68.95						
TYPOTHETICAL		47.168						
PY YOU BACKLI THYPOTHETICAL 21 0 KD PAOTETH	BACILLUS SUBILLIS			Ī				
100000000000000000000000000000000000000	BACILLUS SUBTILIS	17.5						
וואניםונים		165-101 1262-289	1 68			_		
POTEN RECEIV INTRODUCETICAL 61 # KD FROTEIN	BACILLOS SOUTERS	Ī	T				-	L
-	BACILLUS SUBTILIS		7]			+	
THE PROPERTY OF THE PARTY OF TH	BACILLUS SUMTILIS	56.41 15-112	1					
ACSU MINOINE	MACH LUS SUBTILIS	24.30				-		
MYPOINEILA	95 47248474	23:52						
PYXI2 ANASP HYPOTHETICAL 18 V KU PROTEIN	TO COLOR OF THE PARTY OF THE PA	41.0						
POWER CALLA HINDOMETICAL 10 1 KD PROTEIN	CALDOCELCOM SACCIMANOL I IICUM				1			-
Manual Library Strain S	CALBOCELLUM SACCITAROLYTICUM	61.90			+			
	PACHEBICHIA COL	17-10			-			
PAYER ECOL. HATCHELL ALTON MOTOR								

WO 96/19495 PCT/US95/16733

TABLE IX

107 X 178 X 4 SEARCH MOTIF RESULTS SUMMARY

FOR ALL HUMAN PROTEINS

П	107317814 Mottl Search on All Human Protein Sequences	ARFAI	ANYA 1 AR	AREA 3 AREA 4	AREAS	AREA	AREA 7	AKEAT	ANIAS
7	THOUGHT THE MENTION ACTIVED ACTAIN TO	J	_					•	
NALAN MUNICIPALITY OF THE PARTY		\$.3	L						
4=	14.3.3 PROTECN THETA (14.).3 PROTEIN T-CELL) (1151 PROTEIN)	61-92						-	
-	4-3-3 PROTECN ZETA (PROTECN KINASE C DAUBITOR PROTEIN-1) (KC:P-1)	31.55					1	†	Ī
+-	HEA CLASS I HISTOCONDATBILITY ANTIGEN, A-29/AW-19) A-2901 ALPHA CHAIN	2					†		
_	H.A.CLASS I JUSTOCONDATIBILITY ANTICEN, A 14/AW 19) A 2401 ALPHA CIMIN	1	+				T	T	T
•	ILA CLASS I KOSTOCONZATIBILITY ANTIGEN, B-7 B-0702 ALTIA CHAIN I	7		1			Ì		
	LACLASS HUSSOCONDATIBILITY ANTIGEN, B-13 B-1301 ALPHA CHAIN	7	1		1		İ	1	T
	HEA CLASS I HISTOCOMPATIBILITY ANTIGEM, BW-15(B-15) B*1501 ALPHA CHAIN	[4:1]						T	
PIBIL HOMEN	ILA CLASS I HISTOCONDATIBILITY ANTICEN, DW-11(BW-10) B-1501 ALPICA	2	1				1	+	T
FIBIT HOMEN	H.A. CLASS I HISTOCOMPATIBILITY ANTIGEN, B-42 B-1504 ALPHA CHAIN	76-107					1	1	T
+=	HEA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-18 B-1801 ALPIIA CHAIN	14-115			-		1	1	T
•	HI.A CLASS I HISTOCONDATIBILITY ANTIGEN, B-15 B-1501 ALPHA CITAIN	14-115					1		
-	IN A CLASS I HISTOCOMPATIBILITY ANTIGEN, B-15 B-1502 ALPHA CHAIN	84-115						-	
NVAN	M A CLASS I HISTOCOMPATIBILITY ANTIGEN, B-35 B+3503 ALPHA CHAIN	84-115							٦
₽	HA CT ARE HISTOCORPATIBILITY ANTIGEN B-15 B-1504 ALPISA CHAIN	76-107				_			
4	IN A CT ARE HISTOCONDATIBILITY ANTIGEN, B-15 B-3505 ALPHA CHAIN	11.113	<u> </u>			1		-	
	HA A CLASS LINET OCCUPATIBILITY ANTICEN B-15 B-1506 ALPHA CITAIN	\$4.115						-	
_		5						•	
-	THA CLASS I RESIDENCE A HEREITT ANTICEN, 633 B. 150 ALENA CHAIN	84.7.15	-		ļ			-	
7	CLASS TESTOCOM/ATIGICAL ANTICOM, 672 6 720 MINOR CONTROL OF THE CO	11.11			-				Ţ
	RIA CLASS I MISTUCCHE A INDICE I A MISCON SERVICE AND A COLANIA						İ		
E SE	TA CLASS I MISTOCOMPATIBLE I I ANTIOCA, 8-57 8-5702 ALTAN CROSS	10.55					İ	Ī	
	HEA CLASS I HISTOCOMPATIBILITY ANTICEN, BW-60(B-60) B-6001 ALFRA CITAIN		1				+	-	
	ALA CLASS I HISTOCONO ATIBILITY ANTICEN, B-40 B-4502 ALPHA CHAIN						Ì	Ī	Ţ
Ρ.	HEA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-40 B-1001 ALPHA CHAIN	î					1	-	T
r	BA CLASS I HISTOCOMPATIBILITY ANTICEN, B-40 B-4004 ALPHA CHAIN	14-115					1	1	
Т	TA CLASS I HISTOCOMPATIBILITY ANTICEN, BW-41 B'4161 ALPHA CHAIN	84:115						-	
Т	HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, BW-41 B' (20) ALPHA CHAIN	17.114					1		
KYYCH	ALA CILASS I HOSTOCONDATIBILITY ANTICEN, BW-41(B-12) B*4401 ALPHA CHAIN	111.41							
Т	HI.A CLASS I HISTOCOMPATIBILITY ANTIGEN, BW-44(B-12) B*4402 ALPHA CHAIN	11-114					1		
SAAA.	HA CLASS I HISTOCOMPATIBILITY ANTICEN, BW-44(B-13) B*4403 ALPHA CHAIN	17:114						7	
NAME	ILA CLASSTHISTOCOMPATIBILITY ANTIGEN, BW-41(B-12) B*4561 ALPHA CHAIN	34-115	1				1		
PIB4 HUMAN	HLA CLASS I HISTOCOMPATIBILITY ANTICEN, BW-46 B*4601 ALPHA CHAIN	87.114	1				1		
Ι-	HLA CLASS I KOSTOCOMO AT BELITY ANTIGEN, BW-47 B*4701 ALPHA CHAIN	39:115					1		
г	HEA CEASS I HISTOCOMONEMENTY ANTIGEN, B-48 B' 4601 ALPHA CHAIN	14-115	1				1		
~	HEA CLASS I HISTOCOMPATIBILITY ANTIGEN, BANGE, 21) BASSO ALPHA CHAIN	17:114	-				1	1	
Т	HEA CLASS I HOSTOCOMPATIBILITY ANTIGEN, BW-SO(B-21) B-SOOI ALPHA CHAIN	14-115						1	
Т	HEA CLASS I HISTOCOMPATIBILITY ANTIGEN, BW-12(B-5) B-5201 ALPHA CHAIN	\$7.114							
т	HEACLASS I HISTOCOMPATIBILITY ANTIGEN, BW.SK(BW-22) B-S401 ALPHA	17-114					1	1	
1-	HEA CLASS I HESTOCOSO AT THE TTY ANTIGEN, BW-SYBW-12) B' 5301 ALPIN	87-114							
1	HEA CLASS I HISTOCOMPATIBILITY ANTIOEN, BW-34/BW-22) B*3502 ALPHA	17.114		-					
+-	HEA CLASS I HISTOCONO ATIBILITY ANTIGEN, DW. SKIBW-22) B'S601 ALPITA	17.114					Ì		Ì
355	HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, BW-SK(BW-22) B"5602 ALPHA	67.114					1		
•	HA CLASS I HISTOCOMPATEILITY ANTIGEN, CW. I CW 10101 ALPHA CILAIN	17:114							j
	HEA CLASS I HOSTOCOMPATIBILITY ANTIGEN, CW-1 CW-0161 ALPIN CHAIN	17:114	_						
PICE HEIMAN	HEA CLASS I HUSTOCONDATIBILITY ANTIGEN, CW. I CW-0301 ALPHA CHAIN	11.114							
	KEA CLASS I HISTOCOMPATIBILITY ANTIGEN, CW-1 CW-0101 ALPHA CHAIN	17-114							
NAMON MOTOR	HEA CLASS I HUSTOCOND ATTBELLTY ANTIGEN, CW-3 CW-0301 ALPHA CHAIN	11.114							
PICE HENCH	HILA CLASS I HOSTOCONDATIBILITY ANTIGEN, CW-II CW-0101 ALPHA CHAIN	11:48							
•	HAY CLASS I HISTOCOMPATIBILITY ANTIGEN, CW-S CW-0101 ALPHA CHAIN	11.11							
т	HEA CLASS I HISTOCOMPATIBILITY ANTIGEN, CW-8 CM*040) ALPHA CHAIN	17.114							
1-	HEA CLASS I HISTOCOMO ATTRIBUTTY ANTIGEN, CW. 1401 ALPHA CHAIM PRECURSOR	67.114							
PASSE HUMAN	8971 KD (7-370LIGOADENYLATE SYNTHETASE	۰							
PLAKA HUMAN	PROTECH PHOSPHATASE PPIA, 65 KD REGULATORY SUBUNIT, ALPHA ISOFORM		11-16						
	PROTEIN PHOSPHATASE PPZA, 65 KD REGULATORY SUBUNIT, BETA ISOFORM	7	41.68	79.106				1	
3	Protedi Phospikatase PTA, 13 kd regulatory subunit, alpha isoform		†		4	1	1	T	I
P411 MUNUM	EXYTHOLOG PROTEIN 4 I (BAND 4 I, ERYTHOLOCYTE FORM)	32-46	1	_	$\frac{1}{2}$	1	1]

PCCFNE	Italy (The A Blant Canada an All Munnes Prairie Secuences		-	r					Γ	Γ
FILEMANE	PROTEIN	ANGAL	ARTA	AREAL	AKKA	AREA S	AREA1 AREA1		AREAL	AREA?
PAIS HUMAN	HON-ERYTHROID PROTEIN 4 I (BAND 4 I, LYNGHOID FORM)		36.33							Ì
PA1 HUMAN	ERYTHROCYTE MEMBRANE PROTEIN BAND 4.2		25.55							
P4F2 HUMAN	143 CELL-SURFACE ANTIGEN HEAVY CHAIN (431HC) (LYMHOCYTE ACTIVATION	201-322							-	
PSHIE HUMAN	S-HYDROXYTRYPTAMORE IE RECEPTOR (S-HT-1E) (SEROTONIN RECEPTOR)	311.334								
PSHIF HUMAN	J-HYDROXYTRYPTA-GONE IF RECEPTOR (S-HT-IP) (SEROTONIN RECEPTOR)	122-253								
PSHIA HUMAN		8.2			ĺ					
PSHT HUSCAN	SHYDROXYTRYPTANNE PRECEPTOR (3-HT-7) (5-HT-X) (SEROTONIN RECEPTOR)	┪		1						Ī
PAIAC HIDAAN	ALPHA-I-ANTICHMOTRYPSIN PRECURSOR (ACT)	٦	200		1					
PAIAO HUMAN	ALPHA-1-ACID GLYCOPROTEIN I PRECURSOR (OROSOMUCOID) (OND).	93-119	1		1					
PAIAT HUMAN		168-202							+	1
PAIAU HUMAH		_			1	1			4	
NAMES SALES		191-218	365-395							
PASCE HUNAY		104-134	۳							
PASMO HUMAN		53.60	119.349	1013-1112	1402-1429				,	
PAN HISTORY		428-455								
PAACT HODOW		611-24	120-747						-	
PAATH HUMAN	ASPARTATE AMINOTIVANSFERASE, MITOCHONDILAL PRECUISOR (EC 2 6 1 1)	109-136								
PABPT HUMAN		99-19	19:19	2604-2633						
PAC12 RUNAN	-	30-33							-	
PACIS HUMAN	•	14:51	183-209	668.700						
PACE HUMAN		П	179-206	113.340						
PACET HUMAN		П		016-969						
PACE HUSAN	_		100-127	1250-1284						
NYMMY YICKN		48-80								
PACHE HUMAN			İ							
PACHO MUMAN			104-331							
PACHE MUMAN		Η	10-01						-	
PACKO HUMAN	ACROSEM PRECURSOR (EC 1.4.31.10)	122-149				Ī				
PACYN HUMA		26-93	1	1						
PADT INDAM		41:2	1	1					-	
300	ADP.ATP CAUGUA PROTEIN, LIVEA ISCHOOM II (ADPAIL FIRMSLULASE J)	7	1	1					1	
AK 19 HOKAN	A-KINASE ANCHOR PROTEIN 79 (ALAP 79) (CAMP-DE-RAIDENT PROTEIN RINASE	_								
ALLA HUMAN	STRUCTONG BLOCK OF THE ALL AND THE CEL A 7 2 13 7 (PLUCE)			1	1					
ALTER MONTH	PROCTOSE-BISPHOSPRATE ALLOCASE (CC 417 & 17) B (LIVER)	1 2	T	\dagger	T					Ī
NYTHIN I WAY		49.16		l						Ī
PANCH KIMAN		Ŀ	179-700	926.964						T
PALOR HINAN	(AJOHDREGULIN PRECURSÓN (AR)	313:247		l						
PANCE WISKN		20	263-290							
PANTS KUMAN		Н								
PANKI HUMAN		=+	8.63	517.1644						
PANCE REPLAN		344-157	1		1	1				
PANKC HIBAN	I ANK YELN, BRAIN VALLANT 3 (ANK YELN B) (ANK YELN, NONE XTHROED)	=1		T	Ì		Ī			
PANTA HAMAN			7	1	1					Ī
AVAIL HATE	A MANUAL	16.16		\dagger	Ì					T
AANTO COMA		Ť	104-111		T					Ī
PANT HIMAN	ANNEXON IS CHOCOSTON IS) PLACENTAL ANTICOAGULANT PLOTEIN (II)	Ŀ		T						I
PANK HIBAN		Т	626-653	T						T
PANT HUMAN		Ī	137.164							T
PAOLA HULLAN		Î	76.10							
PAOFE HUMAN	ALITHE OXIDASE (FLAVIN-CONTAINING) B (EC I 4) 4) (MONOAMINE OXIDASE)	64.45								
PAPAL HADAN	APOLIDOPROTEIN A-I PRECURSOR (APO.Al).	П								
PAPE HUMAN	APOLITIONROTEIN BLICO PRECURSON (APO B-100/APO B-1)		1073-1100 1353-1380			2074-2117	2132-2159	2181-2215 2240-2271 2360-2389	1220-221	2360-2389
		1002	23.79.7559	2446-2507 (2529-2559 (2850-3000)340-3390	_	3480-3370	3620-3654	4040-4074	4090-4120	41354167
		144.74	Tarania i	T-2.2.	1]				

PEGENE (10717814 Mail Search on All Human Protein Sequences									
PROTECTION AND INCOME TO SEPTIME OF A POLITIC	V S	AKEN E OREGE		1000			1	т-	2
PAPE HAMAN TADEMONATIOUS POLYPOSIS COLL PROTEIN (APC PROTEIN)	=	617-631	134-661	1795-1822	2172-2212 2572-2609	2572-2609			
7-	48-11	147-274							
	4448-4475								
PAGE! HIMAN AGUARGAIN-CHIP (WATER CHANNEL PROTEIN FOR RED BLOOD CELLS AND KIDNEN 19-7)	139-73	ŀ							
PALK HONGAN BETA-ADRENGACIC RELEVIOR MINASE I (EC. 37.1. 129) (BETA-ADA-1)									
PARLY MUMAN AMOUNTAIN SUCCESSION OF ASSISTANCE OF TRANSPORTATIONS OF THE PROPERTY OF							T		
PAREZ MENAN BETA ARRESTIN 2	315.343	305.332							
PARIAL HOBIAN LAURESTON (RETINAL S.ANTIOEN) (48 KD PROTEIN) (S.AG)	294-332								
PARY I MELAN JARY ANDE HACETY, TRANSFERASE, MONOMORPHIC (EC 2.3.1.3) (MINAT)	***							_	
PARYS MINIAN JARYLAMINE WACETYLTIANSFERASE, POLYMORPHIC (EC 2.3 5) (PWAT)	2								
	11.31	343.374							
PATCO HUMAN CALCIUM-TRANSPORTING ATPASE SARCOPLASMIC RETICULUM TYPE (EC.) 61 18)	163-190								
	163.190								
	201-230							-	
	155-183								
PATES NUMBER TRANSCRIPTION FACTOR AYES (FRACKIENT)	19-01								
PATTS HISIAN TRANSCRIPTION FACTOR ATF 4 (FRACMENT).	34.66								
PATFA HIDAAN TRANSCRIPTION FACTOR ATF-A AND ATF-A-DELTA]381-364 }							-	
Ī	129-163								
PB311 HUMAN (NUCLEOLAR PHOSPHOPROTEIN B2) (NUCLEOPHOSMIN) (NUMATRIN)	114-141								
PRIAK KINAN BETA-JADRENERGIC RECEPTOR	292-319	145-372							
	=1							-	
PBM KUMAN BM PROTEIN	╗	23-562	ş Ş					-	
PRANT HANN ERTTROCYTE BAND ? INTECRAL MEMBRANE PROTEIN.	3								
PBASO HIBIAN BASONUCLIN	2	1633	773:807			1		-	
PBC28 HOSAN TRANSFORMENO PROTEIN BCL-3-BETA	6								
PECCH HOUN BEELL GLOWIN PALION PRECUROR (BUCKET)	?!					1			
PROTEINING BENEAUTORY CLUBICATION FOR THE PROTEIN	244.380	164.611				Ī		 	
FORMAL THINKING TO THE CONTROL OF TH	5					Ī	Ī	1	
PRINCE STANDARD INCOME LOS PROCESSES (PRINCES OF PRINCES OF THE STANDARD OF TH	202.236						Ī		I
PRIME WALLE BOOK LODGE CONTROL FOR THE PROTEIN & PRECIDE OF CAMPA.	374.30								
PRICT NIMAN BONE MORPHOGENETIC PROTEIN ? PRECUASOR (BND-3) (OSTEOGENIC PROTEIN !)	192.219					Ī			
Pansi RAMA Busi Moted.	204-311								
	164-195								
	10-37								
PRITE MUNICH BASIC TRANSCRIPTION FACTOR 62 KD BUBUNIT (PN).	120-162	33.115							
PRITCI HERAN (BIGI PROTEIN (B.CELL TRANSLOCATION CENE I PROTEIN)	3								
PCITC HABIAN IC.I. TETRANYDROFOLATE SYNTHASE, CYTOPLASING (NETHYLENETETRAHYDROF	030-363								
PCSTA MEMAN MORE CLASS II TLANSACTIVATOR CUTA	2								
PCA19 HUMAN COLLAGEN ALPHA (IDS) CHADN PRECURSOR.	4								
PCATS HUNGA COLLAGEN ALTHA I(A) CHAN PRECORDIA									
PLACE THE STATE OF THE PARTY OF THE STATE OF	_					Ī			
	277					T			
	94.133	151.14					Ī		
POLICIA INCREMENTATION AND ANALYSIS OF THE CONTRACT OF THE CON		VEN ANT				1			
POLICY NORMAL PROGRAMMENT AND A PARTY MANAGEMENT AND THE PROPERTY OF THE PROPE		38000					Ī	Ī	
	140-167					T	T		I
	397.334	467-494			Ī				
_	361.588						Ī		
	157.314	\$02-529							
PCAPT HIBLAN CALPAIN PM, LARGE (CATALYTIC) SUBUMIT (EC 1.4.22 17) (CALCIUM-	674-701								
	94.								
PCAP HUNGN ADENTLY CYCLASE ASSOCIATED MOTEIN (CAP)	11111	163-197	321.355			1		1	

PCCDAL	1003-178-4 Medi Search as All Itamas Protein Negaring		l	r	ŀ	ŀ			ſ	
THE NAME		PEN	AKEAT AREAT AREAS AREAS	10.1	WAT N	1 5 VIR		143	AREA? AREA!	SHIA.
PCART HUMAN		217.244								
PCASS HUMAN		11-71								
PCATA HISKAN		954-223								
PCATD_HEMAN		335-558				-				
CATH MUNICAL	CATHEFSIN H PRECURSOR (EC 3 4.22 16)	41-68	\mid							
PCATE HUMAN	CATHERSIN LIPRECURSOR (EC.) 4 22 15) (MAJOR EXCRETED PROTEIN) (MEP.)	Ē	-				l			
PCATS HUMAN	CATHERSIN S PRECURSON (EC 3.4.12.17).	30.57	142-169				r			
PCB/B HUMAN	CCAAT-BINDING TRANSCRIPTION FACTOR SUBUNIT B (CBF-B) (NF-Y PROTEIN		19:161	\mid		T				
NO KUKAN	CONTICOSTEROID-BOODING GLOBULIN PRECURSOR (CBG) (TRANSCORTIN)	771-98		l	l	İ	İ			
PCBPS HILLANY	CARBOXYPEPTIDASE B PLECURIOR (EC. 14 17)) (PANCHEAS SPECIFIC PROTEIN)	T	178-305	319.346	t	t	T			
KAN HIMAN	ABROXVERPTIDAGE MARKCING CO 1419 101 CARROXVERPTIDAGE EVICEGI	T	Т	!	\dagger	t	T	Ī	-	
	CONTRACTOR OF CO		1		†	\dagger	1	T		
		20-57		1	1	1	1			
	TAUTUM LIALITY	200-240	1	1	1		1			
200	INCARCULATION INITIATION FACTOR THIS 230 KD SUBURIT (TBP. ASSUCATED	238-1142			1	1			-	
	MONOCYTE DIFFERENTIATION ANTIGEN CD14 PRECURSOR (AYELOID CELL-SPECIF									
PCDIA HUMAN	T-CELL SURFACE GLYCOPROTEIN CDIA PRECURSOR (CDIA ANTIGEN) (T-C13.1.		101-101						-	
PCDIE HUMAN	T-CELL SURFACE GLYCOFROTEIN COIR PRECUISOR (CDIE ANTIGEM) (R2GI)	77.104		_		<u>-</u>	İ			
KON HOKEN	913	226-233								
PCD28 HIBMAN	Ŧ	226.755			t	t	Ì	Ī		
PCD2 MIMAN	TASEL SUBSACE ANTICEN COS PERCENCOS (T. CELL SEDEACE ANTICEN		l	t	† 	<u> </u>	i	Ī	-	1
PCD34 MIDAAN	SCHOOL STATE AND ASSESSED ASSESSED TO SECOND	2		T	1	İ	T	Ī	1	
WALLEY WITH A	LEIN DOUGH A LONG COMMENT OF THE COM		\dagger	\dagger	†	t	\dagger	T		
				1	+	1	1	1		
AUN POINT	I CELL SUR ACE GLYCUPROTEIN CDJ GAMMA CIKAIN PRECURSOR (T-CIELL RICEPT	ī			-		j			
PCDIL HUMAN	CD30 LIGAND (CD30-L)	26.136	183-217			1				
PCD4X HIDAN	CD44 ANTIGEN, EPITKELIAL FORM PRECURSOR (CD44E) (PHAGOCYTIC	55		-						
PCD4 HUMAN	F-CELL SUMFACE GLYCOPROTEIN COMPRECUASOR (T-CELL SURFACE ANTIGEN		140-267							
PCD53 HUMAN	EUKOCYTE SUNTACE ANTIGEN COSS.	67-114		- 			İ	Ī	<u> </u>	
PCD72, HUMAN	B-CELL DIFFERENTATION ANTIGEN CD73 (LYB-2)	161-811	-		-					
PCDIC, HENCY	CELL DIVISION PROTEIN KINASE 5 (EC 2.7.1).	5.33		-	-	-				
PCDK3, HIDAAN	CELL DIVISION PROTEIN KINASE S (EC 2.7.1) (KINASE PSSALRE)	22			-		ĺ			
PCEBB HUMAN	K	000-968		l					-	
PCENTS HUBAN	(B-4N3)	\$66-898		\vdash	┞	\vdash			F	
PCENC HUMAN	CENTROLEME PROTEIN C (CENP.C) (CENTROMERE AUTOANTIGEN C).	13,460			Г	Ī	Т	Г		
PCENE HUMAN	CENTROMENIC PROTEIN B (CENP-E PROTEIN)	112-399	193.520	12 409-155	715-752 76	767-825 8	\$50.884	903-947	\$69-698	1010-1107
2.2				1250-1277 1340-1367			186-1556	646-1610	1466-1556 1646-1640 1684-1724	1808-1846
		1	1290-1917 19	1940-1988 20	2021-2048 33	2 8162-882	2440-2478 2	2498-2563		
PCERU HUMAN	SE).	913-940	-		H	ľ				
PCETP HUMAN	CHOLESTERYL ESTER TRANSFER PROTEIN PRECURSOR	11-106			-					
NOTH HUMAN	CYSTIC FIBROSIS TRANSLABABIANE CONDUCTANCE REGULATOR (CFTR)		802-829 89	226-561	1243-1270		l			Ī
PCOCC JRUMAN	COMP JATED CATION CHANNEL PROTEIN (CYCLIC NUCLEOTIDS	316-245	_		-		l			
PCCL HUMAN	CYSTATHOONDYE GALOA-LYASE (EC 4.4.1.1).	315-349		\mid		\vdash				
POSE A HEMAN	CHLORIDECONE REDUCTASE (EC 1.1.1.23) (CDR)	17:51		H	-	-				İ
PCHOL HUMAN	CHORODELAEMIA-LIKE PROTEIN	÷	330-257 45	451-478						
PCHOR HUMAN	CHOROLDERAEMIA PROTEIN (TCD PROTEIN)	113-139			-					
PCDA HUXAN	SODIUM CHANNEL PROTEIN, CANDIAC AND SKELETAL MUSCLE ALPHA-SUBINHT		943.970							
PCLCA HUMAN	CLATTON LIGHT CHAIN A (BRAIN AND LYPHOCYTE LCA)	121-148		\vdash						
PCLCS HUMAN		133-157		\mid	-					
PCLCY HUMAN	CALCYCLIN (PROLACTIV RECEPTOR ASSOCIATED PROTEIN) (PRA) (GROWTI)	05-6								
POLUS HUBAN	CLUSTERIN PRECURSOR (COMPLEMENT-ASSOCIATED PROTEIN SP-40,40)	F	Г	367.394						
POHON HOMA	CHRONDORANDI A PRECURSOR (CGA) (CONTAINS: PANCREASTATIN AND WE.14)	031-66	430-451		-	l	T			
MONTH HUMAN	CILLARY NEUROTROPHIC PACTOR (CNTF)	26-93	ŀ		F					Ī
PCOG HUMAN	TUMOR-ASSOCIATED ANTIGEN CO-019	25.00	82176	_	-			Ī		Ī
PCO3 HUMAN			593-620 63	133.867						Γ
POOL MEDICAN		~								
NOS MUNAN		7	537-564 97	970-997 12	1270-1304					
PCO HUMAN	COMPLEMENT OF PLECUSOR.	1.74	1	1	+	+				
PCO7 NUMAN		13:361	1	1	1	1				
					[

PCGENE	1971,191,4 Motif Search on AB Muman Project Sequences	1 1				\blacksquare		П		
FILENAME	PROTEIN	┚	7	3	AREA AREAS		TOWN TOWN	Т	4	1
PCOX! HUMAN	CYTOCHRONE COXIDASE FOLYPERTIDE ((EC. LV.)) PRYOCHROWER BASS VIT (CMC) ESTEROT. 1. AL PITA-MONOXY CENASE)	263.290	146.373	T		Ì	Ţ			
PCPCH HIMAN	CYTOCHEOME PASSIBLY RECT. 14 14 (1) (7450-254C) (FRAGMENT).	109-136								
POE HISKY	CYTOCKNONG PASO ILET (EC 1.14.14.1) (PASO I) (ETILANOL INDUCIBLE)	331-358								
POPEM HUMAN	CARBANOYL PHOSPHATE SYNTHASE (ANIMONIA) MITOCHONDRIAL PRECURSOR	П	420-447							
PCPTS HUMAN	MITOCHONDILLA CARATONE PALMITOYL TRANSFERASE II PRECURSOR ,	ĝ		1			1			T
NAME OF THE PARTY	CYTOCKRONG P410 XP1IA1 (P410-C17) (EC 1.14 99 9) (STEROID 17-ALPHA- 1			Ī			Ī			Ī
N KEN		175-475		1			Ĭ	1		
	CONCREMENT RECEPTOR (TPE 2 PRECURSOR (CR2) (CONCREMENT CAD ACCEPTOR)	7	130.420	11.478	137.76	76.780	T	T		T
	COLORECTAL MOTANG CANCER PROTEIN (MCC PROTEIN).		T	Т					_	Ī
NO.	CAMP RESPONSE ELEMENT BUNDING PROTEINS A AND S (CAMP) AND CAMPON A		Ţ	Ī			Ī			Ī
	CAMP RESTORED BLOKEN DESCRIPTION CALLS IN	9	120173	Ī	Ī	Ī	Ī			
717/11		201.111		1	!		:	:	:	
NAME OF STREET	LACEDERACE OF ONY STIME ATING FACTOR I PRECURSOR (CSF-1) (MCSF)	Q - C	Ī							
PCST5 HIMAN	CLEAVAGE STUMBLATION FACTOR, 10 RD SUBUNIT (CSTF 10 RD SUBUNIT) (CF.1	3								
PCTNA HUMAN	ALPHA-CATENIN (CADMERUN-ASSOCIATED PROTEIN)	111.119							·	
PCTYR HUMAN	LPHA-CATEMIN RELATED PROTEIN (CATEMIN ALPHA-1)	610-313								
POSS HUNAN	GAP JUNCTION BETA-1 PROTEIN (COMMEXIN 16) (CX16)	108-134							1	
PCXU1 HUMAN		-	1							Ţ
PCX3 ROWN	GAP IUNCTION ALPHA - PROTEIN (CONNEXIN 11) (CX31)		Ī	Ī	T	Ţ				Ī
PCTB3 HUMAN	THE CONTROL BY THE CONTROL BY THE PRINT OF TAKEN OF THE CHAIN	10.01	126-133	352-396	Ī					
PCTO MUNICIPALITY	CONTINUE DE CICLADA SOCIONE DI SUBLE SOLVENIMA CONTINUE DE SOLVENIMA CONTINUE CONTINUE CONTINUE CONTINUE CONTINUE CONTINUE CONTINUE CONTINUE CONTINUE CONTINUE CONTINUE CONTINUE	10.00								
PYCE KINAN	BERTHAL GUANNIN CYCLASS PRECINSOR (EC 4 6 1.2)	150.25		Ī					-	
PEYRO MIMAN	CYTOKINE RECEPTOR COMMON GANDA CHAIN PRECURSOR (GANINIA-C)	261.162								
PCYTA HUMAN	CYSTATTN A (STEPIN A) (CYSTATD AS)	17.51	П	П						
POBL HUKAN	PROTO-CINCOGENE DBL PRECURSOR (CONTAINS MCF2)	П	П	166.79]	101-145					
POESN HUNAN	DESAID		212-212	┪		Т		╗		
POESP HUMAN	DESKIOPLAKINI AND II (DPI AND DPII) (PRAGRIENT)	-	7	117-244	269-317	765-434	437.467	156	26.39	2000
				10.100	1308:1313				1	
			111.165	116.511	233.710	974-1003	1612.1019	1201-1221	1364-1394	1613-1674
PAND HOMO	_	1838-1869	2158-2189	1113-2343	2752.2278	1-	2912-2958	1014.3041	1496.3333	
PDNJ HUNCH	DAY PROTEIN HOMOLOG	45.76								
PONT HURAN	DNA LIGASE I (EC 6 S.I.I) (POLYDEÓXYNUDONUCLEÓTIDE SYNTHASE (ATP))	130-153	241-550	112-159						
PDPOA HUMAN	DNA POLYNGRASE ALPHA (EC 2 2.7 7)	25.74	1009-1057	138-137						
POPOD HELEC	DNA POLYMERASE DELTA CATALYTIC CHAIN (EC. 2.1.7.)	20,00	14.148							T
POSNI KILAN		16.35								T
AND HOME		10-107	355.398							
PDSQ! HUNAN	DESMOGLETA I PRECIPISOR (DESMOSOWAL GLYCOPROTEIN I) (DGI).	<u>.</u>	171-296	167.331						
PDSG3 HUMAN			22.522							
POLO MONAN	DIVERGENT UPSTREAM PROTEIN (DUP)	5								
PEARL HOWA	VERBA ACLAIM TANIEN ENERGEN 1 (ERI)		Ī				Ī			
PERIO MINAN	EDV-GOOGLO O PAO EMPLOOPERO PACE A ON A COLOR	103:132								
PER INTERN	STONGATION FACTOR LIDELTA	=======================================								
PECPE MIMAN	EPIDEBLAAL GROWTH PACTOR RECEPTOR PRECURSOR (EC 2 7.1.112)	\$ \$	440-467							
PEGF HUNAN	EPIDEBLIAL GROWTH FACTOR PRECURSOR, KIDNEY (EGF) (UROGASTRONE)	47.74								
PELFI HUMAN	-	151-368								
PENT, HUMAN		49.74	246-273							
PENY! HUMAN	_	381-420								
VEN MONAN	IO ESSUON CHAIN C REGION.		3	146,383						
PERSON HOLAN	PROTECH PICKET FIDE ISOMORASE RELATED PROTEIN PRECURSOR (EXP12)	31.00	2	438-483			Ī		I	T
KYN II	SEPTIMENT THE EXCESSION REPAIR PROTEIN ERCC.	340-370	т							
TENE DUTE										

PCCEME	10711784 Motif Search on All Human Protein Sequences						Ī			
THE NAME		П	ARIA L	AREAL	ABEA4	AREAS AREAS	1	AllEA?	AREAS	ARYA 9
PLACE HUMAN			19.913					_	,	
A MONTH	-+	1 895-160								
A HUNAN	ENDOTHEL IN 2 PRECURSOR (ET.2)	133-160								
		183-309								
PEYZA HUMAN					Γ					Ī
NEW MARK	EZAIN (PHI) (GYTOVILLIN) (VILLIN'2)	119-146	361.188	402-429	\$12.539		Ī			
3	COAGULATION FACTOR V PRECINSOR	2103-2137								T
TAS HIDEAN	COAGULATION PACTOR VIU PRECURSOR (PROCOAGULANT COMPONENT)	106-161	007-1034	1194-1230	Γ			Ī	Ī	Ī
PTAP HUDGEN	COACULATION FACTOR IX PRECURSOR (EC 3 4.21 22) (CIQUISTALS FACTOR)	271-298		T	Ī		Ī	Ī	Ī	
PFABI HUSAN	PATTY ACID-BINDING PROTEIN, INTESTINAL	<u> </u>	T	T	Ī				1	İ
PFASA HUMCAN	APOPTOSIS-ACCIATING SURFACE ANTIGEN FAS PRECURSOR (APO-1 ANTIGEN)	T	249-101	106-111			T		-	
PFCEJ HUMAN	LOW AFFINITY DOMINOCLOBULIN EPSILON FC RECEPTOR IL YNOHOCYTE IGE	L	Т						1	
PECEL MERCA	HIGH AFFINITY DAMINOGLOBULIN EFSILON BECEFTOR ALPHA. SUBJINIT JEFFBIN	70.00	\dagger	Ť						
PECKL MOAN	IBROBLAST CADWIN FACTOR RECEPTOR 1 PRECINGOR (FC 2 7) 1131		1	Ì	Ī		Ī	1		
PFIBA HUNAN	HALINOGEN ALPHA CHAIN PRECIDENT	T	131.161	1			1	1	1	
PEGE HONN	IBANOGEN BETA CHAIN PRECIPEOR	Т		1				Ī		
PFIBO HUMAN	IBRINGEN GAMMA. A CHAIN PREMINGIN	1		†				1	-	
PERSON HOSEN	BRINGEN GANGAL CHAIN GIRENOGEN CANNAS	T	8 3						-	
PEDIC HUDAAN	CARCON PERCHASING	٠,	D01-C7	1					-	
PRI HISAN	TILL CANADORNS CREATE TO A MONTH A CONTROL	M17-1017	1	1					-	
PENO! HUMAN	ODG TRY ANT THE MONOCYCENACE OF DAYING BOTTON OF THE TAIL	7	T							
PEOP HIDAAN	SECTION PROTECTION PROTECTIONS	1		321-100	Ī		1			
PFEAT HENCH	OCUPE ATTO AND OF A	61:20	1	1					1	
WALL BALLAN	OCCUPATION OF THE PARTY OF THE	20:00	1	1						
SES IN MANAGE	TENSING IN THE TAXABLE TO THE TAXABL	01-4								
DIAM HAND	TENTEN COM	3								
71 11 11 11 11	COLUMN COM CANA.	î								
PERSONAL MANAGEMENT	CULTULES STRUCKING HORMONE RECEPTOR PRECURSOR (FSH.R.)	500							-	
	TOWN THOUSAND ALPRACE TO SEASON (EC.) 2.1.51) (ALPRA LEFOCOSIDASE	200								
D. Maria	UNIONALE NIONALASE, MITCHONDIAM, (EC 4.2.1.2) (FUNIONASE)	54-45								
NAME OF STREET	DOTATIVE LIMITAGE TIE GOOD SWITCH PROTEIN	2							-	
2771	MOTERNAMEN AND THE STATE OF THE	£1.2								
MONI MOMAN	MAJOR CASTROONTESTINAS TIMOS ACCOURTED BEOTEIN CAST. SEEF IN CO.	200		1						
POATS HUMAN	JALACTOKINASE 3 (EC 2.7.16)		\dagger	T				1	1	1
MAKE HUMAN	JANDARA-AMINOBUTYRIC-ACID RECEPTOR ALPHA-1 SUBINIT PREPINSON (CARAIA		\dagger	1	1		1		1	
POALS HEBANNIC	JAKBALA-AMINOBUTYRIC-ACID RECEPTOR AL PHA-1 SUBUNIT PREFIT IN SOR LOABALA		1	†	1	1	Ì	1	1	
POASK RUNGA	MASTRUNCHOLECYSTOKING TYPE BIRECEPTOR (CCK. N BECEPTOR)		1	1	1			1		
PGB01 HCMAN	JUANDE NUCLEOTIDE BOOM PROTEIN CO. AL PHA STRING T		+	+		1				
PGBG HUMAN			1	+	1	1				
PCBAK HUMAN	GUANDE NUCLEOTOS ADVODAG PROTEDI ORIS AL PHA SERIENT (CALLA DE LA CALLA DEL CALLA DEL CALLA DE LA CALLA DE LA CALLA DE LA CALLA DEL		1	Ì	1					
PCBAS RIDAN	JUANTHE NUCLEOTIDE-BINDING PROTEIN CAST ALPHA SUBURIT (ADENT ATE		\dagger	1	Ì	1		1		
PGBAY MUMAN	SUANTINE NUCLEOTIDE BINDING PROTEIN GIYL ALPHA SUBLINIT (ALPHA. 11)	100	+	†	1			1		
PGBBJ HUSKN	SUANTINE MUCLEOTEDE-BINDING PROTEIN CHINCISTICAL BETA SUBLINIT 1		1	1	1	İ		1		
PUBLIF HUNAN	+	-	344.387	280.114	1	1	1		1	
PGB71 HGA/AN		Т	Т	+	1	1	1	1		
PCBT3 HUMAN	т			†	Ì	1	1			
POCT HUMAN	T	Ļ	201.100	147.104	784.481	1	1	1	1	
POCH! HUMAN	T	T	+	┰	T		1		1	7
POCKA HUMAN	9	70.19	\dagger	\dagger	1	1				
PGCRB HUNAN		101.69	\dagger	t	1	1	1	1		
PCCSP_HUMAN	PLATING) PRECURSOR (EC.) 442)	460.417	1	\dagger	1	1	İ	1		
PGDN_HUMAN			t	t	1	1	1	1	1	
PGELS HUMAN	ÆNZDIG FACTOR) (ADF)	701.73	T	\dagger	T	1	\dagger	†	1	
POTAL HUMAN		Ť	149.376 31	314-411	T	+	†	†	†	Ī
		Γ	Т	\mid		T	t	t	\dagger	T
NOT X	_	1	251-276				T	t	t	Ī
	SELUTE NTUROATMEINTLINAMSFERASE, CYTOSOLIC (EC 2.1.2.1) (SEMINE 3)	32.59	344.37(-	-	-		t		
								l	1	7

FILEMANK INTOCHOND TO THANSELASE, MITOCHOND TOTAL Y MAAN ISEDIC HYDIOXYAETHYL TRANSELASE, MITOCHOND FOLK, Y MAAN ISEDIC HYDIOXYAETHYL TRANSELNEN FECURSOR (GID FOLK) KIDANA (GLYCDIG REEFIOR ALPHAJ CHAÍN PRECURSOR. TOTAL HYDIAN (GLYCH) FORBERT HALAN (GLYCH) FORBERT HALAN (GLYCH) FORBERT HALAN (GLYCH) FORBERT HALAN (GLYCH) FORBERT HANNA (GLYCH) FANNE FERNSE HA SUDINI 7 (EC 13 L. POTT MAAN (GLYCH) FANNE FERNSE HA SUDINI 7 (EC 13 L. POTT MAAN (GLYCH) FANNE FERNSE HA SUDINI 7 (EC 13 L. POTT MAAN (GLYCH) FANNE FERNSE HA SUDINI 7 (EC 13 L. POTT MAAN (GLYCH) FANNA FOR FERNSE FERNSE FERNSE MAAN (GLYCH) FANNA FOR FERN FYRE I. BRYTHUCYTERIALIN	SEADLE HYDROXYMETHYLTIKANSFERASE, MITOCHONDRIAL (EC. 2.1.2.1) (SEADNE SEADNE HYDROXYMETHYLTIKANSFERASE, MITOCHONDRIALAL (EC. 2.1.2.1) (SEADNE SEADNE	777						1	
MALAN HOLLAN POLICY HOLLAN POLICY FOREN HOLLAN POLICY FOREN HOLLAN POLICY HOLLAN POLIC	Γ				_			1	
TOTAL HOLLAND OF THE		165-795	588-625						
TOTAL HUMAN OTHER HUMAN TOTAL HUMAN TOTAL HUMAN	CLYCHAE RECEPTOR ALPHA-3 CHAIN PAECURSOR	142-169	341-368					1	
POTE HOUSE OTTO HOUSE POTE HOUSE		7	89:50	-				1	
POTER HONLAN	RECURSOR (GHOU! RECEPT			1	1				
POTE HUMAN	18) (GTHZ) (CLASS-	<u>.</u>			$\frac{1}{1}$			Ī	
POTRI HIMAN	ACTIVATOR)	2	1012-1047		-				
STATE DISTAN		274.30		-				Ì	İ
	CLUCOSE TRANSPORTER TYPE 1, BRAIN.	272.24						1	١
POTE A HIMAN	GLUCOSE TRANSPORTER TYPE 4, INSULIN-RESPONSIVE.	390 317						1	
	ASTONE HI:	6-89	+		+			1	
-	KASTONE RIA (H. I.).	73-104	$\frac{1}{1}$						١
WALKIN MINAN	HISTORIE NIB CHI 4)	10-101							
-	HISTONE NIC (HI)	11.103	_	_i	<u> </u>				i
	HISTONE HID (HI 2)	101-01							
۲	SISTOME ELT	14-105						-	ļ
٦.	SECTION NAME OF	20.47						-	
	United NATION AND AND AND AND AND AND AND AND AND AN	20-47	-	_					
200	THE CASE IN THE CA	20.47	-	_					
PHILD PHILDS	NATIONS AND INSTACTOR AT THE ITY ANTIGEN DOYS ALPHA CHAIN PRECURSOR	142.169	-					1	
THE STATE OF THE S	THE ACT OF STREET OF A PARTICIPAL DRIVES BETA CHAIN PRECURSOR	19-83	-	-	L				
PHOLIC HUMAN	THE CHASE IN THE CONTROL OF ANTICEN DRIVEN BETA CHAIN PRECURSOR	15	-	_					
	THE A PART IN COUNTY AND IT ANTICEN DRWINGETA CHAIN PAECURSOR	30.33	-		_			_	
	THE CONTRACTOR OF THE CONTRACTOR OF SETA PARTY PROPERTY OF THE CONTRACTOR OF THE CON	3	-					٠	
	TAN CASS II TUSI COMPANIE TO THE SECOND OF THE SECOND SECO	102-129	-		-	L			
	PLY ALLOHOUSE CANON IN TACHON PACED CONT. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1.	16:19	-						
	IN 14 PROTOCOROUSE PROTEIN PROCESSOR (C.C. A) CHST.21	51:13	139.186	-					
PART STATE	PRINCIPLES ON THE FACTOR STATE OF THE POST OF THE PERSON FOLLY.	264.312							
NAME OF TAXABLE	INCHESTIVE INCOME, IN SYNTHAMER (F.C. 4.2.1.75) (UROPORPHYRING GEN-11)	34-110						·	
NVALUE (SECTION	HEFARIN CONACTOR IS PRECURED (HC.II) (PROTEASE DRUBITOR LEUSERVIN 2)	169-196	L]		
PER TRIVAN	SERINE MOTERASE HEPSIN (BC 3.421.4).	23-49						-	1
PHEKA HIMAN	BETA-HEXOSAMINIDASE ALPHA CHAIN PRECURSON (EC.) 1.133) (N-ACETYL-	× 1		1	1	-			
PHEND HIDLAN	BETA-HEXOSANDMOASE BETA CHAIN PRECURSOR (EC 1.1.13) (N-ACETYL-BETA-	38712	1		1				
PHOCKI JALBACAN	HOMEOBOX PROTEDI MSX-1 (MOX-7).	212-21-2	+		+	-		Ŧ	
PHOOF MOLENN	HEPATOCYTB NUCLEAR PACTOR 1-ALPHA (100F-1A) (LIVER SPECIFIC	4	+	1		\downarrow			
PHOL HUMAN	HENE OXYGENASE I (EC I. 14.99.3) (HO-I).		+			\downarrow		Ī	ŀ
NYTH GADIA	4-INDROXYMENYLPYRUVATE DIOXYGENASE (EC 1.13.11.27) (4/07D)	Т	760 719	A84 2444 A444 9744		2340.231A 1419.1744	144£.1474	T	١
PHEX HEMAN	ZINC FINGER PROTEIN KIX.	_	1					Ī	
PHSI_HUMAN	HEMATOPOETIC LINEAGE CELL SPECIFIC PROTEIN		717 077	<u> </u>		-		Ī	
PHS94 HUMAN	HEAT SHOCK PROTEIN HSP 90-ALPHA (HSP 86).		1000	+					
	HEAT-STABLE ENTEROTOXIN MECENTUR PRELIMINAL (UC-L) (UNITED LINAL		0/1/1/1	-		ļ		Ī	
PHSF! HUMAN	HEAT SHOCK FACTOR PROTEIN ((RSF 1) (HEAT SHOCK SANAGER SHOW FACTOR	17.10				\downarrow			
	HEAT SHOCK FACIUM FRUITS A (NOT 4) (NEXT BROOK) INVESTIGATION FOR	43.104				-			
MINZ! HUKKN	TO PER VI CASAN PROCESSOR VILLE ACTION (PASTICE)	47.74							
PHYST MEDIAN		262.289	-	-		-			
PICKII HUMAN		3							
PEGB? HENEY		21.80				ļ	I		
PLATE HEBRAN	ISLET AMYLOW POLYPETIME	181,310	$\frac{1}{1}$	-		-			
NOT HERE	INSULING LACK AND THE PACK OF BEING THE PACK AND THE PACK	1541.274	\dagger						
PICI HUMAN	_	74 65			+				
PICAL HUBAN	DATE OF THE ADDRESSION MOLECULES I PRECURSOR	75 74.7	170						l
TOE HOW	INSULINGIBLE CALLED BACK THE (E. J. 4.37 4.3) (LASOLITABLE) (LASOLITA	113.948	133.346		+	-			
POL HUMAN	EUKALYOTIC MILLATION PACTUM ACTURISMENT	76.1%	1199			-			
PO 48 HUMAN	THE PLANT PROPERTY A PROPERTY OF TACHOOD BETALA CHARACTER TO THE PROPERTY OF T	104.149							
200	INTERIOR STRING ALPHA PRECURSOR (D. I ALPHA) (NEXATOPOETIN-I)	101-08	183-210	-					
DY WALL	THE THREE INTERICTIONS RECEPTOR TYPE PRECURSOR (IL. IR.) (PRO)	76-110	172.199						

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Particle Control of the Control of	PILENAME	PROTEIN	Т	Ŧ	Т	_	т			1000	ABVAG
Head for the Extract ALTACOM (L. U. U.) Head	PILIR HUMAN	INTERLEURIN-I RECEPTOR, TYPE I PRECURSOR (IL-IRI) (PRO).	1	г		7	т			-	
	PIL1S HUSAN	INTERLEUKIN-I RECEPTOR, TYPE II PRECURSOR (IC. 182).	311-451			Ī					T
	PILSA MOMAN	INTERLEUKDA-S RECEPTOR ALPHA CHAIN PRECURSOR (IL. SR.ALPHA)	11:11		l					Ţ.	
The STATE BLOCK ALP, MELLEY GRANT AND ALL AN	PILS HUMAN	INTERLEURING PRECURSOR (12-4) (B-CELL, STIMULATORY FACTOR 3) (BSF-2)	112:139							Ī	
PRINTED AND ALL ALLEGATOR NECESSARY (INC.) 1419		INTERFERON ALPHAL PRECURSOR.	2:3	Ī	Ī	Ī					
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PHOSPHOFAUCTOKDAJE, MUSCLE TYPÉ (EC 2.71.11) (PHOSPHOFAUCTOKNAJE 140-167 HOSPHOFAUCTOKDAJE, LIVER YTPE (EC 2.71.11) (PHOSPHOFAUCTOKNAJE 19-16 HOSPHOFAUCTOKAJE, LIVER YTPE (EC 2.71.11) (PHOSPHOFAUCTOKNAJE 19-16 G KAPA, CHÁMA C REGION. ALALAN BYNAMOZE PROTEIN PROTEIN PROFELLATA REGILATOR Y CHÁNN ALA DEPENDENT PROTEIN KINAJE TYPE I.ALPHA REGULATOR Y CHÁNN ALA GEBENDENT PROTEIN KINAJE TYPE I.ALPHA REGULATOR Y CHÁNN ALA GEBENDENT PROTEIN KINAJE TYPE I.ALPHA REGULATOR Y CHÁNN ALA GEBENDENT PROTEIN KINAJE TYPE I.ALPHA REGULATOR Y CHÁNN ALA GEBENDENT PROTEIN KINAJE TYPE I.ALPHA REGULATOR Y CHÁNN ALA GEBENDENT PROTEIN KINAJE TYPE I.ALPHA REGULATOR Y CHÁNN ALA GEBENDENT PROTEIN KINAJE TYPE I.ALPHA REGULATOR Y CHÁNN ALA GEBENDENT PROTEIN KINAJE TYPE I.ALPHA REGULATOR Y CHÁNN ALA GEBENDENT PROTEIN KINAJE TER (EC 2.7.1.113) (PHITHELIAL CELL. 319-346 HOTOLOGNOCOURE TYROÁNBE-ROTEN KINAJE TER (EC 2.7.1.113) (PHITHELIAL CELL. 464-473 ROTOLOGNOCOURE TYROÁNBE-ROTEN KINAJE TER (EC 2.7.1.113) (PHITHELIAL CELL. 464-473	PLOCA REMAN	KERATDY, TYPE II CYTOSKELETAL SA KD (KAA KERATDA (PRAGMENT)	t	Н	13.54	T	T			1	
PHOSPHOPELCTOKENSE LIVEN TYPE (RC 211.11) (PHOSPHOPELCTOKINASE 69-40 AND COMMOGRIE THOSINE-ROTEIN KINASE ABL (RC 21.1.11) (P159) 64-513 G KAPA CHARIN CERCION CALLALAN SYNDKORGE PROTEIN PRECUISOR (ADMESION MOLECULE-LINE X-LINK 150-11 ALLALAN SYNDKORGE PROTEIN KINASE TYPE I-ALTHA REGULATOR Y CHAIN 111-20 AND GERDOENT PROTEIN KINASE TYPE I-ALTHA REGULATOR Y CHAIN 111-20 AND CERCIOENT PROTEIN KINASE TYPE I-ALTHA REGULATORY CHAIN 111-20 AND CERCIOENT PROTEIN KINASE TYPE II-ALTHA REGULATORY CHAIN 111-20 AND CERCIOENT PROTEIN KINASE TYPE II-ALTHA REGULATORY CHAIN 111-20 AND CERCIOENT PROTEIN KINASE TYPE II-ALTHA REGULATORY CHAIN 111-20 AND CERCIOENT PROTEIN KINASE TYPE II-ALTHA REGULATORY CHAIN 111-20 AND CERCIOENT PROTEIN KINASE TYPE II-ALTHA REGULATORY CHAIN 111-20 AND CERCIOENT PROTEIN KINASE TYPE II-ALTHA REGULATORY CHAIN 111-20 AND CERCIOENT PROTEIN KINASE TYPE II-ALTHA REGULATORY CHAIN 111-20 AND CERCIOENT PROTEIN KINASE TRE (RC 2.1.1.11) (PRITEILAL CELL 111-20 111-	PKAP NUKA	4-PHOSPHOFAUCTOKINASE, MUSCLE TYPE (EC 27.1.11) PHOSPHOFAUCTOKINASE	†	Т		T			1		
ROTO CONCOCEDE TROSSNER PROTEIN KDASE ABL (EC. 7.1.1.11) (#150) 51.15 ALL LAND CREGION ALL DEPENDENT PROTEIN KDASE TYPE I ALL HAL REGULATORY CHAIN ALS DEPENDENT PROTEIN KNASE TYPE I ALL HAL REGULATORY CHAIN THE SERENDENT PROTEIN KNASE TYPE I BERT AREQULATORY CHAIN THE SERENDENT PROTEIN KNASE TYPE I ALL HAL REGULATORY CHAIN THE SERENDENT PROTEIN KNASE TYPE I ALL HAL REGULATORY CHAIN THE SERENDENT PROTEIN KNASE TYPE I ALL HAL REGULATORY CHAIN THE SERENDENT PROTEIN KNASE TYPE I ALL HAL REGULATORY CHAIN THE SERENDENT PROTEIN KNASE TYPE I ALL HAL REGULATORY CHAIN THOSE REGULATOR (C. 2.7.1.11) (FRINGELLUL CELL TROSSE TROTEIN-KNASE ER (CE. 2.7.1.11) (FRINGELLUL CELL TROSSE TROTEIN-KNASE ER (CE. 2.7.1.11) (FRINGELLUL CELL TOTO CONCOCENTE TYROSINER KNASE TER (CE. 2.7.1.11) (FRINGELLUL CELL THE SERENDENT TROSSE TROSSE (CE. 2.7.1.11) (FRINGELLUL CELL TOTO CONCOCENTE TYROSINER (CE. 2.7.1.11) (FRINGELLUL CELL TROSSE TROTEIN-KNASE TER (CE. 2.7.1.11) (FRINGELLUL CELL TROSSE TROTEIN-KNASE TER (CE. 2.7.1.11) (FRINGELLUL CELL TROSSE TROTEIN-KNASE TER (CE. 2.7.1.11) (FRINGELLUL CELL TROSSE TROTEIN-KNASE TER (CE. 2.7.1.11) (FRINGELLUL CELL TROSSE TROTEIN-KNASE TER (CE. 2.7.1.11) (FRINGELLUL CELL TROSSE TROTEIN-KNASE TER (CE. 2.7.1.11) (FRINGELLUL CELL TROSSE TROTEIN-KNASE TER (CE. 2.7.1.11) (FRINGELLUL CELL TROSSE TROTEIN-KNASE TER (CE. 2.7.1.11) (FRINGELLUL CELL TROSSE TROTEIN-KNASE TER (CE. 2.7.1.11) (FRINGELLUL CELL TROSSE TROSSE TROTEIN-KNASE TER (CE. 2.7.1.11) (FRINGELLUL CELL TROSSE	PKAM, HIDAN	4-PHOSPHOFFLUCTOKINASE, LIVER 17PE (BC 2.7.1.11) (PHOSPHOFRUCTOKINASE	T	21:150	T	T	Ī	1	Ī	1	Ī
G KAPA CHAIN C REGION LLILAKANI BYDANGME PROTEIN PRECUISOR (ADMESSION MOLECULE LIKE X.LTMK 136-14 ALM SEPROPERT PROTEIN KINASE TYPE I-ALTHA REGULATORY CHAIN THE SEPROPERT PROTEIN KINASE TYPE I-ALTHA REGULATORY CHAIN AND SEPROPERT PROTEIN KINASE TYPE I-ALTHA REGULATORY CHAIN THE SERVICE RACHAR SUBDITT: (OF KAPA'S PIOS STBURIT) THE SERVICE KINASE GEALTH (OF KAPA'S PIOS STBURIT) THOSDER MOTEIN-KINASE ECK PRECUISOR (EC 2.7.1.113) (EPITHELIAL CELL REG-19 ROTO-ONCOCENT TRADSING-PROTEIN KINASE PER (EC 2.7.1.113) (POM-FER) 219-346	PKABL HEMAN	PROTO-CONCOGENE TYTHOSINE-PROTEIN KINASE ABL (EC 2.7.1.113) (P.150)	ļ.,		Ī	Ť	Ì		1	1	T
LALLANAN SYNDROME PROTEIN PRECUISON (ADMESTON MOLECULE LINE X.LFNK 150-411 AND PERSONENT PROTEIN KANSE FYRE LALLAN REGULATON CHAIN 119-20 AND OBJENDENT PROTEIN KINASE TYPE LALTAN REGULATON CHAIN 119-20 AND OBJENDENT PROTEIN KINASE TYPE LALTANA REGULATON CHAIN 119-20 AND OBJENDENT PROTEIN KINASE TYPE LALTANA REGULATON CHAIN 119-20 AND CLEAR AND CONTROL ROLLAND (FOR KAPPA B 105 SUBUNIT) 119-20 TABLATON KAPPA B GINGOTT (FOR KAPPA B 105 SUBUNIT) 119-21 119-	PKAC HIMAN	IO KAPPA CHAIN CREGION.	2	T	T	T		1	1	1	Ī
AND DEPROPERT ROTEIN KNASE TYPE I-ALTHA BEGULATORY CHAIN 119-26 AND DEPROPERT ROTEIN KNASE TYPE LBETA REGULATORY CHAIN 119-26 AND DEFROEST PROTEIN KNASE TYPE I-ALTHA REGULATORY CHAIN 119-20 AND DEFROEST PROTEIN KNASE TYPE I-ALTHA REGULATORY CHAIN 119-20 AND DEFROEST FOR KAPPA-B SUBDITT I (IFF. KAPPA-B PIOS SUBUNIT) 119-20 TAGATORE KNASE, B CHAIN (E. 2.1.). 110-21 TROSTOR WOTELLANGE ECK PRECANOR (E. 2.1.). 110-21 TROS	PEALLY HUNKAN	KALLMANN SYNDROME PROTEIN PRECINSOR (ADMESION MOLECULE LINE X.LINK	Į	T	T	Ť			T	T	Ī
AAR-DEPENDENT PROTEIN KINASE TYPE I-BETA REGULATORY CHAIN AND-DEPENDENT PROTEIN KINASE TYPE II-ALINA REGULATORY CHAIN (15:302 AND	PRAMO HUMAN	CAMP-DEPENDENT PROTEIN KINASE TYPE I ALPHA REGULATORY CHAIN	30,30	İ	\dagger	T	T		T	1	Ţ
AAA-DEPENDENT PHOTEIN KINASE TYTE II-ALPHA REGULATONY CHĀIN 115303 AUCLEAR FACTOR KAPA-B SUBUNIT-1 (NF-KAPA-B PIOS SUBUNIT) 135-370 ALĒĀDOS KONAŠE GALAN (EC 2.1.1.1.) (EPITHELIAL CELL 646-47) ATOTO-ONCOCENS TYROŠING-PROTEIN KNASE PER (EC 2.1.1.113) (PRIFIELIAL CELL 646-47) AOTO-ONCOCENS TYROŠING-PROTEIN KNASE PER (EC 2.1.1.113) (PRIFIELIAL CELL 135-346	PICANI MUSIKAN	CANG-DEPENDENT PROTEIN KINASE TYPE I-BETA REGULATORY CHAIN	22.20	ľ	t	T	T		T	1	Ī
AUCLEAR FACTOR KAPA, B SIBBUTT - I OFF-KAPP FIOS SUBUNIT) 7364 TOBE KARAGE, B CHAPPE (C. 2.1.1.) (FRITHELIAL CELL GAGGO) 73070 ONCOORDE TATAGEBEEK PRECASOR (C. 2.1.1.1.) (FRITHELIAL CELL GAGGO) 74070 ONCOORDE TATAGEBEEP KOPEN KNASE PER (C. 2.1.1.1.) (PRITHELIAL CELL 71.5.3.6.4.9)			Ť	1	t	T	T		1	1	
ALEATOS KUAJE, B CHAIN (EC 17.7.). TROSDE PROTEM-KONSE ECY PECUASOR (EC 17.7.1.113) (EPITHELIAL CELL 464-93 ALOTO-ONCOCONE TYROSINE-PROTEIN KINASE FER (EC 17.7.113) (PA-FER) 219-346	PKSFI HUMAN	AUCLEAR PACTOR KAPPA-B SUBURIT-I (NF-KAPPA-B P105 SUBURIT)	53.570	ŀ	T	İ			T	1	ľ
TROSDE PROTEN-RDAZE ECK PLECASOR (EC 2.7.1.113) (EPITHELIAL CELL. 464-493 40/TO-ON-COCIENE TRAGEDRE-ROTEIN KINASE FER (EC 2.7.1.113) (P94-FER.) 219-3-46	KOL HIME	CHEATIVE KUNASE, B CHADI (EC 2.7.1.2).	101-328		l	İ			T	Ī	
219-246	WECK HUNNY	TROSDE PROTEDLEDADASE ECK PRECUSOR (EC 27.1.112) (EPITHELIAL CELL							T	Ī	Ī
	TATES HUMON			165-79				9		l	Ī

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FILE NAME	Ī	Ť	┰	7	T T T T	AUGAS ABEAL		T T	4	7
PRIES HUNAN	PROTO-CONCOCENE TYROSINE-PROTEIN KINASE FESTPS (EC 2.7.1.11) (C-FES)	201-143	100.00	T	T	T	T		1	
NATI MENAN	AECEPTON: RELATED TYRUSINE KINASE PLI PROCUNSON (P. 2.7.1.112).	1		Ī	Ī	Ī			-	
A CHARLES	MACHENIALE COLONY STUMOLATING PACTON FACES 100 PACCOCO (COLONY)	98-333		Ī						
PACTOR MINAN	COAP-DEPENDENT PROTEIN KINASE BETA 1502 YAS (COX) (EC 2 7.1.37)	¥.	T	l						
PKICK HIMAN	VALOSIDER KINASE HEX RECEPTOR PRECURSOR (EC 2.7.1.112).	Ē	Г			П				
PKDSH PEDAN	INTERN HEAVY CHAIN	П	425-452 4	471-542 6	019-569	914-689	871-899			
PKKIT RIBAKH	IT PROTO-CINCOCENE TYROSDYE KINASE PRECURSOR (EC.2.Y.1.113).	235-263								
PKINET HUNOWI	IZPATOCYTE GROWIH PACTOR RECEPTOR PRECURSOR (MET PROTO-ONCOGENE	898-925								
PRINT HELIAN	(nanogen, hany precursor (alpha-3-thíol proteimase inhibitor)	85.53								
PK258 IEEEAA	GALACTOSYL TRANSFIDIASE ASSOCIATED PROTEIN KINASE PSPOTA (EC 2.7.1)	╗	٦						7	
PKP44 IRBAAN	INTERFEROMINDUCED, DOUBLE-STRANDED RNA-ACTIVATED PROTEIN KINASE	╗	191-225	215-212						
PKP78 IGBAAN	KITATIVE SEADRE/THRECHINE-PROTEIN KINASE P78 (EC 2.7.1)	21,609			1					
PKPCL KUNKAN	roten kinase C, eta Type (ec 27.1) (nprc-eta) (prc-l.)	7	1		I				1	
HEPTI HISTAN		П	20°23							
PKPY! HIDAN	SOLIC THYROID	20.20	1	1	Ī				-	
PICT RESERVE		£							-	T
PKPYR HUBAN		2.2	1			1				
PKAET HUMAN	13)	103:217							+	
PKEOS HIBANY	ROS PROTO-ORCOGENE TYROSINE KINASE (EC 2.7.1.112) (FRACHENT).	53.203		Ì					٠	
PKSRC HDAN	I PROTO-ONCOCENE TYROSINE-PROTEIN KINASE SAC (EC. 2.7.1.112) (PGO-SRC)	2	1	T		T				
PKU HUMAN	LUPUS KU AUTOANTIGEN PROTEIN P10 (10 KD SUBUNIT OF KU ANTIGEN)	417.667	1	Ī	T	1			1	
PKUR4 HUMANN	UPUS KU AUTOANTIGEN PROTEIN PEE (16 KD BUBUNIT OF KU ANTIGEN)	238-20		1					ŀ	
PKYES HOWAN	ROTO-ONCOGENE TYROSINE-PROTEIN RINASE TES (EC. 2.7.1.112) (POI-TES)	7			14.416	169.494	480.507	410.410	·	
AAN HAY	AMON B1.		т	Т		т				
AAM AGAM	LAKIN A (70 KD LAKIN)	T	7	171.00					-	
A PARCE NOW A	LAMIN C. TAN BROTHEN BRETHINGS OF BURGEYTE ANTIGEN BELATEDITEC 1 (1) 48)		1							
	THE A SECTION OF THE STATE OF THE PARTICULAR STATES OF THE PARTICULAR S	T	33.743	T		Ī				
N A MINAN	PARISHATION CHOINE STEACH ACYLTIANSFERASE MECURSON (EC 2.3.1.4.3)	T		Ī					•	
M DISH MUMAN	LLACTATE DEHYDROGENASE H CHAIN (EC 1.1.1.23) (LDH-B).	П	302-326						ą.	
PLDION HUMON	LLACTATE DEKYDROGENASE M ČKAN (EC 1.1.1.27) (LDH.A.)	115-252								
PLDCR KURAN	LOW-DENSITY LINOPHOTEIN RECEPTOR PRECUNSOR.	443-510	1			Ī				
PLECH HUSLAN	HECH HEALIN ASSALISELYCOPROTEIN RECEPTOR I (REPATIC LECTIN HI) (ASGM).	95.70	+	1		T				
3	P.SELECTIN PRECURSOR (GRANULE MEMBRANE PROTEIN 140) (CAC-140) (TAUNCH)	25.27				Ī				
N.C.	LACTOTLULUIA IMMUNG LI ABOLICE A.M. I. 3 (MAINTUM I CAMANAS)		Ť	T		Ī			L	
N IN INDIAN	LNE. I BEVERSE TANKCRUTASE HOMOLOG.	152.179	133-263	294.356	671-698	174-901	1036-1066			
N DO NOVA	HUACYCOLYCEROL LIDASE PRECIRSOR (EC 1.1.13) (LIDASE, CASTRIC).	154-185								
PLDS JACKAN	HORIMONE SENSITIVE LIPASE (EC 3.1.1) (HSU).									
PLKIA MUMAN	LEUXOTAIENE A-4 KYDROLAKE (EC 3.3.2 6) (LTA-4 HYDROLASE) (LEUXOTAIENE	(T-2)	_	100	1044 1051	1001	9901 3701	2004 2004	9116 1906	
PLAN ICHAN	LAMININA CIALLY MECHINOL		7011-791		1681-1714	723.1781	1000			
1000	TANKAN BY CHARLES CHICAGO	103-115								
N. LOT HILLIAN	I LYSOSOME ASSOCIATED MEMBERINE GLYCOPROTEIN 2 PRECURSOR (LAND-2)	135-182								
PLOXI HUMAN		341-364								
PLOXS HUMAN	A AUACHIDONATE S-LIPOXYGENASE (EC 1.1) 11.34) (3-LIPOXYGENASE) (5-LO).	100								
ACH MUNAN	(ACTASE-HILORIZM HYDROLASE PRECURSOR (EC 3.2.1.100) (EC 3.2.1.42)	┪								
PLEAS HUNDA	4 PROTEIN-TYRIOSINE PHOSPHATASE BETA PRECURSOR (EC 1.1.) 41) (PTP-BETA)		Ž	1						
PLETO HEBAN		180								
PLUZ HOMAN	PROTEDUTY OSING PHOSPHATASE ZETA PRECUNSOR (EC.) 1.3.43 (PTF-ZETA).	22.5	1604-1031	002-1761						
H SHO HUMAN		18-19								
NAO HUKA	NILYSOSOMAL ALPINA-CIUCOSIDASE PILE: UNGOR (EC 3 2 1 20) (ACID MALTASE)	118:913	T							·
PADOM HIBAA	GTOCHONDRIAL 3-OXOGLUTARATIONALATE CARRIER PROTEDY (OGCP)	50.73								
PHACE RUMAN	ALACTOSE SPECIFIC LECTIN MAC. I ANTIGEN) ILIE BINDING PROTEIN) (15 KD	219-246								
PHANG HUMA	PKANG HOMAN WANGE ALPHA MANNOSHIDASE (FC 1.2 L.)	414-44]

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ELL NAME PROTEIN	ARGAL	AREA AREAS	AREAS	AREA 4	AREA 3	AREA	AREAT	AREAT	AREAS
FMAXA RUMA MAMNOSE-FROSPIATE SOMERASE (EC. 5.1.1.9) (FROSPIAMANNOSE ISOMERASE)	3	11/12/1183	Ī					-	T
					Ī				T
	100.444								T
PLAN HIMAN MAX PROTEIN	771711	Ī	I		I				T
PADAGE HANA INDIA PROTEIN PROCESS PROTEIN	216.386	Ī							Ţ
PADAL MINANIMALTIDADO RESISTANCE PROTEIN I (P. GL. YCOPROTEIN I)	\$61-595								T
MEAL MAKAN MELLIN (SCHWARMORM)	177-407	332.566	Ī						
PKEAD HUMANIJEEKOSIN HEAVY CHAIN (LAKININ CHAIN AS) (TRAGMENT).	103		2.43	1112					
PACACT MUMA METHYLATED DNA PROTENCYSTENS METHYLTANSFERASE (EC 2 1.1 61) (4-0-	811.18								
PACLE HUMAN HITOTIC KINESIN-LIKE PROTEIN-1.	207.234	319-346	510-537	349-608					
PALCH HUMAN MELANIN-CONCENTRATING HORMONE PRECUISOR.	T								
•	116.139	31.348						[
MOKSA HOKA METHYLMALONATE SEMIALDEHYDE DEHYDROGENASE	T							1	
PACES HUMAN MOESIN (MEMBRANE-ORGANIZING EXTENSION SPIKE PROTEIN)	119-146	351-403							
PADCY HIBAAN INITIOCHONDRIAL PHOSPHATS CALABRA PROTEIN PRECURSOR	Г							-	
	22.55		Ī	Ī				-	
	05.61				Ī			-	Ī
	286149813	2437-2478		Ī					Ī
	138-421	25.54						Ţ.	I
7=	T		Ī	Ī					Ī
	T	230.366		T					Ī
	Т	119	Ī	T		Ī		1	T
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FROM A RUMAN HE INTERNATION TO MOTASE PRECUEDA (R. S. P. J. (PACA).			Ī			Ī			
_	2							1	
PACE HOMAN INTERPRESENTATED LESS TAKE OF BINDING PROTEIN INCO. (P.M. NELATED ASSAULT	7	670,697							
PATEA RUMA MID-LEATED MOTERN A (PIACHEST).								1	
THE FEMALE STATES AND THE PROPERTY BY	┱			1					
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-	777-777							-	
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THE TEST DURING THE COURTY FOR THE TEST	20.00		1	1				1	
PROTES ACREAN MATERIAN PRINCIPLE.	201.02		1	1					
PRITER HUMAN MATELIA PROTECTION PROTEIN (PLY) (LIPURITIN) (CONTAINS: MATELIA	1	7	╗		╗				
PROTAG BURGAN MOTOSIN REAVI CHADA, CALCAC MUSCLE ALFRA (SOFORM (FRAGMENT).	T	7	-+						
PACTOS PLUMANIMICOSIN PLEATIC CALCUAC MUSCLE BETATOCOUN.	4-73	20-16	104	_	22.22	1264-1332	1360-140\$ 1442-1479		1488-1532
PACYSE KINZANILYOSIN MEAVY CHAIN SACT SKEI BTAI LAISCTE BLABYOUT		1007-1001	771.011.04.001.1874		71.01 191	27.1	7	277 177 1871 1871 1871 1871 1871 1871 18	
	35	127-1858	-					100	C/81-16
PHYSP_HUKAN MYOSIN KEAVY CHADI, PERINATAL CARDIAC MUSCLE (FRAGICENT).	75.77		141.188	215.277	60,483	507-552	316.624	645.736	784.818
	123.907	946-987	10	Г	т	т	т	Т	
PMYSS HIMAN MYOSIN KEAYY CHAIN, SKELETAL MUSCLE (FRAGMENT).	133-160	193-280	304-349	433-450	625.20	28- ES	12.62	143.198	101-135
	Ŧ	146-873							
	╗	_							
PHACA HUMAN SODIUM/CALCIUM EXCHANGER PRECURSOR (NA+CA2+EXCIANGE PROTEIN).	492-519	594-621	205-735						
PNCA3 HUMAN INEUTAL CELL ADMESION MOLECULL, PHOSPHATTO YLINOSITOL-LINKED ISOFOLM	25.283								
PHICE I MINIAM (REUTHOPHILL CYTOSOL FACTOR I (MCF-47K) (4) KD AUTOSOMAL CHOOMIC	134.76	ř.							
THE HUMAN INCUINGING MACHINESS FACTOR (PRICED)	2	┪							
THE A MUNICIPAL WAY BINGING THE PART ARE A PARTICULAR.	7	7	20.00	1					
7	1,021	200		1					
_	7/10/5		1939-1860		Ì				
MATE HISAN NEUROSILANCENT TRIPLET L'PROTEIN (48 KD NEUROFILANCENT PROTEIN (74 KD	92.126	41.46		T				1	T
_	101:101	Т	213.280	115.11	233.364	704.87K	110.673	1	1
_	336-365	Г	1	Т	✝	T		T	Ī
PARKA HUMAN MATURAL KILLEN CFILLS PHOTFIN APPECIATION	166-193		ĺ				Ī	Ì	

		ANEAL	AREA !		AKIAS	-	_			
THE WHIT THE	TRUITER CHANGE CONTINUED DE CORRESPONDATIONAL - KILLER CELLS CYCLOPHILIN-	T	Т		_	(16-84)	1010-1133		-	:
	AKOLA AND NKOLA TYPE II INTEGRAL MUMIKANU PROTUINS					-	Ì		-	
PACKE LEBALAN MITBE	COXIDE SYNTHASE BLAIN (EC 1, 14 1), 39) (NOS, TYPE I).		1116-1146 1292-1319	292-1319		1	Ì	1		
	MITTEL CAXIDE SYNTHASE ENDOTHELIAL (EC 1.14.13.19) (EC-NOS) (NOS,	917-686				1				
	SOUTH- AND CHLORIDE DEPENDENT GABA TRANSPORTER I	151-161		+	1	1	1			
	NEUROTENSIA RECEPTOR (NT.4).	27-14			†	1	1	T		
1	SOCIUM DEPENDENT SELOTONIN TRANSPORTER (SHT TRANSPORTER) (SHTT)	5		1	-	i	1	-	:	;
PWTTA KUMAN SOOU	4- AND CIL DAIDE-DEPENDENT TAUKINE TRANSPORTER	2	1			Ī	İ			
NAME OF	MADH-UBIQUINONE OXIDOREDUCTASE CHAIN 2 (EC 1 6 5 3)	1			+	Ì	1			
PEDAN HERANINADE	JAKOUNONE OXIDOREDUCTASE CHAIN 4 (EC 1.6.5.1)		2		1	1	1	Ţ	-	
	DEMOIN PRECURSOR.	Ħ	66-383						4	
-	NUCLEGIAN (PROTED) C23)	105-291				1	1			
	PUTATIVE NEUROPEPTIDE Y NECESTON TYPE 3 (NPY3-R) (FB22) (NPYRL)	115-142			-		:			
	-000	13.128							1	
MAIAM	SELBINOWING TRANSCRIPTION FACTOR (A (OCT-1A)	139.135								
	OCTAKES BOODING TRANSCRIPTION FACTOR 35 (OCT-38)	17.76					1		-	
KINAN	LOWES OCH DEREBROKENAL SYNDROMS PROTEIN.	704-735							-	
	LIDE ACYL TRANSFELASE COMPONENT (E.) PRECURSOR OF BRANCHED CHA	100-127	175-402							
	DINYDROLLPOANIDE ACETYL TRANSFERASE COMPONENT (EL) OF PYRUVATE	13.44				1			+	
	<u> OLIGODENDROCYTE-MYELIN GLYCOPROTEIN PRECURSOR (OMG)</u>	5.40			1		1			
-	ALLIE SENSITIVE OPSIN (BLUE CONE PHOTORECEPTOR PICHENT)				1	1				
	SENSITIVE OPSIN (GREEN CONE PHOTOXECEPTOR MGMENT).		239-266		1		1		1	
	HED. SENSITIVE OPEN (NED CONE PHOTORECEPTOR PICHENT)		239-266		1	1				╛
	OSTEOPONTIN PRECURSOR (BONE SIAL OPROTEIN I) (UNINALLY STONE PROTEIN)	239-266			j				-	
100	OUNTHING CASEAMON, TRANSPERASE PRECUISOR (EC. 1.1.3.1).	10.204			1				-	1
3	OSTECNECTIV PRECURSOR (BASENZ) I NEWBRANE PROTEIN BM 40)	_	╗	Т			1		ŀ	1
	OXYSTEROL-BINDING PROTEIN.	7	2		\$		1		1	
	CONTECENTOR (OF A)	330-331	***	1	t	T	Ī		ŀ	l
PIOT MEMAN METEN	RETRICOLATIONA - ASSOCIATED PROTEIN-LUCE 107 RUNCHOLOGIA (1707)	Т	1997		T	Ī				L
•1	ALT PERANE ALTER MUCACA FRESANCIAL ESTREMENTO	2					Ī		-	L
PAT HUMAN	PERCENSION (PM).	\$\$ £	191-218						-	
AVAILABLE OF	HANDRIAL MATRIX PROTEDU PI PRECURSOR (PIOL YLOHOCYTE PROTEDY)	Ť	362-142	761-407						
L	PHOSPHATIDY INOSITIOL J.KINASE REGULATORY ALPHA SUBUNIT (PI): KINASE	13.39	431-476	166-613 61	686-715					
PAPE HERAN PANCE	PANCALATHIS ASSOCIATED PROTEIN I PRECURSOR.	17.104								
AXY HUMAN PAINE	PAXI HIMAN PAINED BOX PROTEIN PAX: 5 (9-CELL SPECIFIC TRANSCRIPTION FACTOR)	187-187								
DOA HIMAN PLATE	PPOGA, HIDAAN PLATELET DELIVED GROWTH FACTOR, A CHAIN PRECURSOR (PDGF A-CHAIN)	¥		1	1		1			
ECI HUMAN MATE	LET STOOTHELLIAL CELL ADMESION MOLECULE PRECURSOR (PECANI-1)			†	1					
PER HUMAN PROES	PROBUMENTALISM A PRECINCOL	142.1		\dagger	t		Ī			l
	EDSTROPME PERCENTAGE PRESENCE (EL FILLE FILE DE PARTICION DE PRESENCIAN DE PARTICIO	117117	T		\dagger					L
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TANK MUNICAL PARTY	PARTY AND ABOURD BEOTROMY YEAR COLE PROTEIN PRECINSOR (CSPCF)	3.68			l	Γ				
DIV I WANTED	I ARCH BIBROAL AST PROTEOCL YCAN PRECURSOR (YEASICAN) (CHONDROITIN	2 3	1390-1417 1333-1510	1153-1510						
PRIDE HIMAN ISTO	LHYDROXYPROSTACLANDIN DEHYDROCENASE (NADI+)) (EC 1.1.1.141) (PODH)	11:11								
PODR HUMAN BETA	BETA PLATELET-DERIVED GROWTH FACTOR RECEPTOR PRECURSOR (EC 2.1.112)	394-331	П		Π					
PCDS PRINCING ALPRU	alpha platelet derived growth factor receptor precursor	2.2	347.395	461-488 5	524-551	916-1058				
PGHS_HEMAN PROS	PROSTAGLANDIN OM SYNTHASE PRECUASOR (EC. 1.14.99.1) (CYCLOOXYGENASE)	22:12			†	T	Ī			\perp
	BONE/CARTILAGE PROTEOCLYCAN I PRECURSOR (BICLYCAN) (PG-\$1)	8		1	1	1	T			1
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	PROHIBITION.				\dagger	T	T			1
3	PHOSDOCIN (3) KD PHOTOTIKANSKALING PROTEIN)	1	Ī		t	T				
PHSI MUMAN GLYO	GLYCOCEN PROPRIEKTIANS, LIVER FORM (EUC.).)	532-559			T	Ī			L	ļ
	OUTCOOCH PROGRAMME MUSICE FORM (CC 2 C 1)	411		Ì	t	T	Ī			ļ
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NAME OF THE PARTY	I PHOSPHATIDYLINGSTOLA, S-BISPHOSPHATE PHOSPHODIESTERASE GAAGNA ?	П	130.266				-		
PLAX HUNCA	N PLAKOGLOBIN (DESMOPLAKIN III)	171.400					1		
A PLANT	L-PLASTIN (FUGRIN)	Ş.					1		
775	T-YLASTEN (TUGBRIN)			-			-		
PPG2 HUMAN	EXPREMAL MYELM PROTEIN 22 (PAD-22)	3		1		j	1	1	
WINGS HUM	HOSPHOGL VCELATE MUTASE, BRAIN FORM (EC.S.4.1.1) (PGAM-B) (EC.S.4.1.4)	-			1		1	-	
PPINCN HUNA	PHOSMIOGLYCELATEMUTASE, MUSCLE FORM (EC.) 4.2 1) (MAM-N)		+			j	1	+	
NOW N	PROBABLE INCORPIUM PACTOR PRICT.		1	1			 		
HUMA	N PROBABLE TRANSCRIPTION PACTOR PML-X	31:363		1	-		1		
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4	ANY BLACK AND THE POPULATION OF THE PROPERTY OF THE PROPERTY OF THE PA		7	440-700 /60-010		Ì			
NO. HUMAN	LETROVIAUS. RELATED FOL POLYPROTEIN (REVERSE TRANSCRIPTASE	14.10							
NO.	ETROVIRUS-RELATED FOL FOLYPROTEIN (FRACMENT)	20.5	71-303						
POR HENAN	XITER MITOCHONDALAL MEMBRANE PROTEIN PORIN (VOLTAGE DEPENDENT ANIO	2	189.216						
PPPA HUMA	ROSTATIC ACID PROSPHATASE PRECUASOR (EC 11.1.1)	3.26							
PPPAS HUMAN	LED CELL ACID PHOSPHATASE 1, 1502 YPCE 5 (EC 3 1.3 2) (ACP1)	П							
PPOL HUMA	WIN(*) ADP-RIBOSYL TRANSFERASE (EC. 3 4 2.30) (POLY (ADP-RIBOSE)	626-669	\$72-1003						
PPRC3 HUMAN	ROTEASOME COMPONENT C1 (EC 3 4 99 44) (MACROPAIN SUBUNIT C1)	99-66							
PPICT HUMAN	ROTEASOME COMPONENT C1 (EC 3.4.59 46) (MACROPAIN SUBUNIT C1)	19-16	-				-	 -	
PPRC9 HUMAN	PROTEASOME COMPONENT CO (EC. 3.4.99.44) (PACROPAIN SUBLINIT CO)	197-502	-						
PPRCR HIDAA	PROGESTERONE RECEPTOR (PR) (FORMS A AND B)	061-971							
PPRTS ACCOUNT	MITAKIN K-DEPENDENT PROTEIN S (BLOOD CLOTTING) PRECURSOR.	11.37							
PRETZ HUNA	MTAMON K-DEPENDENT PROTEIN 2 PRECUNSOR	9X 62	+						
PROPERTY AND A	T	45.02		ļ					
PAUD GENT	PROBLEMAAN INELIGIALE SUBFACTANT ASSOCIATED PROTEIN DIPRECUISOR (PSP.D) (SP.D)	124.251	ŀ			1	<u> </u>		
PTIN HIMA	PARATHYROD HORMONE PRECIESOR (PARATHYRIN)	19.	$\frac{1}{1}$						
NALES INTER	PROTEST, TVBOSTNK PROCESTACE IN FPC 1 1 1 481 (PTP. IN)	14-177	-		-	Ì			
A PARTY	P. CELL PROTEIN, TYROKINE PHOKEHATAKE (F.C.) 1 ASI OF PETEL	71.05	116.19				1		
PPTN6 HIBA	PROTECULTYROSINE PHOSPHATASE IC (EC.) 1 41 (PTP. IC) (NEMATOPOLETIC	Ŀ	\$12.540				+		
PPTAR HISAA	MOTER, TYTOSING PHOSPHATASE 2C (EC.1.) 401 (PTP-2C) (PTP-1D)	Т	218.245			ļ			
PPTAC HISA	PROTED/TYTOSINE PHOSPHATASE OF (EC.) 1.3 (4) (PTPO)	Ŀ	405-722					-	
PITTER RESEA	ALATHYROD HOLLIONEPARATHYROD HOLLMONE RELATED PEPTIDE	Т							
PPTO AUGUN	ENTAXONAELATED PROTEIN PTX3 PAECURSOA	74-101							
PURT HUMAN	HOSPHONDOSYLANDNE—GLYCINE LIGASE (EC.6.3.4.13) (GAIS) (GLYCINANIDE	009-000							
PUT HIDAN	KILL THUNCTIONAL PROTEIN ADEZHI (PHOSPHORIBOSYLANGNOINIDAZOLE:	191-160							
PPUTE HUMAN	ADENYLOSUCCINATE LYASE (EC 4.3.2.3) (ADENYLOSUCCINASE) (ASL)	104-231							
PYTES HEBRAN	URLINGNE S'-MONOPHOSPHATE SYNTHASE (UNO SYNTHASE) (OROTATE	130-150							
PYTO KENEY	CTP SYNTHASE (EC. 4.1.4.1) (UTP -AMMONIA LIGASE) (CTP SYNTHETASE).	╗	_	_					
12 KG	PRECRAMENT ZONG PROTEIN PRECURSOR		116	1162-1189 1405-1432	20				
ACM VA	TANGCALTION PACION III, ALTHA SUBUMI (1918), ALTHA SUBUMI)	000					1	-	
TANK MUNICAL	WASTELLIEU TRUIBIN INDIA								
TANK TANK	CAPACIAL POLICE PAGE.	201.00	137 777	610 613		1	1		
PLATE ACMAN	RACEPELATED PROTEIN BAB-11 CAKOL (YLB)	1	Т						
PRESS HUMAN	RETINOBLASTOMA BINDING PROTEIN 1 (RBBP-1) (PRB-BINDING PROTEIN EXF-1)	20.00	161.123					 -	
PLDS HUSLAN	ND PROTEIN	S3					1	 -	
PREMI HUMAN	NEWNY PRECURSOR, RENAL (EC. 3.4.23, 13) (AMGIOTENSINGGENASE)	136-163	-					+	
PILEST HUNAN	RESTTY (CYTOPLASADE LINKER PROTEIN-170 ALPHA-2) (CLIP-170).	100-217	333-370 44	445.472 571.619	744.771	784-052	023-1050 1088-1139	1139 1157-1164	
		1216-1306				†		_	
PIUAI HUMAN	REPLICATION PROTEIN A 70 KD DNA-BRIDING SUBURIT (RP-A) (RF-A)	П	425-455						
THE HORSE	TRANSFORKENO PROTEDY (NET) (NET PRINCER PROTEDY)	113-217							
PRH HUMAN	BLOOD GROUP RH(D) POLYPEPTIDE	181-188							
NEE HERE	ALBOPHOLIN I PRECURSOR.	101-11	196-530				-		
PLD: NOVEN	REPORTOR II PRECURSOR		161.388						
PLO HOMAN	ALBONUCLEOSUBE-CUPHUSPIKAT BIRLDUCTASE MI CHAIN (EC. 1.17.4.1)		370-400	1					
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THE MUNICIPAL PARTY	SAS ACTIVE REDACTAGE PROTEIN POLITION	31.163								
	STATES AND SELLING STATES OF TABLE A ANTIGEN (SS.A))	Γ	116.265							
T	AND NO PROTEIN CHOCKEN CAMBONIE TYPE A ANTIGEN (SS-A).	192-145							1	
Т	PRESCRIPTION OF THE BIRDWING FORBOTTE IN SCHOOL AND WINNE	7								
т	DESCRIPTION OF STREET STREET (STREET)	301.328	Ī							
┱	CACACACACACACACACACACACACACACACACACACA	410.617	Ī							
PROUPLE PROPERTY	HEIRAGENOUS LIGHT CALCATANT SIN OF WESTING	Т	665.720	906-64	1314-1341	1371-1398				
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FRED HUMAN UP	UNA-CARLE LED WAS TOLIMERASE II JUNO INC. II CO.	525	Ī	Ī				Ì	F	
PRACKA HUMAN RE	RETINGE ACID RECEPTOR RATIONAL PRA	1		Ī				Ì		
PRUCE HUMAN RET	RETINGIC ACID RECEPTOR EXR.BETA ISOFORM I	10000	Ì	;	•		1	-	-	
PRINC HUMAN REI	RETINOIC ACID RECEPTOR RXR-BETA ISOLORM?	70-06	Ī		1		Ī		Ì	
PRS12 HUMAN 405	OS NBOSOMAL PROTEIN SIZ			Ī			1	Ì	1	-
PASIS INDMAN 405	405 NIBOSCHAL PROTEIN SIG	=							٠.	
FRS35 HUNTAN 405	405 RIBOSUMAL PROTEIN \$25	36-53					ļ		-	
_	405 KIBOSOMAL PROTEIN S27A	17-7	i	i	:			1		
•	405 KUBOSOMAL PROTEIN \$1 (S1)	73.100	į		!	-		-:	:	•
PRSE HUMAN 405	405 RIBOSOWAL PROTEIN SA	16.161	!	1	:		-		-	
1,	KAS-LIKE PROFEIN TC31	133-150								
PRUIA RUMAN UI	UI SALALL MUCLEAR MIDOMUCLEOPROTEIN A (UI SNRWP A PROTEIN)	13-47								İ
PRUZB HUMAN UZ	US SAIALL MUCLEAR MISONUCLEOPROTEIN B"	П								
PEYNOR HUMAN BY	AYANDODE RECEPTOR, SKELETAL MUSCUE	1 201 951	148-525	166-19)	1140-1111	2020-2047	3304-3331	3520-0256	3012-3939 4921-4941	1051.494
PETAL UNIVERSITY	C. IMPROTEIN ALPHA CHAIN	12.54								
TO THE PARTY OF TH	CONTROLLER DESTRUCTION	2.2								
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PSATI ROMAN	A-BUNDEND FROITING AND BUILDING AND	30.104						Ī	ŀ	
PSOCA HUMAN SO	SQUANQUE CALL CALLENGA ANTIGER (S.C.A.) ("ROTEIN 194)	10176	Ī							
NO MON	STEM CELL 7 ACTUM PROCESSION (SCHOOL SCHOOL AND COLORS	Ť	76.236	388-129	34.34				-	
PSEAL MUNAN	SECRETARION OF THE CONTRACT CO	T		104.144	405.430	510.535			Ī	Ī
NO MARK	ACADAGE IN IL PACCURON (SAN)	T	24					Ī		
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7.	SECRET CONTRACTOR OF THE PROPERTY OF THE PROPE	٢	Т	356.213						
-	LASCINICA CHARLE THE ANY CHIEF TOWN ACTIVATOR SNS 21	Ĺ	Т							
THE PERMANENT	STAND THE PROPERTY OF THE PROP	Г								
PEPCA KITHAN SP	SPECIALIN ALPHA CHAIN.	193-220	370.621	812-559	1000-1126	1461-1502	6061-7111	1028-8801	0522-1222 1512-0212	233-3350
-		1346-2373								
	SPECTRIN BETA CHAIN, EXYTICNOCYTE		316-350	025-917	619-819	987-1021	1027-108)	1287-1324	1347-1374	1834-1861
	SENAPTERDN REDUCTASE (EC I 1 I 153) (SPR)	П								ĺ
	SERUM RESPONSE FACTOR (SRF)	٦	20.20						1	
	SIGNAL RECOGNITION PARTICLE RECEPTOR ALPIN SUBURIT (SR-ALPHA)	2							T	
PSSRI HUMAN SO	SOMATOSTATIN RECEPTOR TYPE I.	203-2110								
PSTIBLE HUMAN ST	PSTICK HUKKN STATICAN (PHOSPHOPROTEIN PIS) (ONCOPROTEIN PIS) (LEUKEARA-ASSOCIATED	× .	I	-					Ĭ	
PSUIS KUNAAN SU	CLASE-ISOMALTASE, INTESTINAL (EC.) 2 : 41) / (EC.) 2 1:10)								1	
	WAYNOOLEVIN I									T
PSYDS HUMAN AS	ASPARTYL-TRUA SYNTHETASE ALPHA-1 SUBUNIT (EC 8.1.1.12) (ASPARTALE—		140 331							T
PSYEP HUMAN IN	A TO UNCTIONAL ANGROACYL-TIUM STRING I ASB (CONTAINS GLUTANITIES	107-1-1	1/1-00/						Ī	
_	HOSTIDYL, TANA SYNTHETASE (EC 6 1.1 21) (HISTIDINE-TRNA LIGASE)	Т	704-70							
	SYNAPTOTAGMIN (PS).	9	1300							
_	THE CONTLITUE STRING ASE, CT 107 ASMC (EC. 8.1.1.1) (THE UNITED AS A STRING TO	т	411.440						Ī	ŀ
_	VALYETTAMA STRINELASE (CC 0 1.1.7) (*ALINE-1704 LIGASE) (*ALINE)	T							T	
PSYN HOMOS IN	THE ANY CENTRAL PARTICIPATION FACTOR HE BETA CHAIN (TRIPEBLA)	Т							T	T
VI 420 RUMON	FIRE THE ALL THE ALCOHOLD FACTOR AND CRACKEN	8	245-272							
FIATE DUMON III		7								

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TILE MANE PROTEIN	বং	3	7	1	4	7 42 4	A SEA	1	A TEN	1
PTAPO NUMAN TRANSCRIPTION FACTOR JUN-D	29	291-333	Ī	T	Ī			Ī		
PTAUL HUMAN MICROTUBULE ASSOCIATED PROTEIN TAU	12	278-305								
	5	\$11:23						Γ		
	20	101.241	130-357							
	16	316-343								
PIDT HUMAN DWA NUCLEOTIDY LEYOTRANSFERASE (EC 2 7.7 31) (TERMINAL ADDITION ENZYME) 81.93	TONENZ YNIE) 61							1		
PTEK IIUNIAN IRECEPTOR TYROSINEIPROTEIN KINASE TEK FREGURSOR (EC 2 71.112)	(FII'K-6)		20.00	903-1036						
PITZB KONIAN TRANSCRIPTION MITTATION FACTOR III (17118)			т				Ī	Ī		
PARTY DIRECT TOP INCOME SALIDATED TO SECTION 6.1		T	2				1			
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PICK TONAN PROTECT ORGANIC CAMPE CAMPA OF LITANY TRANSFERACE (FC.) 11	-			Ť			1		-	
		1	214-314	T		Ī	T		-	
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PIXMS HOMAN PROTACITY NIN BETA PRECURSOR (CONTAINS SUBSTANCE P. NEUROKININ A		<u> </u>	Ī	Ī			l	Ī	1	
	Ī	636-653	Ī	İ	Ī		İ		1	
	2	84-125								
	2	100.30							Ţ.	
	1	9	101-533				Ī			
PTOPB INDIAN DNA YOPOISOMERASE II, BETA ISOZYME (EC 1991.))	25	33.63	616-647							
PTPAIS_HUMAN TROPOMYOSIN, FIBROBLAST ISOFORM TMJ.	16.	16.74	911-28							
PTPATA HUMAN TROPCHIYOSIN ALPHA CHAIN, SKELETAL MUSCLE	=	7	5:34	9:1:0	147.174	191.237	10. US			
PTPAGE HEMAN TROFOMYOSIN BETA CHAIN, SKELETAL MUSCLE.	11.	17.116	193-240						-	
PTPING HUMAN (TROPOMPOSIN ALPHA CHAIN, CANDIAC MUSCLE		П	911-29	143-211						
PTPNG KIMIAN TROPOMYOSIN, FIBROBLAST AND EPITHELIAL MUSCLE-TYPE (TNI)6) (210-240	7				Ì		
PTPMO HUMAN TROPOMYOSIN, FIBROBLAST NON-BRISCLE TYPE (TM30PL)			=	T	201.134				-	
STATE TOWARD TROUGHT USING CONTRACTOR THE CONTRACTOR TO STATE OF THE ACCOUNTY	Ī					Ī	İ		-	
PTERS ACREA TREPERTING ACTIONS HISTORIA TO THE TO THE STREET TREET TO THE TREET TO		Ī.	Ta	1140.1167		Ī	Ì			
PTPR HUMAN TPR ONCOCENE (PRACNENT)	22	۲			T	T	T			
	Ī	T	343.369			Ī	T			
		2			Ī					
PTILC_HUMAN TROPONIN I, CALDIAC MUSCLE		(9-9)							l I	
PTRKA, HUMAN HOGH APPINITY NEAVE GROWTH FACTOR RECEPTOR PRECURSOR (EC 2 ? 1113)		П	117.148							
PTRSK HUMAN (TRANSPERUM NECEPTOR PROTEIN (TR) (ANTIGEN COVI) (T9)		ℷ	366.393						1	
TIBER RUMAN INTRUINGEN RULE TON PRECUNSOR (1981-R)	4.	1 101	91	773 013	117 077		1			
FILE ADMINISTRATION ALTERNATION FOR THE PROPERTY PROPERTY (SEC. 8.7.1.1.5)		1	7	Т		1	T			
PLEAT HIMAN IDEICHTIN-ACTIVATING ENZYNG ET (A159 PROTEIN)	1	\$ 17.00 P	Ī		Ī	Ī	T			
PUBET MUNCAN INOCLEDICAR TRANSCRUTTION FACTOR ! (DPSTREAM BINDING FACTOR !) (UBF-!)	=	221.134					T			
PLIDIO HUMAN UDP-GLUCURONOSYLTIKANSFERASE PRECURSOR, MICROSOMAL (RC 1 + 1 17)		227-154								
PURO HUMAN (RECEPTOR TYROSDIE-PROTEDI KINASE USO PRECURSOR (EC 17 1 113)		489-522			Ī					
		2								
=		7								
PVILL HUMAN VILLIN	2	╗	Т	117.764						
PYDAR HUMAN VENENTEN	2	1	3 2 2 3 3 3	1	1	1	1		1	I
PVDVC HONCAN VONCOLIDA PVDVC	2	101.13	Ī	T	1	1	1	1		
PAPEL BOXAN REINOVINOSHICA ED PROJESSE (EU 1422)		10.72	1	1	1		1	1		T
	34	347-374		T		Ī	1	Ī		Ī
PXBPI HUMAN X BOX BINDING PROTEIN-I (XBP-I) (TREB) PROTEIN)	5	31.13		İ	Ī	Ī	T	Ī		
PYDAC HUMAN DNA REPAIR PROTED COMPLEMENTING XP-A CELLS (XEXODEBNA PIGMENTOSUM) 180-111	IGMENTOSUM IR	П								
PXPCC HUMAN IDNA-REPAIR PROTEIN COMPLEMENTING XP-C CELLS (XEXODERMA PH	IGAEENTOSUM 13	134-169	101.728							

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1	PCCEAC [107x173x4 Model Search on All Mannes Protein Sequences	TIEMANE PROTEIN	YOU'C MULAN DUA REPAIR PROTEIN COMPLIANCE IN A CHELL THE OWNER MAY PROMINED IN	ADOC HONAN DHA NEDATH PROTEIN CONDITIONED IN COLUMN AS C	XSICE HAMAN BEPAUM PROTEIN XCCCI.	TABLE CONTRACTOR OF THE PROPERTY OF THE PROPER	ZNIO HUMAN ZINC PINCER PILITER VICTORIA PARTIER PROPERTIENCY VIETS TYPE I ENIANCISE 11-62	FZNAO HUNAN ZINC FINDER PROTEIN AD HUMAN HANDINGAN	ZN45 ILINIAN ZINC FINGER PROTEIN 45 (UKC1744) [FRACMENT	THE RESEARCH PROCESS PROPERTY AND PROCESS WORLD

TABLE X

Search Results Summary for PCTLZIP, P1CTLZIP, and P2CTLZIP Motifs

910		PICTLE					•	_
	-	LIBRARY FILE			A257	LIGHARY FILE		
JEHANY FILE	-	PENY BYON	434,460		AGA	PENV BIVOG	249-929	
PENV FOAMV		BA111	461.470		PENV	PENV BIV27	224-671	
PERV HVIMA	139483	TENY BILLY	407.707	AA4.ARO	PENV	PENV FENVI	3047	030-647
PENV HVSMP	183-198	PENV POAMV	200		PEN	PENV PIVPS	781-798	
PENV HVIRH	446-460	PENV HVIKB	007-707		300	PENV FIVED	770-788	
PENV HV18C	102-201	PENV HVIMA	437-463		238	PENV PIVIZ	780-787	
PENV HV122	123-138	PENV HVIMP	183-188		Sula	DENV FLVCA	39-55	024-041
PENV HV12H	439-463	PENV KVIRH	444180		Na Park	DENV EIVOI	AOK-822	
DENV MV2RE	750-765	PENV HV181	739-764				62E. 649	
DEUV LIVIDA	741.756	PENV HV18C	166-201		KENA	PENV FLVLO	040.04	
20000	741.756	PENV HV122	123-138		YEN'S	PENV PLVOA		760 000
ENV NVCIII	27.0 36.3	PENV KV1Z3	117-133		AEM -	PENY FOAMV	/10-/2/	100
PENV HVZNA	1	MAINN MAIN	437-463		PENV	PENV FBVOA	020-042	
PENV HVZRO	751-760	TENY TARREST	TEO. 7AR		PENV	PENV FBVOB	90E-622	
PENV HV28B	743-768	PENV NVABE			PENV	PENV FBVBM	608-625	
PENV HV28T	746-760	PENV HVZD1	/41/00		AN36	PENV HV10Y	123-140	
PENV JSRV	104-119	PENV HV201	/41-/00		DENV	DENV LIVI79	410-427	
PENV MMTV8	618-633	PENV HV2NZ	742-767			DELLY LIVING	184-171	
DELLY MUTVO	616-633	PENV HV2RO	761-700		LENA	PERIO DE LES	760.243	
ENV MINITO	110.164	PENV HV28B	743-758		LENA	LANCEA		
PENV SIVER	73, 40,	DENV HV28T	746-760		PENV	PENV MCFF	1600	
PENV BIVML	138-104	Vien Vien	124-110	641-557	PENV	PENV MCFF3	601-616	
PHEMA CVBLY	391-406	VEAV JOAN	207.413		PENV	PENV MLVAV	630-647	
PHEMA CYBM	391-408	PENV MCT	202,413		AEK.	PENV MLVCB	625-642	
PHEMA CVBO	391-406	PEND MCPF3	200		PENV	PENV MLVF5	630-666	
PHEMA CVHOC	301-106	PENV MLVAV	427-44-3		PENS	PENV MLVFF	639-656	
PHEMA CVMAS	402-417	PENV MIVEB	422-3B		NJ4	PENV MIVED	630-656	·
PHEMA CVMS	403-418	PENY MINHO	423-439		A CONTRACTOR OF THE CONTRACTOR	PENV MICHO	626-643	
PUEMA WRAA	295-310	PENV MLVMO	420-442		Citize	DELIV MI VYI	167.184	
PUENT MEDE	303-318	PENY MLVRD	424-440	-	TEN	NATE .	1	
DEM WOOL	302,208	PENV MLVRK	424-440		MENA	PENV MIVMO	0.0.0	
PHEMA INDUO		DENN MATAN	618-633		PENV	PENV MIVRD	624-041	
PHEMA INBEN	301-318	SALIN MILITAGE	618-633		PENV	PENV MLVRK	024-641	
PHEMA INDPU	285-301	Series April	804.880		PENY	PENV MSVFB	170-187	
PHEMA MOOL	206-311	PENS OFFI	881-877		PENV	PENV RMCFV	603-620	
HEMA INBAK	203-208	TOTAL STATE	97.59		AENA 	PENV BPV1	710-727	057-074
PHEMA INBIB	288-303	PENY GIVES		003.010	NI A	PENV BINGE	707-724	054-071
PHEMA INBID	280-314	FENV BIVMK	7.00	210	PENV	PENV BIVMS	766-783	
PHEMA INBLE	302-317	PENY BIVML	101.104	/10:100	AN SE	PENV BIVAK	765-762	
PHEMA INBMD	202-307	PENV BIV84	229-009		ZNEG	DENV ANA!	764.781	
PHEMA INBINE	200-311	PENV BIVEP	610-626		ANSO	DENY ANA	760.788	
PURMA BURNA	288-303	PHEMA COVO	36-62			2000	705 444	
PURMA TABOR	301-318	PHEMA CVBLY	391-400		PEN	PENV BIVEY	00/-0//	
יייייייייייייייייייייייייייייייייייייי	201.318	PHEMA CVBM	391-406		AENA AENA	PENV BMHVM	F00-0F0	
LUCKY HOO!	404.414	PHEMA CVBO	301-406		SEA.	PENV BM3AV	42-DB	
PHEMA INDEA	212.30	PARTA CAGO	391-408		786	PHEMA COVO	30-53	200-217
PHEMA NEUB	ang and	BUTTON COMME	402.417		PAER	PHEMA CVBLY	301-408	
PHEMA INBVI	730-311	COMPANIE COMPANIE	817.07	-	73FE	PHEMA CYBM	391-408	
PHEMA INSVI	303-318	THEMA LYMS						
				_				_

44 AMILTORA	977.00		PUFMA IABAN	1221-237		PHEMA CYNOC		-	
PHEMA MUMPIN	200		PHEMA IABUD	234.250		PHEMA IAAIC			
AA MUMPH	201.00		TALL THE PARTY	274.980		PHEMA LABAN	N 306-323		
PHEMA MUMPS	133-148		LUCHA MACA	21.91		PHEMA IABUD	320-337		
PHEMA FISHW	345-350		PREMA MCAG			DUENA 14CKA			
PHEMA PIZH	95-60		PHEMA MCKV	230-240	+	Carry version	Ī		
PHEMA FIZHT	68-90		PHEMA IADA1	234-280		CACAL ALICANA	Ī	-	
IA RINDK	366-383		PHEMA IADAS	237-263		CHICK CHICK	T	+	
PHEMA BV6	7.04		PHEMA IADCZ	134.260		PHEMA IACK	T		
PHEMA BVBCM	7.04		PHEMA IADHI	221-237		PHEMA MCKS	1		
PUTILIA AVECE	7.04		PHEMA IADH2	1221-237		PHEMA LACKY			
BUELLA BURLU	7.04		PHEMA IADHS	221-237		PHEMA IADA1			
5040	13.63		PHEMA IABMA	221.237		PHEMA MOAS			
PVENV DHVII	100		PULLIA INDIA	991.997		PHEMA IADCZ	2 320-337		
PVFP7 CAPVK	5					PHEMA IADHI	1 306-323	-	
N VACCO	72-67		PREMA IAUGO	700.00		PHEMA IADH2		-	
PVG01 BPP22	242-257		PKEMIA IAUM	757.175	 	CHOM AMBUS		-	
PVG01 HSVES	169-164		PHEMA IADM2	237-283		TOTAL VENEZUE	T	+	
PVG01 MSVI1	210-226	317-332	PHEMA IADNZ	234-260		THE AND A PARTY	T		
PVOOR RPTA	184.199		PHEMA LAENO	221-237		PHEMA IADHO			
BAJONS BOTA	ARE DOD		PHEMA IAEN7	1237-253		PHEMA MDH7			
1			PURMA IAEDS	230.248		PHEMA IADM2	2 322-339		
LAGOR MENT	10136		S CHARLES	246 AEA		PHEMA IADNZ	7 320-337		
PVOTO BPPH2	183-106		PHEMA WHAL	430.207		PURITALISM	Ī	-	
PVG10 BPPZA	163-190		PHEMA LAHAN	230-201		District Account	Ī		
PVQ10 H8V8A	109-124		MEMA WHEN	230-240		NICE OF THE PARTY	Ī		
PVOIG BPP1	81-88		PHEMA LAHC7	230-248		MEMA MEN	1	+	
PVOTA APT4	468-483		PHEMA IAHCO	230-248		PHEMA LAFFE	1	1	
DVANK BETA	07.112		PHEMA LAHDE	230-248		PHEMA IAGRE			
20,010	36.46		PURMA IAHRO	236-262		PHEMA_MOUZ			
PVUZN MBVII	200		PUELLA JAHKA	236-252		PHEMA MOUA			
rvd30 Brrno			BUENT TAUE?	938-989		PHEMA WHAL	1 321-338		
PVG16 BPOX2	/c-zz		TAKE AND A	876.016		PHEMA IAHCO	316-332	-	
FV036 HBV8A	£21-901		ביינייי ייינייי	976-048		PHEMA 1AHC7	·		
PV037 BPT2	1263-1268		PHEMA IANEO	200 460		PHEMA IAHCD			
PV037 HBVII	264-289		PARMA LANGE	200		SHEWA LANDE			
PV056 MBVII	72.37	143.100	בשנישי ושונים	430 462		CENT THE		-	
PV050 HBVII	268-283		PHEMA IANHO	230-202		WALLA LAURA	Ţ		
SO MBVII	102-117		PHEMA IANDA	730-507	1	CAMP ASSESSED		+	
PVG59 HSVII	267-282		PHEMA IAHBP	230-240		AND ARBUT	Ī	+	
PV066 HBVII	618-633		PHEMA IAHBW	230-248		THEM AND			
TVOS SPPH2	234-240		PHEMA IAHTE	230-282		PREMA JAHLO		+	
PVGB BPPZA	234-240		PHEMA IAHTO	236-252		PHEMA WHIMI		+	
PVIG BPVIR	87.72		PHENIA IAHUR	236-252		PHEMA JAHNM	Ī		
Anda sonx	234-240		PHEMA IAKIE	238-261		PHEMA JAHNN			
2010 CVB	284.270		PHEMA IALEN	236-251		PHEMA IAHPR			
	284.970		PHEMA IAMAA	233-240		PHEMA_LAHRO			-
אמוק כאפות	20.00		PUTINA IAMAR	239-264		PHEMA LANGA	A 321-338	_	-
אפול כאפוא	202-202		CHECK CHICA			SHIPS AUTO		-	
PVOL2 CYRM	264-278		PHEMA IAMAO	23/-203		WESTA AMENA	Ī	-	
EVOL2 CVBO	264-279		PHEMA IAMET	23/-283		THE PERSON NAMED IN COLUMN			

Color Philika Jumes 221-237 Philips Jumes													-						380.387																								-			-
PHEMA IAME 221-237 231-247 231-247 231-259 231-250 2	321-338	321-330	317-334	310-336	324-341	322-338	322-339	322-339	306-323	316-333	322-339	320-337	206.329	200.20	130.117	121.138	316.332	120.117	T	T	25.000	300 300	200-200	200-263	322.77	011.01	101.118	011.01		200	0.110	93-110	03-110	03-110	03-110	03-110	36-63	466-503	111-120	111-129	111-128	111:128	111-128	111-128		1111-128
O	PHEMA JAHTO	PHEMA LAMUR	PHEMA IAJAP	PHEMA IAMAA	PHEMA IAMAB	PHEMA JAMAO	PHEMA LAME!	PHEMA IAMEZ	PHEMA LAMED	PHEMA IAMIN	PURMA IANTO	PUEMA IAPIL	Margaret 18 Or 13	WHEMA MADO	WIELD SEED	PHEMA INDEA	CALETA MATA	MALE INTERN	MINISTER IN THE	PARTY PARTY	PHEMA LAVIV	PHEMA IACO	PAEMA JACHA	PHEMA IAZKIS	PHEMA WZUK	PHEMA MUMPM	PHEMA MUMPR	PHEMA MUMPS	PHEMA NOVA	PHEMA NOVO	PREMA NOVO	PARMA NOVI	PHEMA NOVM	PHEMA NOVO	PHEMA NOVTO	PHEMA NOVU	PHEMA PHODV	PHEMA PITHW	PHEMA PIDB	PHEMA PISH4	PHEMA PISHA	PHEMA PISHT	PHEMA PICKU	PHEMA PISHV		PHEMA NOWW
O																								-																						_
PHEMA IAME 121-237		231-247																					296-310	303:318	203-308	301.316	286-301	200-311	283-308	200-303	200-314	302-317	284-307	100.30	301.316	301-318	208.313	294-309	208-311	303-318	286.301					
	Г	Γ		221-237	234-250	234-260	234-250	230-248	226.381	107.057	234-280	233.249	230-248	220-246	237.263	238-261	238-264	236-251	237-263	221-237	221-237			123-130	110-132		П	119-136	116-132	108-124	120-138	123-130	27.128	261-011	100-14	123-139	119.138	116-137	116-132	123-139	108-124	133-148	133-148	173-148		715.300
	PHEMA IAMES	PHEMA IAMIN	PUFMA IANTO	PHEMA IAOU?	PUFMA IARUD	PHEMA 148E2	DUELLA (ARM?	AUCUA IARTA	TIEM IN NSME	PARKA MENA	PHEMA MOUN	OUTENA MIRE	PARTY PROPERTY	CUELLA BURY	SUPERIA INRVE	PUFUA NEVE	PURITY MISMEN	OUBLIA MIMBS	Principle Antiques	PREMA MUMP	LOUISING SHOUND																									
	467	Τ	T		100.	0101	200		-1070		718	216	087	460	442	103	•	•	280	280	280	260	280	280	280		202	916	758	616	910	441	442	440	636	300	202	Car	300	980	300		,		9	
	e de la constant		PVOL2 CVPPU	PVOLZ CVPHB	PVOLZ CVPRIN	PVGLZ IBVG	PVGLZ IBVE	PVOL2 IBVD2	PVGL2 IBVX	PVOL2 IBVM	PVGLE HSVBA	PVGLS PRVIP	BVOLC HRVBC	PVOIC HSVE4	PVOLC HEVE	PVOLC PRVIE	PVOLD HEV!	PVOID HBV2	PVOLF BRBVA	DVOI P RRAVC	200	W/01 8 1040	AVAIL DAY	1000	2000		PVOLP MUMPS	TANK TO TO	E STORE	BYOLK SECTION	BOOK WILLIAM	PVOLY LABBO	PVOLY	PVOLY MOPEI	PVM3 REOVD	PVMSA HPBOS	PVMSA HPBVO	PVMSA WHV1	PVMBA WHV69	PVM8A WHY	PVMBA WHVB	PVM9A WHV8	PVMBA WHWWB	PVMT2 IAMN	:	PVMT2 IABAN

PVMT2 IALES	26-40	PREMA TIBE					Secretary Divis	84-101	
PVMT2 IALE2	28-40	PHEMA PIOH4	324.340	į			LINEWA BYO		
OVUT2 IAMAN	26.40	PHEMA PISHA	324-340				PHEMA BV6CM	101-101	
AVEATS LABINE	28.40	PHEMA PISHT	324-340				PHEMA BV6CF	84-101	
DVIVE INDIN	35.40	PHEMA PISHU	324-340				PHEMA BV6LN	84-101	
MINE TANK	36.40	PREMA PISHV	324-340				PVF06 VACCC	1280-297	
District Land	35.40	WHENA PISHW	324-340				PVFOS VACCP	280-207	
1000		XHEID WHEN	324-340				PVF08 VACCV	281.208	
PVMIN MITAVE	1	PUFLA BINDK	366-383				PVF08 VACCC	176-103	
		BUSIN SUR	7.64				PVF09 VACCV	176-193	
		BUELLA BUTCH	7.84			_	PV027 H8V9A	200-226	
	†	PARTY BOOM	7.04				PVG28 HBVI1	173-180	
	+	TOTAL PARTY	7.04				PVG39 HBVI1	646-668	
	†	TAKENA OVOICE	49.87				PVG43 HBVII	109-128	621-638
	†	BAREN RAN	26.4				PVG67_H8VI1	171-168	
	1	Contract Court	RR-104				PV072 HBVI1	1252-1289	
	1	TALLES COME	20, 98				PVQF! IBVB	3073-3090	
		LALLY COLAR	10.01				FVGL2 (BV6	1084-1111	
		PVFUS VACCO	/0-7/				PVQLB H8VE!	736-763	
		PVGOI MBVEB	100	413.93			PVGLB HEVEA	675-692	
		INSH IODA	200,200	317.738			BVAIR LIBVEA	736.783	
		PVG08 H8VII	134-146				EVOLS URVER	734.783	
		PVG10 HBV8A	109-124				MANOT BIOLOGIC	71A.7K1	
		PV011 H8VII	103-110				PVOLD MOVEL	K97.414	
		PVGL2 HBVII	270-288				TVOKE ILIVO	760.600	
		PVG1 BPV1R	70-02				PVGLB ILIVB	100,100	
		PVG28 HBVII	20-35				PVGLG INTVI		
		PVGBB BPOX2	22-37				PVGLC PRVIP	100	
		PV036 HBV8A	108-123				LVULB VEVU	004:804	
		PVG37 HBVII	284-288				PVOLF SV5	401.418	
		FVG41 H6VII	244-280				PVOLH HCMVA	366-382	
		PV048 HBVII	1244-1280				PVOLH HCMVT	364.381	
		PVOSS MEVI	22.37	143-168			PYGUH HBV11	245-202	803-820
		PACKS LAVI	288-283			L	PVOLH HSV1E	248-262	803-820
	†	TACK DESCRIPTION	101.117				PVOLI HBV11	43-60	
		ABORD MACAN	130-146	330.346			PVOLM BUNL7	81.08	
	1	בייהים השינים	287.582				PVOLM BUNBH	81-08	
		PANORE UBVIT	369.378	618.633			PVGLM PUUMH	712-720	
	1	ABOUT STORY	80.108				PVGLM PUUMB	712-728	1
	1	COARD SONS	234.340				PVGLM RVFV	344-301	
	1	4 CORD BOX 1	374.340				PVOLM RVFVZ	344-361	
		Carrie Day	100				PVOLY LASSO	12-04	
		WI A 40 BOA	30100				PVOLY LABBJ	12.04	
		LAGLI (BAB	2012		300		AVEN VINE	19.01	
Ļ		PVGL2 CVBF	123-138	174-180	204-279		PYGLY LYCVA	17.0	
		PV012 CVB19	123-139	174-180	204-279		PVOLY LYCVW	12:04	
-		אונאס בופאא	123-130	174-180	264-270		PVOLY MOPEI	12.94	
		PVOL2 CVBM	123-139	174-180	264-279		PVM1 REOVD	280-207	
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101.2				147.184	147-164	147-104	147.164	11.04	186-202	188.302	13.76		•	174.10	174-101	1-04	174-101	185-202	185-202	11:04	134.101					7,02	79.9	200	3	78-42	28:42	26-42	26-42	28-42	7.2	79.42	1	\downarrow	4	1	1	1	1	-	4	1	1	-
WHAT MEAN	LAMA MENA	PVMP CAMVG	PVMP CAMVO	PVMP CAMVE	PVMP CAMVN	PVMP CAMVS	PVMP CAMVW	DVAGA MPRVO	DVAGEA MERV?	TARREST TOWN	TANGE TOTAL	PVM6A HFBVA	PVM8A HPBVD	PVMBA HPBVJ	PVMSA HPBVL	PVM8A HPBVN	PVMSA HPBVO	PULLEA MPRVP	PANA MPRAR	SALARA MODUE	WALE A LIBERAL	LANGE STORY	PVM3A MPBV	PVM8A MPBVZ	PVMT2 IAANN	PVMT2 IABAN	PVMT2 IAFOW	PVMT2 IAFPR	PVMT2 IAFPW	PVMT2 IALE1	PVMT2 IALE2	PVMT2 IAMAN	PVMT2 IAPUE	PVMT2 (ABIN	PVMT2 IAUDO	PVMT2 IAWIL									-			
					1272-1288																																											
264-278				1274-1200	70A.814	1050-1088	000.000	2001-2001																																						٠		
174-180	1287-1283	1216-1231	1126-1142	810.818	2000	200	0/0-07	740-070	1277-1203																			266-280	265-280	266.280		265.280	265-280	265.280	266-280						276-292						_	101,101
123-130	111-90	08-111			105240	80	216-233	215-233	803-818	1066-1071	1056-1070	1066-1071	1086-1070	1085-1070	201		202-218	622-638	475-490	444-469	427-442	448-461	160-166	150-160	79-94	79-84	3.04	308-321	206-223	20E 936	108.414	208.921	206-221	208-221	205-221	286-302	289-306	288-302	276-202	276-292	6-04	273-289	273-280	273-288	273-289	273-280	273-289	200
PVOL2 CVBV	INVOIS CVM4	PVOL9 CVMAR	2000	TVBLZ CVMVII	PVGL2 CVPFB	FVGLZ CVPTU	PVOL2 CVPRB	PVOL2 CVPRN	PVGL2 FIPV	PVGL2 IBV6	PVOL2 ISVB	INVAL 9 IRVD2	200 a 100 to	בינוני פינוני	FVGLZ IBVM	PVOLB HBV5A	PVGLB PRVIP	PVOLB VZVD	IPVOLC HISVBC	PVOLC HIVE	PVOIC HOVE	PVGLC PRVIF	PVGIC VZVD	PYOLC VZV8	PVALD MBV11	EVOID MAY	STATE SEVE	A 101 B BB0VA	CARDO STOAL	TVOCT BASE	PVG P BROVE	CAST STORY	AVEUE LEVEL	Naga a rock	SVO S MERVE	PVOLP MEASE	PVOLD MEAS!	PVOLP MEABY	PYOLE LINIMPIA	BYCIE LAIMBR	PVOLE MUMPS	DVALE NOVA	BYON BIDYS	NACE BY NAVA	PVOI B NOVE	PVGI P NDVTG	1000	מאמע אמא
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		_	3	1 900-015	9	2			9		901-916	900.016	~		426-441	427.442			426.440		210		0 -				9	7	132-148	4	4	•	4	4			2	~	9					-			-
262-288	282-298	176-191	278-203	356-371	499-515	400-615	499-615	743.768	609-625	609-625	356-371	356-371	826-642	869-985	12.84	12-04	12.84	12.04	12.84	12.84	1031.1017	621.63	20.170)?:\A	135-161	135-151	189-205	188-205	11-96	119-134	110-134	118-134	110-134	110-134	1118-134	116-131	380-396	187-202	1376-303	383-388	383-308	383-388	363-398	1		26-40	5
PVQUE RINDX	PVOLF RINDS	PYGL! TRTY	באפרו אבאם	PVOLM HANTB	PYDLM HANTH	PVOLM HANTL	PVQLM HANTV	VOTA PTPV	PVOLM PULMY	PVOLM PUUMS	PVGLM SEOUR	PVGLM BEOUS	PVOLM UUK	PVOLP BEV	PVOLY LABSO	PVOLY LASS.	PVOLY LYCVA	PVALY LYCVW	PVOLY MOPE	VOA! V PIABV	Mineral County	AE S ESTA	PVM3 HEOVU	PVMAT MUMPS	PVMAT NOVA	PVMAT NDV8	PVMAT PIZHT	PVMAT BV41	PVMAT 6VB	PVMP CAMVC	PVMP CAMVD	PVMP CAMVE	PVMP CAMVN	PVMP CAMVS	PVMP CAMVW	PVMP, FMVD	PVMBA HPBQ9	FVMSA HPBV9	PVM9A WHV!	PVMSA WHV50	PVM9A WHV7	PVMBA WHVB	PVM9A WHV8	PVM8A WHVW6	PVMT2 IAANN	PVMT2 IABAN	
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28-40	25-40	ş	6-40	25-40	26-40	26-40	26-40	26-40	226-241		-			1	1	†							1	1	1	+			1														1	1
	PVMT2 IAFPW			7			•						+	1		1																												
PVMT	PVMT2	PVMT	NA.	PVMT	PVM7	PVKT	PVAT	PVMT	DVACT.		1	1	-	-	-	-		L		-	1	1	-			-	-	1			1	1	1	1			4	-			-	-		;
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TABLE XI

Search Results Summary for P3CTLZIP, P4CTLZIP, P5CTLZIP, and P6CTLZIP Motifs

			A LANCE GAR									
Poch2IP			14010			LIBRARY FILE			LIBRARY FILE			
LIBRARY FILE			LIGHTHY FILE	100		PENVI FREEV	380-400		PENV BIVOS	47.69	626.840	
PENV BIV27	147.166		PENVI PASTV	2000		DENY FREEV	380-400		PENV BIV27	47.68	147.168	564.575
PENV CAEVC	810-928		PENV AVIBU			DENV RAFVM	170-190		PENV FENVI	225-248	630-061	
PENV CAEVO	808-828		PENV BIVZ/	147.100		DENY RIVER	781.801		PENV PLVCB	624-645		
PENV HV286	760-768		PENV HOLKH	723-122		SENT FIVED	270.700		PENV FLVOL	447-488	806-828	
PENV HV2D1	741.760		PENV HV2D2	9.78		DENY FIVE	780-000		PENV FLVL®	467-488	625-646	
PENV HV201	741.769		PENV HV258			BENY ELVAL	0.30		PENV FLVSA	444-405	602-623	
PENV HV2NZ	742.760		PENV JSRV	541.660		BENY EDAMY	266-276	924.044	PENV FOAMV	163-174	867.078	
PENV HV2RO	761.769		PENV RSVP	293.662		ACTIVITIES TO SELECT	9.30		PENV PSVOA	467.489	626.846	
PENV HV25B	1743-761		PHEMA VACCC	173-102		PENV PSVGA	97.007		BEND SEVOR	447.460	806-626	
PENV HV2BT	746.703		PHEMA VACCI	173-182		PENV HVICE	000000		DENIV RRVALL	480.471	808.828	
VAL VARA	376-304		PHEMA VACCT	173-102		PENV HV2CA	2//00/		SELV REVET	467.488		
SURLIA BIOM	118-136		PHEMA VACCV	173-192		PENV MINFO	078-00		7100	E 9 7 9	610.640	
PUENA DISMT	118.128		PVENV BEV	62.61		PENV MMTVB	643.663		YENV UALV	11000		
ביינים ביינים			PVENV MCVI	61.80		PENV MMTVO	643-663		PENV MVZBE			•
PHEMA BV4:			DVENV MCV2	91.80		PENV OMVVS	76.86		PENV HV201	741.702	1	
PVENV THOUS			BATELLE ABENT	28.48		PENV RSVP	42.02		PENV HV2NZ	742-763		
PV018 8PP22	101-101		STATE OF THE PERSON AND THE PERSON A	1.00.188		PENV BFVI	024.044		PENV HV2RO	761-772		
PV024 BPT4	116-133		2300	336 308		PENV SFV3L	821-841		PENV HV26T	745-766		
PVG36 HBVBA	344-362		באמסו אשכרר	2000		DENV SIVIN	766.786		PENV MCFF	600-621		
PV040 HSVII	14-32		PVG01 VACCV	210.27		BEAV BIVING	366.786		PENV MCFF3	601-622		
PVGSO HSV8A	10.9		PVGOI VARV	375-385		TEND AND	364.384		PENV MIVAV	630-661	_	
PVOR1 RPT4	63-91		PVG08 BPT4	027.046		PENV BIVML			BON MINO	675.846		
PVAR HRVI	84-102		PYOTO HEVIT	36.64		PENV BIVES	201.401		DEUV MIVER	430.600		
SVOAE LEVIS	166.173		PVQ11 H9V11	103-122	160-189	PENV SIVSP	113/83		PENY MUNT	930.00	-	
1000 HOLD	1788.280A	3374-3382	PVOI BPPH2	31-60		PHEMA COVO	403-513		FENV MLVF	200.000	 	
DAG LADA	1007		PVOI BPVIR	859-678		PHEMA CVBLY	391-411		PENV MLVP	000-000	-	
PVGL2 CVR24	100		PV020 BPT4	231-260		PHEMA CVBM	301.41		PENV MLVHO	040-04		
PVGLZ 18V6	1000		PVG32 V2VD	90-109		PHEMA CVBO	301-411		PENV MLVKI	10/-100		
PVGL2 IBVB	1000-100		BVA1A RPK3	132-161		PHEMA CVHOC	391-411		PENV MLVMO	629.620		
PVGL 2 IBVD2	10001		BV013 RPT2	18.38	820.848	PHEMA CVMAB	402-422		PENV MLVRD	824-646		
PVGL2 IBVK	1000-100		BV012 GP14	10.38	625.844	PHEMA IACKO	81-101		PENV MLVRK	824.645	\downarrow	
PVOL2 IBVM	1000-10/3	.0.	PV048 L9V	1038-1057		PHEMA IADMA	91.101		PENV MSVFB	170-101		
PVOLG HSV81	9009	1	1041 MEVIL	A2.81		PHEMA MUMPM	397-417		PENV RMCFV	903-954		
PVOLE HEVBC	682.710		1300 TAUNO	380-388		PHEMA MUMPA	397-417		PENV BEV1	067.078		
PVQLB HSV9A	584.602		avea uppet	117.386		PHEMA MUMPS	397-417		PENV BFV3L	167-178	054-076	
PVOLB ILTVB	740-756		1767 03076	142.181		PHEMA PHODV	403-613		PENV BIVAS	437-469	_	
PVOLE ILTYS	760-788		TARE ASSAULT	117.136		PHEMA PINKW	322-342		PENV BIVAG	442-483		
PVOLD ILTY	760-768		LAGU LODAL	200.000	1073.1081	PHEMA PIZH	13.33		PENV BIVAL	421-442		
PVOLC VZVD	431-440		PVGB/ HSVII	10000	3100 3133	PUEMA PIZHT	13.33		PERV BIVAT	435-466		
PVGLC VZV8	431-449		PVGF1 IBVB	1687-1606	4100.2167	SUSTAIN DIND!	407.817		PERV BMSAV	42.63		
PVQLF PISH4	2.04		PVOL2 CVBF	0101-1010		DURMA CENTR	122.342		PHEMA CVMAB	402-423		_
PVGLM MSV60	314-332		PVOL2 CVBLG	0101-1010		BUENA BENDE	322.342		PHEMA IADE1	200-287		
PVOLH HBVE4	614-632		PVOLZ CVBLY	001:1010		TOWNS SERVICE	133.343		PHEMA MUMPH	225.246		
BVOIN HEVER	807-826		PVOL2 CVBM	991-1010		TOTAL BENDE	440		BUTTA LIMBO	228.246	-	
BUGH 144V11	5.04		PVOL2 CVBG	001-1010		PHEMA SENDS	346.346		PHEMA LAUMPA	228-248		
VALUE ALVOVA	678-696		PVGL2 CVBV	991-1010		PHEMA BENDA	7,4,4	140.00	+-	913.234	-	
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		370-60	378-400	379-400	379.400																																												463-474
		7.28	7.28	7.20	7.28	169-160	589-610	314-336	96.00	167.178	369.300	4E.10A	100.100	0/11:011	102-502	30-61	238-269	1866-1877	167-178	1269-1280	1250-1280	1269-1200	1260-1280	1250.1270	200	1200-1400	1317-1338	1265-1288	1176-1197	83.104	82-103	62-103	83-104	136-166	446-467	338-367	224-245	227-248	224-246	440-407	446-487	448-467	308.328	AEA 4731	177	460-471	450-471	450-471	405-426
The state of the s	PHEMA PIZHT	PHEMA BVB	PHEMA BV6CM	PHEMA BV6CP	PHEMA BV6LN	PVG01 HSVEB	PVG01 HBVII	PVG25 HSVII	PVG17 BPOX2	LIVER CACVE	PACE LOVIE	ANORE HEVER	COACH COOL	PVGSG HBVII	PVGEB HSVBA	PVGBO HSVII	PVG63 HSVI1	PVGFI IBVB	PVGH3 HCMVA	PVOL2 CVBF	PVGL2 CVBL0	PVGL2 CVBLY	DVG12 CVBM	08/3 610/4	אפרל האפת	PVQL2 CVBV	PVDL2 CVM4	PVOL2 CVMAS	PVOL2 CVMJH	PVOLD HBV11	PVOLB HGV1F	PVOLE HEVIK	PVGLB HBV1P	PVGLB MCMVS	PVOLC PRVIF	PVOLF COVO	PVOLF MEABE	PVOLF MEAB!	PVOLF MEABY	PVOLF MUMPM	PVOLE MUMPR	PUBLIC LAUMES	VOCHS SIGNS	Val. 7 514110	PVOLF FIIMC	PVOCE PIZH	PVOLF PIZHO	PVOLF PIZHT	PVOLP PISB
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366-378	296-318	237-267	200-318	31.61	11.61	26.45	161.171	300 320	T	T	25.07	007-077	11/13/	124-144	328-348	327-347	328-348	328-348	327-347	Γ	Γ	732.782	250.270	2000	761-771	79.00	79.09	98.86	72.02	279-209	63.63	738-768	263-303	164-474	464-474	464-474	464.474	464-474	670-680	1328-1348	1125.1346	4100		101-101	1000-1020	1001-1021	1001-1021	1156-1170	1000-1000
PVENV THOOV	PVGO1 VACCC	PVG01 VACCV	PUDDI VARV	DVOOR VACCC	VAAV AONO	OVOCO REPET	PVO19 MRVII	Non cone	1000	100 A 100 A	PVG61 H3VII	PVG63 MSVII	PVG66 HSVII	PV074 HSVSA	PVGL2 18V6	PVOL2 18VB	PVGL2 (BVD2			PVG12 IBVM	BVG1 9 IBVII2	200 E 000	AND THE PARTY A	VOLD HCMYA	PVGL8 HCMVT	PVGLB H9V23	PVGLB HBV2H	PVGLB HSV28	PVOLS HBV6U	PVOLD HSVB2	PVOLB HBVBA	PVOLE MCMV8	PVGLF PI3H4	PVOLO PABVE	PVGLG RABVH	PVOLO RABVP	PVGLO RABVS	PVGLG RABVT	PVOLH MCMV8	OVOI 14 BILLI 7	NEW BUILDING	TACKE BOTTON	A COLOR MAN	PVOLM MANTE	PVOLM HANTH	PVOLM HANTL	PVOLM HANTV	PVOLM RVPVZ	PARTIE SECTIO
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900:000	047.986	AKA. 877			Ī,	814-833	200	+	7	Ì			٦	706-725	707-726	117.130	256.276	266-285	266.28K	Ť	Ī		476-494	430-466	1372-301	44.63	278-297	117.136	162-171	007-1018	166-174	166-174	B30-849	830.640	AKK.A74	80.108	11185.1104	E31.840	121.180		001.00	7	174-183	174-193	171-100				
PVGL2 CVM4	PVOL2 CVMAS	M M A 10/4	LOW AS TO ALL	PVGL2 CVP/8	שאפון ב כאונות	PVGL2 CVPR8	PVGL2 CVPRM	אמול צואא	PVGL2 IBV6	PVGL 2 18VB	PVGL2 IBVD2	PVGL2 1BVK	PVGL2 IBVM	PVQ18 HCMVA	PVQ18 HCMVT	PVQLB MSV6U	BVALE II TVA	OVOI B IN TVE	2/4	1000	PVGIC NOVI	PVGIC HSVIK	PVBIC HSVBC	PV010 CHAV	PVDLO RABVH	PVOLI H9VEB	PVGLI VZVD	PVOLM BUNDE	AND IN PHA	VOTA M IOVA	WILLIAM PURINE	PVOLING PLINA	SVALLE BVEV	DVOI IN BVFV7	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	WO WAY A 10/18	AVOVE CELEV	0,000	מייים עביים	LAWE! CADM	PVME1 CVHZZ	PVME! CVPFB	PVME1 CVPPU	PVME1 CVPRM	PVME! CVTKE				
126-144	l																													-																		+	_
183-101		27.722	227-248	44-62	100-208	190-208	183-201	183-201	163-201	183.201	163.201	183-201	160.108																			1												_		-		-	
VAPEL	A NO.	VMI REOVO	PVM1 REOVE	PVMAT HRBVA	PVMAT NDVA	FVMAT NOVB	PVMP CAMVC	PVMP CAMVD	PVMP CAMVE	PVMP CAMVN	PVMP CAMVS	PVMP CAMVW	DVMP FMVD																																			+	

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	220-241	220-241	460-481	160-481	460-481	460-481	460-481	481.434		440-40/	991-712	680-711	304-326	297-318	066-670	2.23	2.23	107.218	180-211	160-211	103-214	217.25.0	926.00	20000	07.00	291-302	230-281	189-180	200-221	122-143	64-86	201-222	70-01	244-206	244-265	244-205	233-264	70-01	233-264	233.284	233-264	70-01	233-264	244-208 1	244-205	70-91"	233-264	233.284
AUGUL LIBAL	PVGLF RINDK	PVOLF RINDL	PVOLF BENDS	PVQUE SENDE	PVOLF SENDH	PVOLF SENDJ	PVGLF BENDZ	9770	PVOLT BYA	PVGIF EVE	PVOLH HCMVA	PVOLH HCMVT	PVOLH HBVE4	PVGLH HBVE®	PVOLH HBVSA	PVQLI HBV2	PVQU HBV23	PVOLM BUNGE	PVQLM BUNL7	PVOLM BUNSH	WANTE MINA	Daniel Contract	2000 2000	WOLY LABOU	PVQFB EBV	PVMOI VACCC	PVMO! VACCV	PVMAT HRBVA	PVMAT RINDK	PVMAT TRTV	PVM81 CVHOC	PVM0A HPBD8	PVMBA MPBVO	PVM9A HPBV2	PVM8A HPBV4	PVM8A HPBV8	PVM8A HPBVA	PVM8A MPBVD	PVMSA HPBVI	LVBAH ARMV4	PVM6A HPOVL	PVM8A MPBVN	PVMSA HPBVO	PVM8A HPBVP	PVM8A HPBVR	PVMOA HPBVB	PVMBA HPBVW	WINDS ANDROV
900-101	925-945	12-52	12-32	12.32	141.161	310,330	300.130	200.768	308-328	308-328	312-332	312-332	308-328	300-328	74.04	70.7	34.04	74.04	901.991	300.330	410.000	263-313	722.102	212-232	212-232	212-232	212-232	63-63																-	 - -			
PVOLM BEOUS	PVGLM UUK	PVGLY LYCVA	PVOLY LYCVW	DVOIV PIABV	VINE COUNTY	Distant Latitude	PVMAI MUMES	PVMAT NOVA	PVMAT NDVB	PVMAT PIZHT	PVNIAT PIEMA	PVMAT PIAHB	DVIDAT AVEL	BULLAY BUR	DVALET INVA	P. (1) (1) (1) (1) (1) (1) (1) (1) (1) (1)	PVME TOVO	PVME I DVDA	PANEL INCH	PVM3A HPBDS	PVMSA NPOUP	PVMSA HPEME	PVM8A WHV!	PVMSA WHV60	PVMBA WAV7	PVM9A WHV8	PUMBA WHVBI	PVMSA WHVW6																				
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WO 96/19495 PCT/US95/16733

TABLE XII

Search Results Summary for P7CTLZIP, P8CTLZIP, and P9CTLZIP Motifs

202-224 409-616 409-616 603-626 409-616 603-626 609-627 609	176-103 176-103 176-103 1776-1	1187ATY FILE PENN BLVAE PENN BLVAE PENN BLVAE PENN BLVAE PENN BLVAE PENN BLVAE PENN BLVAE PENN BLVAE PENN BLVAE PENN BLVAE PENN BLVAE PENN BLVAE PENN FLVBE PENN FLVBE PHEMA CVBC PHEMA CVBC PHEMA INCEN	303-327 303-327 303-327 303-327 303-327 303-327 303-327 303-327 303-327 303-416 430-464 430-464 430-463 430-463 430-463 430-463 430-463 430-463 430-463 430-464	
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496-520 489-511 123-146 487-518 506-527 506-527 506-527 506-527 506-527 506-527 506-527 506-527 506-527 506-527 51-43 51-43 51-43 51-43 51-43 51-43 51-43 51-43 51-43 51-43 51-43 51-43 51-43 51-43 51-43 51-43 51-43 51-43 51-56 51		PHEMA INCEN PHEMA INCAT	430-454 430-453 42-453 420-453 420-453 420-453 420-453 420-453	
469-611 123-146 406-617 489-620 489-620 213-236 213-236 21-43 21-56 21-56 21-56 21-56 21-56 21-56 21-56		PHEMA INCOL PHEMA INCHY	420-453 423-453 423-453 420-453 420-453 430-454	
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219-22/ 219-236 219-236 219-236 219-236 21-43 21		PHEMA NCM PHEMA NCPA PHEMA NCP1	429-453	
219-236 219-236 219-236 219-236 21-43 21-4		PHEMA INCNA PHEMA INCP1 PHEMA INCP2	420-453	
21.526 21.525 21.525 21.526 21.43 21		PHEMA INCPI	430-454	
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27-69 21-43 21-43 21-43 21-43 21-43 21-60 27-60 27-60 37-60		PHEMA INC.	430.484	
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21-43 37-60 27-60 37-60 37-60 37-60	VBF 10-33	PVENV BEV	62.66	
27.60 28.60 37.69 21.43	VBL9 651-674	PVF06 VACCC	280-304	
28-60 17-69 21-69		PVF08 VACCP	280-304	
27-59 27-43 37-50	VM4 1267-1290	PVF08 VACCV	281-305	
21-43	VMA6 1215-1238	PVF09 VACCC	176-200	
37.60		PVF09 VACCV	176-200	
20.76	Ī	PV001 V2VD	20-03	
ĺ		PVQ10 H6V6A	365-370	
20.75		PVQ12 HBV8A	69.02	
		FUGIO HEVIT	00-112	
		PV018 HSVII	173-107	
75-17	Ī	PV043 HBVII	108-133	
17.00		IVORY HEVIS	108-132 1006-1028	528
21.43	Ī	PVG72 HBVII	720-744	
33-56			3001-3828	

PHEMA LAX31 37-88 PHEMA LAX20 37-69 PHEMA LAXH2 21-43							_
	-	FVGL2 IBVM	912-501	PVOLB ILTVO	1	1	
		PVAL 2 IBVUI	175-201	PVOLB ILTVB			+
		1 P. O. P. C. P. P. C. P. C. P. P. C. P.					
		PVOLE IBVOS	178.301	PVGLE H9V!	1 413.437		
1		COAR PRO		PVOLE VZVO	469-483		
PHEMA IAZUK 37-69		TVELS TOWN	KARKO	PVQLF SV6	401-428		
		MANUEL COURT	48.508	PVOLH HCMVA	VA 874-588		
		STORE WORLD	600-600	PVOLH HCMVT		7	+
		TARES BANK	443.480	PVGLH H6V11	11 443-487		
٦		2000 2000	703.400	PVOLM HSV1E	16 443-467	603.627	1
PVPUS VACCE 72:04		PVOLC HSVIR		PVGLM BUNL?	17 31.66		
		MOLC HEVZ	005-07-0	KENDY TIONS	Γ		
		PVGIC HSV23	430-40	MAN TIONS			
		PVOLM BUNLY		Cave is love			
PVGO4 VACCC 11:33		PVOLM BUNSH	139/-1410	SVEVE IN RVEVE			
PVGO4 VARV 11-33		אסוא חחצ	383.008	2011 14 10/10	Ī		
PV018 H8VII 88-110		PVOLY JUNIN	2.20		,		
		PVGLY LABBO	12.36	LAGNA CT	T		
		PVOLY LABSU	12.35	PVGP2 EBV			
		PVOLY LYCVA	12.36	PVGP3 EBV			
		WCVI VION	12.36	PVM1 REOVD			
		10000	19.36	PVM1 REDVI		,	1
PVG58 HBV6A 256-255		TOTAL MONEY	100	PVM21 REOVD	VD 108-192	2	
٥		מוני מינית	¥ C.	PVM22 REOVO		2	1
PVGS 8FV4 42-64		בייניים בייניים		PVM2 REOVJ	109-192	2	
PV080 HSVII 63-78		אמרו ועראו	13.38	PVM2 REOVE	168-182	2	+
		PVGLY IACVI		PVMAT MEAS	481 87-111		
		PVDNM CPMV	T	ARALATY PUMAT BEPVB			
1056-1078		PVM1 AEOVD	1	7	Ī		
1058-1077		PVM1 REOVI	464477	PANTE CAMP			
		PVMAT MUMPS	227.250	A A A	T		
Ī		PVMSA MPBOB	280-282	PVME1 CV IKE	T		
100 June 100 J		PVMBA HPBDC	268-201	PVMET IBVO	Ī		
		PYCHSA HPBDU	231-264	PVME1 IBVB	DO: 42		
T		PVM8A HPBDW	269-292	PVME1 IBVB2			-
TYDIO NEVOL		PVISA HPBHE	236-259	PVME! BVK			
		-		POMBA HPBB	1		
T				PVMBA WHVI	١	3	-
,				PVMSA WHV59		0	
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TALL BREVR 484-506				BVHA AMVA			
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014-636	807-628	186-180			427-440	426-447	657-670	884-876	11.450	414436	304-320	106-217	132-164	196-217	108-217	186-217	132-164	121-163	203.516																		
PYOLH HOVE			PVGU- BEV	PVOLY LABBO	l	l		İ	PVINI REOVO	l		PUMAT PINC	PVMAT PI2HT	PVMAT GENDF	PVMAT BENDH	PVMAT SENDZ	PVMAT 8V41	PVILST FRV	PAUD CEDY																	+	

WO 96/19495 PCT/US95/16733

TABLE XIII

SEARCH RESULTS SUMMARY FOR PI2LZIPC MOTIF

PCGENE	PLICTLY										
THE NAME	PROTEIN	VEUS			7	+					
PIME TRVSY	POTENTIAL 194 KD PROTEIN	TOBACCO RATTLE VIRUS (STRAIN CYM)		S	DRIA.	ARTAN	ABGAL	AMEA	4364.	A I V	1 1 1 2
PUBLIS VACCC	10ETA-HSD	VACCINIA VIBISE SETEMA CONTRIBUTION				ş 3	1011.1030	2	315.1400		
PIBIIS VACCV	TOETA-HSD	VACTIVIA VISITS AND WITH								İ	İ
PITHS VANY	UNI(A-1141)	VARIN A VIRIN		E		_					_
PATIL FOWPE	ANTIHITOMOIN III HOMOLOK	FOWEROW VINCES STATE OF A SECURE SEE	,		:		:	•		_	
PATH VACCV	4 KD A.TYPE INCLUSION PROTEIN	VACCINIA VIRUS ISTRAIN WAS		-		į					
PATTI VARV	DIKD A-1 YPE INCLUSION PROJEIN	VARIOLA VIRIIS		İ	-					İ	i
LYTIZ HSVII	7 7 5	CORPES SWORLEN CHANGE CONTROL IN THE COMPANY OF THE	101 011		į	-			!		
PATIS HISVIE	U. 46	HERPES SIMPLITY VIRITE IN THE LASHABILL				:					:
PATIS ISVED	ALPHA TRANS-INDUCINED ACTION 02 KID PROTEIN	CHINE IN ACT AND A COUNTY AND ADDRESS AND				-					-
VAID VACCC	PUTATIVE A.TYPE INCLUSION PROTEIN	VACCING VIEW COMMENDED	1			•	į				_
PATE VEW	ALPHA TRANS INDUCTING FACTOR 14 KD PROTEIN V	VARIORI A 2001 ED VISITA INTERNATIONAL DE LA CONTRACTORIO DE LA CONTRA	-		-	-			i		1
PA III) VACEV	PUTATIVE A. TYPE INCLUSION PRIDITIN	VALUE AND	2	13.13				į	1	:	!
PATH HAVE	ALPILA TRANS. INDIETING PROTEIN					-		:	į		:
PATER	ALPHA TRANS.INDIRCING PROTEIN	Control of the Contro	101	271.272			: i	:			
PATIN HSVER	Al Min Thank they willed be digital	COUNTY TOTAL STATE OF THE STATE	2			•					
	AT PAINT PRINT PRINT BE COME TO	COINE HEAVES VIRITY TO FILL (STRAIN ALLA)	174.14	!		:-		:	:	;	:
A CANON	A TOTAL PARTY AND A PARTY AND	AUCELLA-ZOSTER VIRIS (STRAIN DIINIAS)	201.230	_	:	į -		-	: 1 1		
200	STATE STATE OF STATE STA	COWPOX VIRIS	120.01	1.11.01	:	i		; !	: i	. 1	:
	DATE OF THE PERSON NAMED IN COLUMN NAMED IN CO	LACK BEET E VIPIS	15:53	_		1	:	1	:		
	IRAMSCRIPTIONAL REGULATORY PROJECT	GRESSIMPLEX VIRUS CIVET 47 ATP AIN CA	15	:		<u>-</u>	i			•	_
	DCRF I PROTEIN PRECURSOR	EPSTEIN BARR VIRUS (STRAIN 1195.1)	161		_	• :	:				_
78FL1 EBV	TRAMSCRIPTION ACTIVATOR BALL!	EPSTEIN BALL VIAILS (STRAIN NOS 3)			i	:		İ	-		_
PCAPH VACCC	CELL SUNFACE BROOKS PROTEIN	VACCINIA VILUS (STRAIN CONTINUACION)			: :	-				:	:
PCAIBI VACCV	CELL SUN ACE BINDING PLOTE IN	AACCINIA VIBILICACIDADO MAIL	P-11		-:	1			i	i	!
VEN VAIV	CELE SUM ACE. BINDING PROTEIN		2	_			İ		!!	:	:::::::::::::::::::::::::::::::::::::::
KOH KSVSA	COMPL CONTROL PROTEON INVESTIGATION		107		:	!	!	 - !		!	;
KELL KIVII	CELL SEIGNAL DE CAREND DE CAREN DE CAREN DE CAREN DE CAREN DE CAREN DE CAREN DE CAREND DE CAREN DE CAREN DE CAREN DE CAREN DE CAREN DE CAREN DE CAREND DE CAREN DE CAREN DE CAREN DE CAREN DE CAREN DE CAREN DE CAREND DE CAREN DE CAREN DE CAREN DE CAREN DE CAREN DE CAREN DE CAREND DE CAREN DE CAREN DE CAREN DE CAREN DE CAREN DE CAREN DE CAREND DE CAREN DE CAREN DE CAREN DE CAREN DE CAREN DE CAREND DE	SECTION SALISMENT OF THE SECTION OF	7		 		!	-	i		
MARIN ARROLL		LEFES SOUTH A VINCE TO THE ACCIDANCE AND	38 - 56	:	P6 100	-	ī 	!	:	:	1
100		CAPES SIMOLEN VIRUS (TYPE 1/ STEASIN KOS)	2	,	-	i		İ	-	-	1
	Ì	TAPES SINOLEX VINUS (TYPE 27 STRAIN 110-13)	2	1	100 100	Ì				!!	
	CELL FUSION PROTEIN PRECURSOR	IERPESVAUS TYPE I (STILAIN REMTUCEY A)	101.23	;	 -	Ī					
		VARICELLA-ZOSTER VIRUS (STRAIN BUNIAS)	746.346		!		Ì	Ī			
AND POST		HELVES VIRUS SALMINI (STRAIN !!)		216.347	!!!		j				
7	COAT PROTEDI VPI	SUDGESUGAR PLEDGLING DISEASE VIRIS	9		i	Ì		-			
٦		OLYOMAVILUS BK (STRAIN AS)	T	1	-	j					
ī	COAT PROTEIN VPI	POLYOMAVIRUS BK	Ī			İ					
		BOVINE FOLYOMA VIAUS	Ī.	ī	-	İ					
7	COAT MOTED VAL	HAMSTER FOIL YOUAN VIRUS			i	ĺ			-		
MOV AVIC		POLYDMAVINIS IC			-	İ					
_		YACHOTROPIC POLYGNIA VIRIUS		ī		j					
Ķ		MOUSE POLYOMAVIRUS ISTRAIN RITIGANI	Ī,		İ	j					
	13	SDGAN YRUS 40	ī			Ì				<u> </u>	İ
À VO	200	HERMOPROTEUS IENAX VIRIUS I ISTRAIN KRAIN		ī						<u>. </u>	!
_		BOVDVE POLYGALAVIBUS								:_ 	
200		LYNGHOTROPIC POLYDMA VIX US		j	-	j					
2000	COAT PROTEDIATE	MOUSE POLYCINA VIRUS (STRAIN 3)		Ī		j				<u> </u>	ļ !
30		PREJUDENOTEUS TENAX VINUS I (STRAIN KRAII)	270	Ī		İ					
NOV AND		ABUTTLON MOSAJC VIALIS (150LATE WEST INDIA)		İ							
POOT POOL	OR	BOOLARIA VIRUS			-						<u>.</u>
- NO.	PROTECN		Ī	1	-	j	1				İ
COAT CLYK	PEOTEIN	CASSAVA LAIENT VIRUS (SIIIAIN WEST KENYAN 114)			i			į	j		
- 1	FOIEN			-				İ	i		
- 1	MOTEON	PHODDIUM MOSAIC VIRUS (STRAIN STRICAPORE)		i	 	İ	1	i	j		
KOAT ON		KUMBER NECROSIS VIRUS			-	1			j		_
- 1	MOTEIN		116.211	!		Ì	j	j	į		
- 1	MOISIN	CITAUS TRUSTIZZA VIAUS (ISOLATE TIB)	1	İ	i	<u> </u>	İ	-	<u> </u>	-	
200	NA COLUMN		Ī	3	İ	İ	İ	İ			
	MINION		Е	150	-	i		İ		<u>.</u>	
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PCCLNE	Pricriale	All Virours (Ne Bariteringhaget)		\Box	1					1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	
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PCOAT PPV		I EL INE PARI EURUPERIA VIRUS				ļ			1	-	
PCOAT PPVIS	W	FEI DOE PAIN EUROPENIA VIRTIS (STRAIN 191)	5	::	;	1		1		-	:
PCOAT DEVS	COAT PROTED	INTERIOR VINUS S	63-66			_				1	-
AVAN PAR		REINK ENTERSTIS VIAUS ISTRAIN ABASSITAL)	605.700								
		TAGE ON MECHANIC SPOT VIRILS	2.2								
	1	MAINS CIENT VIRIA	176-197	701.27	<u>:</u>	i	<u> </u>		!	-	
		PARACTECINE ALINE ALC CIDILIS	43.64				1	:		2	
	COALPROTEIN	MANUSCO MOSAL VINOS		1	l i	1	:	:		:	1
>	COAT PROTEIN MECUASOR	MODAMURA VIRUS	7.5	į	İ						i
	MILL OF THE PROPERTY OF	COONTOCLOSSUM RINGSPOT VIRUS	2.2								
ı,		Character very from Lenscarie Village	13:43							<u>-</u>	
	COAT PROTEIN		127 641		İ	-		-		-	
		CANINE PARVOVIRUS (TYTE 17 STRAIN ATZ)	2		-					: :	
MCOAT JAWC)		CANNE FARCOVINIS (SIRAIN 160419)	8			-	1	1		_	
		CANINE PALYOVIEUS (SIBAIN CPV.D CORNILL 120)	28 15			•				_	
	COAL CROSSING CO.		314		-	ľ	ļ		1		:
PCOAT PAVCH	COAT PROTEIN VPI	CAMPR. PARTONIRUS (STRAINT)			-	-		-	1 1 1		
PCOA? PELOY	COAT PROTEIN PRECURSOR	PEPER MOTILE VIAIS	373.285						;		
	Sant Back Italia	DAPAYA MOSALC POTFINING	18:10								
		December 1411 State of Control of the last Control of the last	1	12.1		:		1	!	•	
PCOAT PPMVS	COATPROILEM	TENTED PION INC. TINGS IS INC. TO THE PION IN THE PION		!!	;		1			:	:
COAT PVSP	COAT PROTEIN	POTATO MRUS S (STRAIN PERINTAN)				-					:
Print hev	COAT PROTEIN	AICE STRUE VIRUS	131-137								
	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	STARTING LINE CHITE INC MOCALL VIBER	13	:	•	į					İ
COAT SMOTH	COALPROILIN	SATELLIE POLICE WILLE LINE PLOSAL VINOS		İ	-	Ī	İ		1	-	Ī
PCOAT SMMEA		STRAWBERRY MILD YELLOW FOCE ASSOCIATED VIRUS	2	į				1		İ	
APPL AVEN	GENOME YOU YPROJEIN	TAMARILLO MOSALC VIRUS	227-773								
	-	TOWARD BINGIN CRIME VIBILITIES AND REIL	136.11								
PCOAT 183VB				-	•	-		!	İ		:
MOAT 10V	COATPROTEIN	TURNIP CRIMILE VIRUS		į		•				1	
ATU. LVUJA	POLY PACTED	LOMATO COLDEN MOSAIC VIRUS	<u>2</u>								
	2516 615 325	POBLACTO LOT DI CHERN LIGITATION VIBILS TINIV VIRAIN US	102.128			-					
	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1		1 20.00		İ	Ì	!	-	:	i	:
KOAT THV	COATTROILIN	COMPLETE PROPERTY OF THE PARTY	1					1		:	
PCOAT TWOOL	COATPROTEIN	TOBACCO MOSAIC VIRUS (STRAIN DE)	1				1				
MONTH INDO	COAT PROTEIN	TOBACCO MOSAIC VIBUS (STRAIN DALIL ENENSI.)	103-128		į	1	į		:	:	-
PCDAT TAVEL	COATPROTECH	IOBACCO MOSAIC VINUS (STRAIN ER)	103-131			7					
	COLT BESTER	TOBACCO MOSAIC VIBUS ISTRAIN NOUNES RIDGAASS (181)	107.136			-					
1		TOTAL STATE LANGING SETTINGS	15.50					ĺ	!		
CONT.	CONT. CONT.	THE COLUMN THE PROPERTY OF THE PARTY OF THE	1		-						:
PCOAT THINGS	COAT PROTEIN	CORPLETE THE STATE OF			1				İ	i	i
PCOAT TMM10	COATPROTEDA	I DBACCO MOSALC VANOS (SI MAINT)		-	1		-			1	i
PCOAT TNVA	COAT PROTEIN	TOBACCO MECROSIS VIRIIS (STRAIN A)	2								1
KOAT THYD	COATPROLEIN	TOBACCO MECROSIS VIRUS (STRAIN D)	8		į	Ì			1	j	-
PCOLL HSVSC	_	PERFESYTALIS SABARU (SUBGROUP C / STRAIN 411)	¥			į				İ	
PCOLA MOBY		IGPATHIS B VINUS (SUBTYTE ADW2)	8								
PCORA SPRVA	-	ILEPATITIS & VIRUS (STRAIN ALPILA!)	==		i						
THE TANK	7	INDEATITIES NAMES (SUBTIVE ADVW)	8 6								į
	AND AND A PAIN BROWN BE OVER	HANDAN AND WALLS TYPE Y	19:16	1							
1	THE PERSON NAMED IN COLUMN TWO IS NOT THE PERSON NAMED IN THE PERSON NAMED IN THE PERSON NAMED IN THE PERSON NAMED IN THE PERSON NAMED IN THE PERSON NAMED IN THE PERSON NAMED IN THE PERSON NAMED IN THE PERSON NAMED IN THE PERSON NAMED IN THE PERSON NAMED IN THE PERSON NAMED IN THE PERSON NAMED IN THE PERSON NAMED IN THE PERSON NAMED IN THE PERSON NAMED IN THE PERSON NAMED IN THE PERSON NAMED IN THE PERSON NAM	PROPERTY NAME OF SECOND AND ROLL OF	117 977		İ					Ī	
	MANUA UMA-BINUMO PROTEIN	Carlotte Anna Ca			Ī				Ī	Ì	Ī
∢!	MAJOR DHA-BOODEO PROTEIN	PUDPON CT IOMEGALOVINOS (SI PAIN ADIOV)				ļ					
	MAJOR DNA-BENDONG MOTEIN	JEAPES SCOLEX VIRUS (TYPE I / STRAIN 17)	459-476	397-610						1	
PENCEL HISVIE	PLANOR DNA - BONDEO PROTEIN	I IEAPES SOULEX VIAUS (1 YPE I 7 STRAIN I)	***	507-610							
1	INTERIOR PROPERTY IN	HEAPES SUCLEX VIRUS IT YPE 17 STRAIN KOSI	20.05	507-470		i					
	WALCAST BROWNING BROISIN	BOVAKS ISEPESVIELS TYPE STATE AIN BLIVE	1	94.616					i I		
_ L		FOLIMA INCOME CARRIE PARE 1 ACTOR IN A FLAS.		-		Ī					
	MACON DIAMENTO TROUDING	CANAGE TENEST AND THE CALL THE ABOUT				1000				İ	
	MAIOR DNA-BRODNO PROTEIN	PEALLY WOOD SAGRING (STRAIN 11)	2	1000		25				1	Ī
	MAJOR DNA BINDING PROTEIN	MUNINE CYTOMEGALOVINUS (STRAIP SMITH)				Ī		Ī		Ī	ĺ
PONE SOM	MAKIN DNA RINDBAD PROTEIN	SPACEN CYTOMEGALOVINUS (STRAIN COLIUMN)	190-313	641.670		Ì					
	DHA LIGASE	VAZIOLA YIRUS	366.384		_						
POPOL ADEGS	DNA POLYMETASE	INDMAN ADENOVINIS TYPE 1	=	121 850							
i	DNA POLYMERASE	HUMAN ADENOVIRUS 1 YPE 5	21.11	828 850							
	DAY BOLVERALL	HILDAAN ADENOVIRUS 177E 7	331.386	496.517	910.76						
	Part and some and	IN PLAN ADENOVIBILE TYPE 13	185.586	10.50	175.75						
PIPOL ALE	DIM FULT MERASE	HUMBER MICHAEL STEE 14				$\left \right $				1	

_	PROTIZIP	All Virgan INe Barterlanbares									
FILE KAME FI	PROJEIN	YIRUS	12786	AMEAL	ANTAL	ALCAI	ARCAS	AREAS	AHEAJ	ARCAI	ARTAI
		CIKINISTONFURA BIEMNIS ENTOKIOTOXVIRUS	430-434		112.757						
	WA POLYNEBASE	(18 ORELLA VIRUS NY.3A	434-443								
	DNA POLYNGBASE	PANAME CIUMI BURSARIA CIGINEELLA VIRUS I	20.00	24.40		-					
		PASTEIN BARR VIRUS (STRAIN BOS &)	154.374	=	20.00	19.194	013.970				
DOC 7047		FOWL MIN VIRIS	5	20.20						-	i
NO S		PRIMAR CYTOME GALOVINUS (STRAIN ALILEY)	169.507	943.960	103-1013						!
DOC 10409		DUCK HEPATITIS B VIKUS (BPOWN SHANGILAL DIKK 1501, ATE 54)	4:30	3.5	533-541	354.572					
Poror ignoc	POLYNGRATE	DINCK HEPATIFIS B VIRUS (STRAIM CHINA)	4.29	23.53	\$21.540						i ;
-	NUL THERASE	OUCK REPAILITS B VIRUS	907 · I	Ē					-		
200		DUCK IRPATITIS & VIRUS (WITTE SHANGITAL DUCK ISOLATE \$11)	£.	2	13.72	26.53					İ
		GROUND SQUIRGEL HEPATHIS VIRUS	441.475						İ		!
ŧ	DHA POLYMERASE	HEAON (LEPASITIS IN VIRUS	\$	20.5				i i	!		;
	NA MA. THERASE	PREPARING DVINES (SINIVE)	11.1	=		:	:	:	:		
POPUL LPOVE 19	INA PRI PROBASI	THE ALLIES IN VINITE (MINISTER ALMA)	=======================================								_
=	INA MA. YARINASE	INPATERIST VIBILS (MIDIATE ADMINATE AT	3	#	11.	•					
POPOL JOBVA DI	NA POLYMERASE	INEPATITIES WINUS (STRAIN ALPITATI	200	127	414.415	750.76	:	-		1	Ì
POPOL NEW DIO	DEA POLYMERASE	HEPATIFIS & VIBILS (SIMIYES ADW.) STRAIN INCOMPSIANTING	9.0								
	DHA POLYNEAASE	HEPATIFIS IN VINUS (SUBTIYES ANY / STRAIN JAPANAROW)	2	-	_	111111					
	NA POLYNERASE	INPATITION VINUS (STRAIM CITY CHING ANY PINGE ATT)	70.01	18	_				1		
1_	DNA POLYMERASE	HEPATITION VIBILATION VALUE AND AND AND AND				-					
	NA PON VIAFILASE	INPATITION CINES AND AND ARRESTS OF THE ACCOUNTS	8				:		:	:	!
1	NA POL VACERASE	THE ATTRICE CHILD AND TANK AND TANK THE TENTON OF THE PERS				-				Ī	
T	DNA POLYMORASE	Š			110					Ī	
Τ	THE POST VALUE A CO.	100 D A TITLE & LABOR 12 H 5 VIR 1500.				-				Ì	
•	PAIN PAIN STATE THE										i
S CANADA		TECATION OF THE CONTRACTOR OF	2	20.00		730-767					-
		ILEPATICIA B VIRCIS (SUBTITIE ADTW)		2	-						
		MENUS SUCCES VINUS (TYPE // STRAIN IT)	13:		000						
TOTAL PAYA	LINA FOLTALASE	HEIVES SUPPLEX VIRUS (TYPE I / STRAIN ANGELOTTI)	=	=	201						
		TERPES SECTEX VINUS (TYPE I / STRAIN KOS)	2	=	107) 1090						İ
		ICEPES SIMPLEX VIRUS (TYPE I / STRAIN SCIA)	=	2	1073.1980						: !
			200	2 2	1078-1015						1
		HEAVES SIMPLEX VIRUS (TYPE 6 / STRAIN UGAMDA: 1101)	20.53	9.00	131.413					İ	İ
	MA PULTALEASE	EQUINE DEATHS VINOS LTFF (STRAIN ARAT)		Ē	1	101-11	874.191				
		ICTALUADO 16 IVESVIRUS I		=	_						į
The Court of		AND THE PARTY OF T			344.164	2	200				
_		Ī	200		-					İ	
-	DNA POLYNGRASE	Ī		46.0	1					İ	
Τ		VARICELLA-20STER VIRUS (STRAIN DUNIAS)		141.183	448.441	711.146	116.63	100		Ì	
Г	DNA POLYMERASE		1					1		İ	Ī
POPOL WITVE DI		WOODCIRICK IEPATITIS VIRIUS SY	\$ 47								-
POPOL WHY!			16715							Ì	
		WOODCINICK IRPATITIS VIRUS I	2071	15.5						İ	ĺ
		WOODCHUCK HEPAILITS VIRIES 9	100								
POPOL WHYNE D	DNA POLYNGLASI	WOODCHUCK HEPATITIS VIRUS WAS ITSRILATE PWS23)	<u>2</u>							Ì	İ
ᄀ		IEPATHIS B VIRUS (SUBTYPE AYW)	20.00	4)4.450	750-767					Ī	
i		MUNICAL CYTOMEGALOVIRUS (STRAIN AD169)	107.126								
POST HINEA		EQUINE ICERPESVIALIS TYPE 4 (STILAIN 1941)	<u>×</u>							Ī	
		EQUINE IERDESVIALIS TYPE I (STRAIN ANAP)	130-149							İ	
מאון וואון		ICTALUND IGUPES VIPUS I	11.65							i	İ
POUT HSYLA		TERPESVINUS SALVINI (STRAIN 11)	7	79.18	181.181						!
TO THE PERSON IN		MOUSE ADENOVIRUS LYPE I	Ž.	İ	į						: ;
TELL THE E	EAST VEIN THE PROTEIN	THE MALE ADDITIONAL STATE OF THE PARTY OF TH	ŝ	-	i						
		HIGHAN AREMOUTH TOPE T	2		-					j	!
L	EALLY EIA 18 KD PROTEIN	SDADAN ADEMOVILUS TYPE ?	11.	318.344						İ	
_	FIB PROTEIN LANGE F. ANTIGEM	13			-						
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ī	PROTEIN		T	AREAT	AREAS	AREA 1	AREAS	ARFAG	AREAT	ARFAIL	ABTA
PEIBL ADECT	Ī	CANDE ADENOVIRUS 11 PE 2	= : 0		1	1	Π		ī	;	1
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PEDIO ADEGO EA		INFIGURA ADENOVIBLES 15TE 1	Ī	3	İ					-	1
FELIO ADEO! - EX	1	INDIAN ADENOVINUS TYPE S		3					<u> </u> 	Ì	į
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		HAMAN ADEMOVIAUS TYPE I	2	İ	Ī	İ		Ì	-	į	; ;
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100 ADCM	FROM A BLE EAST, YEA 11 KD TROTE IN	MOUSE ADEMOVIRUS TYPE I						j		<u> </u>	
ī			8	-	-					İ	
	EAST Y ANTIGEN PROTEIN D	B05:0)	263 786			-					
Ī		EVSTEEN BARR VINUS (STRAIN BOS 6)	159-184			-					
		EPSTEDA BARR VINUS (STRAIN BY) 6)	Ī							<u> </u>	
		EPSTEIN DAUR VIRUS (STRAIN BYS.6)	1(1)(1)	[19:29]		-			i I		!
=	PERO SUBURIT		7								
PENNI FREEV EN			100.001						Ī	İ	
	ENV POLYPROTEIN PRECURSOR	FREND SMEEN FOCUS FORMING VIRUS	100.401		i I						!
PENV AVEU		A VIAN RETROVIBUS RM 10	106.135			Ī					1
l		AVIAN SARCONA VIRUS (STRAIN URZ)	П							<u> </u>	i
3			8	201.124	-		 				!
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1			Γ	7	•	63.474	\$14.375		İ	İ	!
	ENV POLYMOTER	BOYDYE LEUKENDA VIRUS (AND INCAN ISOLATE FILK)	141.100							<u>:</u> 	
			101.111							<u> </u>	
J			161-151							İ	
_			101.117							<u> </u>	
-			101.11							İ	
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_1					630-651				<u>-</u> 		!
- 1			Ì	_!	630.651						:
1				514-645							- :
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•		FELDIE LEUREMIA VIRUS (STRAIN LANBOA DI)								<u> </u>	
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_ 1		S (FOANIY VIRUS)	131.174	355.315	20 001	897.	10.11	164-117	150 760	116.110	;
اما		TRAIN CARDNER, ARNSTEIN)	467.466	625-646	<u>. </u>					-	: :
		TRAIN GA)	Γ	929-509					-	<u>:</u> !	!
_1	ENV POLYPROTEIN PRECURSOR		430.471 AC	A01.679		 				i	:
. ,		TRAIN SNOTTH THE HITS	467.488			<u> </u>		!		i	;
אס מאר א	IV POLYPROTEIN PRECURSOR	IIA VIRUS	\$19.540								:
ī	CP160 PRECUMSON	KIENCY VIPUS TYPE I (MIND ISOLATE)	461.510								:
7	GATEGORISM	CIENCY VINIS TYPE (DISTRIBUTE)	83:518 13:518								
TO WATER	CATE MECANON	HUMAN DOUTHODERCIENCY VIBILS 1YPE I (DRAIN ISOLATE)	=	j	-	ĺ					
٦	I BO FRECUENTA	FILTER Y VINCE TYPE [IRLI] SOLATE)	22.	1	1	1		1	1	1	7
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١	610,000										
TALE NAME	PERCENT	AM Virume (No Becierophages)		_	г			Γ			
	TOTAL STATE OF THE		25.2	7F.	- Y.E.Y	1	. J. V. D.	a rail	7 Y H.V	Africa	3111.3.9
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ī	CP 146 MECINETAL	MELLON FOR THE PROPERTY OF THE PARTY OF THE PROPERTY OF THE PARTY OF T	3			,					:
ISINI AKIL	GP 145 PAT CAR COR	ICLEMENT VINUS TYPE I	5	116.74							
ī		MONTH OUT IN THE TANK A MINE TANK	300-323	_						1	İ
Į	September 2	CIENCY VIRES 1YPE	133-145	410-427	455.417	-				Î	
-1	UNION FRECUREDA.	HIDMAN INCAUMODES ICIENCY VIRUS TYPE I (ZAIRE 3 ISOLATE)		175.190	!	j-	Ī				İ
BY HAR	WIND PLECUISOR	JCIENCY VIRUS TYPE I	_			1				İ	
ŧ	CATEGORISON	PORTAGOR ICIENCY VIRUS TYPE I	\$03.527			Ī				İ	
_1	OF 160 PRECURSOR	INTERIOR DOMPHODE FICIENCY VINUS TYPE I (ZAINE 12371 ISOLATE)	-		1 25 30				Ì	İ	
		INDIAN BOADNODEFICIENCY VIRUS TYPE I USOLATE BENT		ī	2		Ī			Ī	
_!		INDIANA DORUNODEFICIENCY VIRUS TYPE 2 (150), ATE CAMI)	-	7	İ	Ī	İ		İ	Ī	
ı		INDIAN BORDADEFICIENCY VIRUS TYPE LINGS AFF BIOM	_	741.744	111 300	-	İ				
i I		INDALAN DANDADDE FRIENCY VISUS TYPE 3 HERY A 18 had y		ī		-				į	
LΙ		INDIAN BORDODE ICENCY VIEWS TYPE 3 HER A TE CHANA. 11	776	1,12,11	Ì	-	Ì	Ì			
		HUBAAN BEARNODE FICIENCY VINUS TYPE 3 JISOLA FF MILL ST		- 100	Ì	Ì					
PEN MYTE	CP 146 PRECURIOR	INDAM BORDHOEFICIENCY VIRUS TYPE 2 (ISOLATE ROD)	141.73	3		1	İ	Ì	İ	Ì	
		HUMAN BARINODE ICIENCY VIRUS TYPE 2 (150LATE SBLISY)	_	170.00	İ	Ì			İ		
		MAKAN BOADHOBEFICIENCY VIRUS TYPE 3 11501 ATE STI			Ì	1	İ			i	
	ENV POLYPROTED PRECUISOR	SPEEP PALMOMARY ADENOMATOSIS VIRUS	ī	100	146.186	1	1				
Į	ENV POLYPROTEIN PRECURSOR		100	ī	Ť		Ì			Ī	
	ENV POLYPROTEDY PRECIASOR	ECH	101.63	İ	<u> </u>	İ	İ	Ì		İ	
۰I	ENV POLYPROTEIN PRECURSOR	1		İ	İ	İ	İ	İ			
_!	ENV POLYPROTEIN PRECURSOR	CAS.BR. E MURINE LEUKENIA VIRIIS	413.646		İ	İ	İ	İ		į	i
DV MAY	ENV POLYPROTEIN PRECITISOR	FRIEND MURING LEUKEMIA VIRIIS (ISOLATE 51)	099-619	1		İ	İ	Ì		-	
The second	ENV POL YPROTEIN PLECITISON	Γ	034 619	1	İ	Ì	Ì	Í	Ī	İ	
NA PLANCE	ENV POLITICISM PRECINSOR	FUEND MURINE I EUKENIA VIRUS (ISOLATE PVC.211)	019 619	<u> </u>	!	İ					
Take To Varia		CHARLE V MUTURE I LIMITATIA VIRUS (MUS HOR TULANUS VIRUS)	19.00		<u>.</u>	İ		İ		İ	-
PEN LA WA	ENV POLYMENTERS DESTRICTS		107-116			<u> </u>	İ	İ	Ī	İ	1
PENV MENTO	ENV POLYPROTEIN PRECIETOR	PARAMETER MARKET RUNE PILA VIROS	629-650							Ī	
	DAV POLYPROTEIN PRECURSOR	277 277 277 277		Ī	İ	İ					
PENV MATIVE	ENV POLYMOTEIN			Ì	i	Ť	İ	j			
NEW MATYO	ENV POLYMOTEIN		77.17	İ	İ	İ	İ	j	Ī	Ì	
-	DAY POLYPROTEDI	SOUTH MASON PFIZER YIRUS	10:02	İ	†	İ	İ	Ì	Ì	j	
	ENV POLYPROTEIN	FBI MUNDAR OSTEOSARCONIA VIRLIS	170-191	İ	İ	İ	1	İ	Ì	İ	j
ī	ENV POLYPROTEIN PRECURSOR		636-603		İ	İ	İ	Ì	İ	Ī	-
Ĭ	ENV POLYPROTED PRECURSOR	RAUSCHER MINK CELL FOCUS-INDUCING VIRUS	¥ [9]	İ	İ	İ	Ì	İ	İ	İ	
1	INC BOLD CONTROL	ROUS SARCOMA VIRUS (STRAIN PRAGUE C)	Г	11.51	Г	İ	İ	İ	i	Ť	1
i.	National And	SOCIAL POLICY VINES (179E 1)	2	Τ.	: -	934.93	653.038	İ	İ	Ì	
1	DP 160 PRECLIFISOR	GINTAL BANDON FIRE TO STRAIN LET	ı		101.774	ī	631.64E	16.6%	i 	İ	i
PEN SIVAG	CP 140 PRECLIRSOR	SOCIAM DOUBLES IN THE WAY VALUE AGAINST TOOL AND	3							<u>-</u>	-
1	SPI40 PRECURSOR	ADDITION OF THE STREET ADMINISTRATE ADMINISTRATE ONE CALL		<u> </u>	1						
	GP146 PRECURSOR	Т	7	İ	†	İ				j	
PENY SIVE	SPISOPRECIENCON	ARRIVATED IN IN T STATES CINCLA IF CAN	100	İ	†	+		İ		j	
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PCGENE	Pi3CTL21P	All Virgies (Na Batteriaghages)		1	Г	Г	Г				
ı		VIRUS	43.4	AHA	V.	NAME OF THE PERSON NAME OF THE P	48145	AH LAS	1	16.41	17
1 1		SIMIAN INDITINOUSFICH NOT VIRUS (AINH O'D) ISOLATE)	1							_	
FEN SIVA	CP ING PRECURSOR	SIMIAN INDIDNODES ICIENCY VIRUS IKEW ISOLATE)	l t	. ,	107 625						
		SIMIAN INIMINODE FICIENCY VINUS (K78 ISOLATE)		٠,	101-124	- 1					
1		SIMIAN IMPRIMUTE ICIENCY VIRUS (FILESALITA ISOLATE)	Ī	200							
PENV SIVE	CP166 PRECURSOR	SIMIAN IMMINOUFFICIENCY VIRIS (FB) MC11 ISOLATE)	_	110.011		i				•	
PENV SMSAV		SIMIAN SARCOMA VIAUS	6.63		-						
PENY SRVI	ENV POLYPROTEIN	SUMBAN RETROVINITESAV.	211.235								
PERDA AVIER		avlan erytiroblasiosis virus (strain es4)	221.246								İ
JEH FOWF		FOWLPOX VIRUS (STRAIN PP.1)	21.41	13.62	l						į
PETFI STVICA		SHOPE FIBROMA VIRUS (STAAIN KASZA)	-				!	-			:
PET VACCE		VACCINIA VIRUS (STRAIN COPT NITACITY)	1		İ	: -		:	:		٠
PETT VACCV		VACCINIA VIBITS (CIRAIN WE)				†		!	-	-	1
THE PARTY OF PARTY.	TELET TELEVISION STATES OF THE PROPERTY OF THE		Ī			1		Ī		İ	
				7	7	ī					
	5	VACCINIA VIRUS (STRAIN WR)	2		_						
PETT2_VARV	EARLY TRANSCRIPTION FACTOR 13 KD SUBUNIT	VALIOLA VIRILS	<u> </u>	111.10	145.187	115-100	\$16.915				!
	ALKALINE EXOMOCLEASE	HERDES SIMPLEX VIRUS (TYPE 17 STRAIN 17)	65:00			_				į	i
	ALKALING EXCONDICTEASE	ICENES SUAPLEX VIRIS 17 YP. 21	2			-	-	:		:	
iq.	AL RATING EXCONNESSE	EOLIDIE DERPESVIRUS TYPE DISTRAIN ABAPT	134.30	Ï	1	1					!
	AT IT AT 1M S WOMEN IN S A CO.	PEET CON A DIEG VINE CEN ALV NIA 11	F	İ	1	1	-		:		i
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VE AUT VE VI	ALALINE ENORAL PROPERTY	THE PROPERTY OF THE PROPERTY O		7		• ;	-				
- 1	STANDINGE PROJECT	MUMAN ADEMOVIRUS 19FI, 40	2	-	-		j	-			
200	41 4 KD FIBER PROTEIN	MINAM ADENOVIRUS 1YPE 41	16-133								
MIRP ADES	FIBER PROTEIN	IEDAAN ADENOVIRUS TYPE, 1	132-173								!
	FIDER PROTEIN	HUMAN ADENOVIEWS TYPE 5	41.43		!	j		1	İ	İ	-
•	FIRST PROTEIN	BOVING ADEMOVISING TYPE I MARCHADEMOVIETIC BOCT	Ī	100 000	İ	1		Ì			
A THE VALUE		CANAGE ATHEROCOMES A CARE LIGHTANIA COLATON	Ī		1	İ		:	;	:	:
	STATE STATE	CARING ADJINOVINOS LITE I SALANIA (ILANIA)	:			1 - (22.2.2.2					
- 1	PINE FROILIN	MOUSE ADENOVALIS LYFE I	ī		_	_	2.52		:	-	
	GAG POLYPROJEIN	AVIAN ENDOCEMOUS VIRUS EV.	2								
- 1		AVIAN ENDOCENDUS ROUS ASSOCIATED VIRUS O	1:31								
		AVIAN HYELOCYTONIATOSIS VIAUS MC24	2 2		!					:	
MON A VOICE		A VIAN MYELOCY TOMATOSIS VIRUS IIBI	E.S		!	-		!	1		
POAD AVISU		A VIAN SARCOMA VIRUS (STRAIN URZ)	1.15			-				İ	
1		AVIAN SARCOMA VIRUS (SIRAIN Y 2)	2.5			ĺ				-	i
1	CAS POLYPROTEIN	AABOON ENDOCENGUS VINUS (STRAIN KIT)								İ	i
PGAG ILVAU	GAG POLYPAGIEN	BOVING LEUK EAGA VIRUS (AUSTRALIAN ISOLATE)	111111	İ		İ	İ			Ì	
		BOVING LEUK EMIA VIRUS IJAPANESE ISOLATE BLV. II	2	Ī		İ	Ì		İ		Ī
ķ		CAPENIE AR MILITIS ENCEPTIALITIC VIRTE (CIRAL CORE)		Ī	1	İ	j	Ī		i	
1		HINAMI SABCOMA WHILE		Ì	 	İ	Ì	Ī		Ì	Ī
١.	GAG POLYPEGIEN	INCALANT CELL PERENIA VIRIIS TYPE LICTRAIN ATEL			1	İ	Ī	Ī		Ì	Ī
ı	GAG ANI VPROTEIN	CALAN P.CELT. LEINEAGE CIRCLE COR LICER GREAN ICH AVE.		Ì	İ	İ	İ	Ì	j	j	
	MAC POS VPB ATEIN	STATE TO STATE OF STATE		Ì		1		Ì	Ī		
CAIN DAD	CAC BOX VBIOTED	Ī				1	j				
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		SOCALC)	1	i		j	Ī	Ì		-	
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		IX.431 ISULATE)	-	: : : : : :		: !	-	:	!		
- 1		LI ISOLATI.)	16:0		_				- 3	•	
- 1	GAG POLYPROTEIN	1	16.59				<u> </u>			i	i
MOAD INTO		() ISOLATE)	16:59						!		
		CIENCY VIRUS TYPE I (IRCSF ISOLATE)	10.59					Ī		ĺ	
		TENCY VIRING TYPE I (MAL ISOLATE)	267-785		<u>-</u>			İ		<u>.</u> 	j
		JEN Y VIRUS 1YPE I (AIN 1001.ATE)	16.39			į		1		:	<u>:</u>
CAG IN IN	GAC POLYROLEON	I (NI.W YORK S ISOLATE)	1					İ	- ! !	:	1
		TENCY VIAUS TYPE I (NDK ISOLATE)	10.50	11.33							
	DAD POL YPIOTEIN	I (DY1 ISOLATE)	63.91								
POAD IN:PV	GAD POLYPROTEDA	VIRUS TYPE I (PV23 ISOLATE)	16.59							İ	
POAD HVIRH	GAUPOLYPROTEIN	IRMAN MAKINOKE FICIENCY VIRIUS TYPE I (REALAT ISOLATE)	16:59		_						

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FILENAME	PROTEIN		AREAL	ABEAL AB	ABIAL AL	SEC. S	AREA S	28141	AREA	ANTAI	AREA?
POAD IEVIUA	GAD POLYMOTEDA	SOMINODEFICIENCY VIRUS TYPE I (STRAIN UGANDAN/ ISO	16-51			_				Π	
PGAO IIVIWI	DAD FOL YPROTEIN	SALINODE ICIENCY VIAUS TYPE I (WAIT ISOLATE)	14.59	<u> </u>							
MOAD INIE	GAG POLYPROTEIN	CDC.ZW ISOLATE)	63.61			_					
POAG IPMA	RETROVINGS-RELATED GAG FOLYFROLEIN		151.172					. :		=	
POAG MMTVD	DAD POLYPROTEIN ,		16.2	<u> </u>	<u> </u> - -	<u> </u> 	İ			ĺ	-
POAD MATVC	GAO POLYPIUS EIN	MICHIES MANIMARY TURKUR VIRUS (STRAIM COIL)	 	1	<u> </u>	-			Ì		
DATE OF DATE	CAG POLYROIEM			1	1	+	Ì		Ì		Ī
	THE PART PROPERTY			1	1	1	Ì		İ	-	:
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1000	N.X. N. C.	: !		!		<u> </u>	!	:	:		
TOYOU SEE THE		SUMMAN POANT VINCE (LITTLE / STRAIN LAS)		1	1	<u>!</u> -¦	Ì			İ	
210101010101010101010101010101010101010	SALVE CANONING	SUPPLIES THE PROPERTY OF THE P		1	1	1	İ				-
2000	THE COLUMN THE PARTY OF THE PAR		_	<u> </u>	1		İ	Ī		-	-
POAU SIVA	CACTOLITICIES	SINIAN IMMUNISHER LIGHT TO THE STATE OF THE	-	- : :	1	- -					
TAN TAN	DAG POLYPROTEIN	CHIPOTANCE IMMINISTRACTOR A VINISTALIA (C.)	7		-	- :					_
LOVO SINCE	IIAO POLYTROFEIN	SINIAM INNITIATION IN THE CHAIN TO THE CHAIN	7	<u>:</u>	:	. · !		-		-	:::::::::::::::::::::::::::::::::::::::
POAG SIVIAI	DAG POLYPROJEIM			<u> </u> 		- <u> </u>					
POAD SLOWY	GAG POLYPROTEDI	SQUIRREL MONREY RETROVIRUS (SMRV-11)	246-307								i
нь	POSSIBLE CLUTAREDOXIN		1		<u> </u> 	<u> </u>	Ī		İ		i I
•	POSSIBLE GLUTAREDOXIN	VARIOLA VIRUS	71.87		<u> </u> -	<u></u>					
POLLIN OVAS	ORANG.IN	ACAOTIS SEGETUM GRAINITINS VIRUS	208.136	<u>. </u>	:	-	<u> </u>	•	<u>.</u>		
	ORANUL IN	THEORETUSIA NI CHANILLONIS VINUS	7E-113			_	_			_	
iu	GROWTHI FACTOR	VACCINDA VIEUS (STRAIN COFENIAGEN)	2		! ! !	<u>-</u>	İ			<u> </u>	-
MOLEN VACCO	CROWTH FACTOR	VACCINIA VIDUS (STRAIN WR)	1 2		<u> </u>	<u> </u>	Ì			İ	
PORTA VARV	CROWTH FACTOR	VARIOLA VIRUS	100		<u> </u>	<u> </u> -	İ	Ī	Ì	İ	
VALUE AND	PENNANT BITE ICACI	EPSTEDLIBASE VIEUS (STEAD) hot.a)	ī	141.111	757	 -	ĺ		Ī	İ	
PIE DICAVA	PECBABI RIPITASI	IN MANN EVICAME CAL OVIRUS (STRAIN A DIAS)	ī	į	1 251 25	<u> </u>	İ	ĺ		İ	i
. 1	PROBABLE (ELICASE	HEAPES SIMPLEX VIRUS (TYPE T/STRAIN IT)	ī	618-646	<u> </u> 		Ì	Ī		İ	ĺ
ı	PROBABLE INC.	-	Т	236.544		-	İ		Ī	İ	
Ł.	PECCEANI R 1001 ICASS		Τ	Т	107.00		İ		Ì	Ì	
	PROBABILE INC.		ī	ī	119.05	<u> </u>	İ			İ	
1	PROPARITE IOT INCACE		ī	ī	ī	761.786	İ			İ	Ī
HEMA COVO	IEMAGOLUTDINA RELINAMINIDASE	CANINE DISTEMPER VIRUS (STRAIN ONDERSTENORS)	ī	18	ī		İ		Ī	-	-
HENT CVS!	IEMAGOLUTINAN ESTERASE PRECUISOR	ĺ	Ī		<u> </u> 		İ	Ī			
PIEMA CVBLY	IEMAGGLUTININ ESTERASE PRECIPISOS	Ī	\$17 BE	1	1		İ			Ī	
HENT CVBH	ENACOLUPININ ESTERASE PRECUESOS	ĺ	111111	<u> </u>	<u> </u>		İ			İ	
PIEMA CVBQ	HEMACOLUTION ESTERASE PRECURSOR	BOVING CORONAVIBUS (STRAIN QUEBEC), AND (STRAIN LS)			<u> </u>		Ì	Ī			
PIEMA CYHOC	HEMADOLUTING ESTERASE PRECURSOR		391-415								
PIEMA CYMAS	PENADOLUTOM-ESTERASE PRECURSOR		602-413								
PER CARS	SEMAGOLUTION ESTERASS PRECURSOR	MURING CONDNAVIALIS MOIV (STRAIN S)	_	1		- 					
PIEMA MAIC	HEMADOL UTIMIN PRECUESOR	INTUDAZA A VIJUS (STRAIN A AICHUZAS)	Ì	=======================================	<u> </u>	1	İ			Ì	
MEM WEAR	IESAAOQLUTININ PRECUESOR	INTLUDERA A VILUS (STRAIN ADANGKOK/I/TV)	T	- 13		i	İ				
THE PARTY	I EMACCALUS INTROPERCURSON	T		1	1	$\frac{1}{1}$	Ì				
CALL THE PARTY OF		T	Т	211.347	1 11/3/1	†	Ť				
HELL LAND	-	DOTTED A VIEUS STEAM ACTOR ENDENNY VANALATI	Ţ.	ī			Ť			Ì	
HELL LACED	-		101.110	-	İ	t	Ť	Ī		I	Ĭ
PIEM MCKS	HELLA COLLUTION PRECUMSOR	DATUENZA A VIRUS (STRÁIN ACIDEKENSCOTLANDIS)	119-336	<u> </u>	<u> </u>		T	Ī		Ī	Ī
PIEMA IACKV	HEMADOLUI DADI PRECURSOR	ACIDEKENMETONAVIS	Т	115.332	l	l	Ì			Ī	
	REMANDEL UTININ PRECURSOR		120-311	l	<u> </u>		İ			Ī	
MEMA TABAS	JEMAGGLUTING PRECURSOR	DATE LENGA A VIRIS (STRAIN ADUCKVALBEATAMEN)	Γ	33.336			İ				
	HEMAGGE LITTON PRECURSOR	INTLUDICATA VINUS (STRAIN ADUCINCE CHOSLOVAKIAS)	110.01	_			Ì	Ī		Ī	
PIESCA CADE!	INEMAGOLUTININ PRECURSOR	INFILITIVE A VIRITS (STRATH AMERICANGLANDVINS)	П	116 316	<u> </u>						
MENA IADHI	SEMAGO UTININ PRECURSOR	INFLUENCA A VIRUS (STRAIN ADUCKAIOKKAIDOSAT)									
VIEW ADIE	HEMAOGLUTINEN PRECURSOR		1	2			Ì				
NEW YOR	HENAGGLUTDON PRECURSOR	RATUREZA A VINUS (STRADA ADUCKARIOSKIAIDO) MOSTO ARTICOLOGIA	12.43	100	\dagger	†	1	1	1	1	Ī
PIPMA IADIIS	HEMAKOLULIANI TRECURSON		7		1	1	1			1	7

Proper	P13(T121)	All Virgon I've Bacterionhoers!				ŀ		Γ	ſ		
THEMAN	PROTEIN		3	3	7.1	3	SPEAL S	ARTA L	PLV.	AHEA	AMEAS
PICKA ANDIII	ILEMACGLUTININ PRECURSOR	VIBUS (STRAIN ADUCKAIOKKAUOGIAZ)	21.43								
PERT ADM	DEMA COLUMNIA PRECIASOR	INTI LENZA A VIALIS (STRAIN ADUCKAIOKKAIDOMAS)	10 12	106.321							
MENA LABIN	DEMACCIFICATION PRECIATION	INDITIENZA A VIDUS (STRAIN ANDICKAIOKKAIDOVIDAS)	2 2	106.33							
PIEMA ADM	IEMA DOLUMPHY PRECIESOR	INTITENZA A VIBIUS (STRAIN ANDICE ANDREADMISATERA)	25.25	113:336							
PIENT INDAM	JOSEPH PROPERTY SON	DALLENZA A VIBUS (STRAIN ADIRECARNITOBATIVE)	26.50	101:18							
PIEMA LADYZ	HEMADOLUIDIN PRECIPSOR	PRICERZA A VIRUS (SIBAIN ADIKINGEW ZEALANDVIVA)	120.317			i					
PIESTA LABUS	INCHARGE EPIDAN PRECURSOR	INFLUENZA A VIRIISESTRAIN ADUCKAURRAINE/1/61)	Ī	113.119							
PHEMA LADAS	HELLAGUCTERIE	INTLUENZA A VIRUS (STRAIN AENGLAND/S71849)	9:12	104-131							
	HOMACKE ITTENDA PRINCINSOR	INSTITEMENT A VIRIUS OF BASH AS NOT AND THUS	65.26	31.116		ŀ		ĺ			
WAY ALK	AS LA COL IT IN THE PARTY OF COL	DASTIFICATE A VIRTUE OF BAIN AFOUNT PLACIFF VIRTUE OF CONTROL		1		1.					
THE PARTY	THE LANGE THE PARTY AND PA	A VIEW CATE A IN	136.117		Ì	Ī					
THE CLEAN AND ADDRESS OF THE PARTY.	THE PROPERTY OF THE PROPERTY O	TANDESCRIPTION OF THE PROPERTY		-		-				-	
3	MENACOLO INGINI PARLURSOR	INTEREST A VINCE (21 AND AND LANGE LANGE LANGE)									ļ
MON MON	IEMADOLUTININ PRECURSOR	INTLUENZA A VIRUS (STRAIN AGULL/ASTRAKHAM/21/44)				-					
PICHA MAI	HEMAGOL UTBAN PRECURSOR	MOLLENZA A VIRUS (STRAIN ACQUINEALCIERS/17)	321.538								
PIENA INICA	HEMACOL UTDAN PRECURSOR	INTLUENZA A VIRUS (STRAIN ARQUINE/CASIBRIDGE/IM))	330-246	115.111							
MENA IAIC!	HEMAGGI UTINAM PRECURSOR	INTLUENZA A VIRUS (STRAIN AECHTHEACANDRIDGE (71)	30.24	115.111		ļ-					
PIBMA (AHCO	HEMAGGLUTHING PRECUESOR	INTLUENZA A VIRUS (STRAIN ACOUNTAC DETROIT/144)	330.244	135.331		.			1		i :
PICKE INDE	HEMACOL LIFTHIN PARCHINSON	INSTITUTE A VIBUS (STRAIN ACOUNTACOUNTINA)	330.244	115.311	Ī	ŀ					ļ
PURELLY TAIRED	SCHOOL STANSFER STANSFER SCHOOL	THE LIBERT A VIBIL OF PRAIN A SCHIME SONT AND BILLIAN	114.345			1					
TATE VICE	SCHOOL STATE OF STATE	DATE THE LAND A CONTRACT OF THE PROPERTY OF TH		1		İ				-	
1000	HEATT AND ADDRESS BORDERS FOR	Child September 2 A Company of the C	114 941		I	1		İ			
4	STEWARD COLUMN THE CURSOR	THE PROPERTY OF CONTRACTOR AND ADDRESS OF THE PROPERTY OF THE		- 11		!	į	:	: :		:
VIEWA IANG	HEMAQUEUTININ PRELURSOR	VIRITALISM ACCUMANTEAING CONTROL			!	İ			İ		
MEMA MILO	IEMAGGLUTING PRECINSOR	A VIRUS (STRAIN ALQUINALIGHMI)	20.2			j		İ			-
PIEMA LANGE	HEMAGGLUTININ PRECURSOR	VRUS (STRAIN AEQUINEARIANIMI)	216-252	31:31	į	-				ļ	į
PIEMA MINN	I IEMAGGLUTININ PRECURSOR	A VIAUS (STRAIN AÆQUINEÆE W MARKETØ)	236-252	121-338		-					
MENT MON	I DEMACCILITION PRECURSOR	INFLUENZA A VIAUS (STRAIN ARQUINENEW MARKETHIN)	315.312								
PIEKA MOR	HEMAGOLUTBAN PRECIMSOR	A VIRUS (STRAIN A/EQUINE/PRAGUE/1/34)	315.312		-	ļ					
PIEMA MIGO	IGNACIO DI PRECIPIONE	VIRITS (STRAIN AVEOUNE/ROBIAMIA/10)	236-233	11:31	Ī					-	!
HIELDA TANKA	SOLLAND PRESIDEN	ī	216.313	11.330		L			:	!	! i
ALL ALL		DESTINATE A STREET COURSE AND ENTRY AND PAIN DAIRED	210.346	116.113	-				1		
WELL 1417 F	STATES OF THE PRINCIPAL OF THE COMMENTS	INCLUSING A VIRGIS (STRAIN ACCUING SWILL FREE ANTICION)	710.344	115.113	İ	-	Ī	Ī	Ī	İ	
	TOTAL PRINCIPLE STATE OF THE ST	THE PERSON A CHAIR ASSESSMENT ASS	111	_		†	Ī		1		
THE WALLEY	THE STATE OF THE CONTRACT OF T	CONTRACTOR A CIRCLE AND A CONTRACTOR AND			-	Ī					
THE PARTY	THE WALL OF THE PART OF THE PA	THE PROPERTY OF THE PROPERTY O			Ì	Ì			-		
MENG WICK	HEALDCOLD INDIVIDUAL CONSUM	INTEREST A VICE STATE AND COMPANY OF THE PROPERTY OF THE PROPE	7		ļ	Ì	Ī		Ì		
	THE PROPERTY OF THE PROPERTY O	THE PERSON AND THE PE		- 711		Ī				Ì	1
	TEMACOLO ING PACCERSOR				1	i	1				
NAME OF TAXABLE PARTY.		CALIFORNIA CIRILI (SIEZIN ANIA) ARIONALO CERTALINALI			ļ	Ì	T				
	THE LANGE THE PARTY SEES THE PARTY S	CALLE STEAM			İ	Ì	Ì		-		
1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	THE CLASS THE COLUMN TO SECOND STATE OF THE COLUMN THE	Charle Asset Area	1		Ì	1	Ī	I			
1	THE CLASS OF THE CASE OF STATE				İ	Ì	İ	Ī	Ī		
	THE PERSON NAMED IN COLUMN TO THE PE					1	Ì		j		
	Section bearings	A VIET A STATE				İ	Ī				İ
THE PERSON NAMED IN		MAPLIFACE A VIRIS (STRAIN APRIOT WINTER FAINERS)	1		İ	Ī	Ì	Ī			
HEAT LAND	HENLACKEL LITIOUR PRECLIESOR	VIEUS (STEATH	9	106.121	- !	Ī	Ť	Ì		-	
CHIEFLA IABILE	HENLANCE LT DVD4 PRECITESOR	INFLIBIOLA A VIBUS ISTRAIN ANITODY TURNSTONEME W TRESEVAN	100			Ì	Ì	Ī	Ī		
HELL TARES	TO SELECTION OF THE PROPERTY OF THE PERSON O	VIETE ISTANT	170.117	Ì	i		Ì	Ì			
HOLLA LACKS	JEMACKE LITHON PRECINSOR		9	111.111			Ì	Î			
TAX VICE	SELECT INDON PEFCINSON	VILLE STANK	330.344		Ì	Ī	Ī		İ		
HOLL LINE	HE MACCILLININ PRECINSOR	VIRUS ISTRACT					Ī	Ī	-	1	į
PIEMA LATEO	BELIACOL INICIA PRECISION	PAIN AT STEEVEN ARIOTIZAN			:		<u> </u>			:	i
HENG ATTER	HEMAGGLITININ PLECIESCE	VINIS (SIRAIN ANIMAE YOUR CONTIL	236-746		:		Ī	!	1	!	
PIEMA INTRW	SELLA GOLLITING PRECIESOR	VIRIIS (SIRAIN ACTURKE YOWISCONSINJINA)	319.244	,						İ	
MENA IAUDO	IEMA OCI. UTININ PRECINSOR	2	11.51		10.10						!
PICEMA LAVII	IEMAUGLUTININ PRECIMSOR	INSTURNZA A VIRUS (SURAIN AVICTORIA) INS	99-91		1				 		
HEM WOI	IEMACOLUTION PRECURSOR		19.50								
PHEMA IA2CO	HE MADOLUTININ PRECIESOR	I VIRUS (KIRAIN A/KWINE/COI ORAINO/1/P)	17.59	122-174			İ				
											1

PCCEME	PRICELLE	All Virgani INs Bacterlanhances									
TILLHAME	PROTEIN	VIRUS	VALUE OF	, VALV	1.4.1	-37/487	ABEAG	10564		┰	
אפאע נאנוונו	HEMACOLUTININ PRECURSOR	INTLUENZA A VIRUS (STRAIN A/SWINEAIONG KONGAIMS)	Т	ī	1			-	ī	7	7
HEMA (AZH)	HEMAGGLUFININ PRECURSOR	INT. UENZA A VIRIUS (STRAIN A/SWINI/AIDNG KONG/12/82)	2:10	100 100		1		:	İ		!
PIEMA IAZUK	HEMAGGLUTHNIN PRECURSOR	ARUS (SIR	i		: ! :	· -	:	:	:		ì
MENT INDA	HEMAGGLIFTON PRECINSOR	e VIIIS (S	10.51	95.30		ļ		İ	İ	i	!
MON WHILE	IGMAGGLUTING PRECINSOR	PAT CENZA B VIRUS (STRAIN BORGING/1/17)	111111	91 71				} 		-	
	PENACCIO DAR PRECINSOR	THE LIENS A VIBILS (SIBAIN BROWNESS)	116-132	5							
	JEMAGGI UTININ PRECURSOR	INTI UENZA B VIRIJS STRAIN BENGLANDATZUETI	131 130	9	!		İ		1	:	Ī
MEN MAN	HEMAGOLUTININ	INTLUENZA O VIRUS ISTRAIN INFURUNKAMMIN	100.124	16.30		:		:			
NEW MICH	HEMACCEUTININ PRECIESOR	INCLUENZA & VIRUS (STRAIN B/CL/34)					; 	İ	!	:	:
MEMA INDICA	HEMACCI LITININ PRECINSOR	INTELENZA & VIRUS (STRAIN BACONG KONCA/7)	1 1 1 1 1	100.00	-				į	<u>;</u>	:
PIEMA NEE		INT DENZA & VIRUS (STRAIN BABARKU294)	1 2 2		į į	-	-	-	i	,	-
PIESAA DABID	HEMADOL UTININ PRECINSOR	THE UNITED STATES (STRAIN BADDES)	36.136	18	-	Ì			İ		1
PIENA DIE		INFLUENZA D VIRUS (STRAIN BA EL KO)	Ī			-					1
PIEMA INDIMO		INSTITUTAL IN VIRIOS (STRAIN BALABY) ANIMAS	ī			-		į	1		
PIESCA DIRECT		TATEL TENTA IN CASE OF SIX BACKLESS SALES	ī			1			Ī	1	
HELL KINA		THE TRUST B CHAIR SEE ALL BALLY AND ALL SE				-					
PURKA MAGA	Par Cinton	THE PROPERTY OF STREET AND STREET	Ī			-					
PLINAL NAME		THE COURSE OF THE COLUMN STATE OF THE COLUMN S	ī			-					
THE PERSON NAMED IN		INTLUENCE B VIRUS (STEAM BISINGAPORE/72279)	Ī	2		1					
TIENT INEM		POLUENZA B VIRUS (STRAIN G/SINGAPORE/64)		91.315							
CORNE WATER	PENAUGULUI INIM PRECURSOR	POTUENZA B VIRUS (STRAIN BASSIA/IOOLI)		294.306		-					Ī
	ALCOHOLD TO THE	MOLUENZA B VIRUS (STRAIN BAYICTORIANAI)		10.45						İ	İ
MONT DONE		INTLUENZA B VIAUS (STAAIN BAICTONIANAT)	Г	107.101						İ	
HENC MAY	IEMAGGLUTDA	INTLUENTA B YITUS (STILAIN BIYAMAGATA/IG/11)	198-134	10.4						Ì	Ī
HIEMA INCCA	HEMADOLUTINAN PRECURSOR	INTLUENZA C VIRUS (STRAIN OCALIFORNIA/18)	42.484		Ī	-				İ	
MEMA INCEN	HEMADCH UT ININ PRECURSOR	INTLUENZA C VIAUS (STRAIN CENGLANDAPZIS)	Ž			+				İ	İ
HEMA INCOL	IEMABOLUTININ PRECURSOR	INTLUENCA & VIAITS (STRAIN COREAT LAKES/1167/31)	75700	Ī	I	1				İ	
HIGHA DICHY	INTERACTION IN THE PROPERTY OF	SIN	411.451	Ī		L				Ì	İ
PIEMA DICTI	HEMAGGLUTININ PRECURSOR	GRAIN	197			1	Ī			İ	Ī
PIGERA DICKY	HENA OCT UP INFA	STRAN	57.067	Ī		ŀ			Ī	1	
HIGHA BICAT	HEMADGLUTING PRECURSOR	STRAIN		Ì						Ì	Ī
PIEMA BICHA	HEMACOLITIBIEN	STAIN			Ī	+		Ī		İ	Ī
PIEMA DECPI	HEMADOLUTION PRECINTOR	PAGE TRACE OF COMMENT AND			Ī	1			İ	j	
PIEMA BICK	HEMACON ITTOON PRECIMENT	THE PARTY OF THE PROPERTY OF THE PARTY OF TH				•				j	
BULLY NAMES	DESCRIPTION SECTIONS							Ì			
MEMA BACTA	HELLACOL LY INDA PRECIDENCE	TABLE TO THE PARTY OF THE PROPERTY OF THE PA				Ī			Ì		
PIEMA INCYA	HEMAGOLUTININ PRECIASOR	INCLUSION OF STREET OF ALL DATE OF STREET		Ì	Ī	Ì			Ì		
HEMA MADO!	HEMADOLUT DADA WELMAMINIDASE	MANAGE COM A COLLIN	Т	T	i			1	Ì	j	Ī
HEMA MADE	I BLANDOL DI INDIANE MELINALIMIDASE	ACENDS VIRILIE SCHEAN MINALIANA VALCHNET	Ŧ		1			ļ	Ì	İ	
HELLA BUBOR	EMAGGI LITININ MELITAMINIDASE	LANGE CHILL STRAIN DW.	ī	ī					Ì		
HENLY MUNDS	IEMAGOL DI DNOS NEL DIAMONIDA SE	MANAGE VINITE STRAIN SOLI	T	ī	2						-
ICALA NOVA	EMAGGLUT BATA NELIT AMBRIDASE	NEWCASTI POSFASE VIRILE ASTRACT ALICTRIC IN VIPROSITION	T		I	Ī				Ī	
HEDA NOVE	SMAGGLUTION NEI MANIMINASE	OC WCASTI F DICEASE VIETE SCHOOL BEALTH THE TAIL				Ì	Ī	Ī			
MENA NOVO		NEWCASTLE DISEASE VIRUS (STRATM DACA)			Ì	Ì					Ī
HEMA MOVIE		NEWCASTLE DISEASE VIRUS GITAAN BILLITCHERUST		Ì	Ī	Ī	Ì	İ	Ì		Ī
PICEMA NOVI		NEWCASTLE DISEASE VIRUS (STRAIN ITALIENAS)	9	ĺ	Ī	Ì	Ì		1		
HENCH NOW!		NEWCASTI E DISEASE VIRUS (STRAIN ADVADERAS)	9	İ	Ì		Ī		j	İ	j
MEMA NOVO	IGENACOL L'I DADI-NEI MANDINDASE	INEWCASTI E DISEASE VIRIUS (STRAIN OUTENSLANDMA)	9			Ī			İ		Ì
HEMA MOVIO	IEMAGCI UTONIN-NEI MAKUNDASE	NEWCASTLE DISEASE VINIIS (STRAIN TEXAS C BAR)	-	Ì	1	Ī	Ì				İ
וונדאל אחשו	IEMAGG UTING NEI MAMINIDASE	MEWCASTLE DISEASE VIAUS (STRAIN UL STERA)	1	Ì			Ī	Ì			1
IGMA PHODY	IEMAGGI IJI MIN'NEIMAMINIDASE	PHOCINE DISTENDED VILUS	T					İ	Ì	İ	
HEMA PHIN	IEMAGGI UTININ NEUTAMINIDASE	INMAN PARAMILIENZA I VIRUS (STRAIN WASHINGTON/1957)	Ī	122.163	9	100	1	Ī	1	-	İ
HELL PIZI	IEMAGGITI ININ'NEURAMINIDASE	INDIAN PARAPPLIENZA 3 VIRIIS (PIV. 2)	9	1	1 1 1 1 1		Ī		İ	i	
MEMA PIZIT	IEMAGGLUTININ-KEUNAARDADASE	INDIAN PARAINFLUENZA I VIRUS (STRAIN TOSTITIA)	Ī	1		Ì	ĺ	Ì	† 	İ	
ENA PIS	SEMACCE UT BITH NEURANIMIDASE	BOVING PANAMPLUENZA 1 VIRUS	Ī	1	91.2	Ī		Ī	Ī		
TEMP TOTAL	HEMACCLUTION: NEURANINDASE	INDIAN PARATURI UENZA I VIRUS (STRAIN MII 41885)	İ	1	14.10					 	
TEM PINA	EMAGGLUT DOD: NEUTAMONDASE	HEMLAN PARAINTI LENZA I VIRUS (SIRAIN AUSII)465474)	Г	ī	91.3	ļ			İ	İ	Ī
III MA PINIT	HEMACCH UTININ NETRAMBRIDASE	INMAN PARAINT INFINA I VIRITS (STRAIN TEXISTRO)	- FE :	272.700	100	İ		ĺ	İ	 	Ì
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PCGCME	PUNCTURE	All Virgan (No Berreinphogn)			111111	1222		1 1 1 1			
אפאי איפיי	DEMAGGLUTININ WELDAMINIDASE	HIGHAN PARAING US XZA 3 VIRUS ISTRAIN TO X 3 10 4 3 3		18	700	The sale	Prof. St	T Company	:		
PIEMA PINITY	HEALAGOL CHININ-MEURANINIDASE	HUMAN PARAINT (JENZA) VIRIJS (STRAIN TI. VIJS 17/1)	181	311.37	2	1		-	-	,	
HEMA HISTOR	INTRACECUTION NEURANIMITASE	HENNEN PARAIMILLENZA I VIRUS (STRAIN WANDALITY)		£	:	. -	:				
PIEMA PISHX	PERIAGGLUTINA-NEURANIMITASE	HERAN PARAINICIPERA PARCS (CIRAL WASIFISHED)	- E	33.33	:2:	•	• • •				
PIEMA PIAHA	HELIA COLUTINIM MELIEALINIDASE	HEMAN PARAIN LIGHTA IN VIRUS (STRAIN TOSHBA)	19:02	<u>!</u>	•	<u> </u>		!	:		
HELEN ADOL	HEMAGGLUTIMIN-MELIRAMINIDASE	RINDERPEST VINUS (SIRAIN KARE TE O)	1		<u> </u>					1	:
MENA RING.	JENIAGGLUTININ NEJ PLANINIDASE	ADDERPEST VIRUS (FIRAIN ()	2						; ;		
PIGMA SENDS	I PATAGO LA IMPANIMINA SE	SENDAL VIRIS (SIRAIZ VIII VIII ANI VIII ANI VIII	? ?								
HEAL SENS	IN RECENT OF INDIVIDUAL INTERNATIONS OF THE PARTY OF THE	SI MIDAL VIETING (SI MANUAL CALIBARI)	? ?	•							_
MENA SENDI	IL HACCLUTINIM NEURAMINIDASE	SENDA! VIRUS (SIBAIN HARRIS)	2							-	
NOW YOU	PEALACOLUTININ NEURANIINIDASE	SENDAL VIRUS (STRAIN IIV.)	22.70			_					
MONEY TOO	GEALACKE UTINGON NEUTRALIINII) ASE	SENDAL VIAUS (STRAIN 2)	123.343								
MENA IVE	DECKACE UTWO-VELIAMINIDASE	SINDAN VIRUS 4:	\$5.13	2	107 113						İ
MENA SVS	HEMAGGLUTININ-NEURANINIDASE	SIMILAN VIBUS S (STRAIN W1)	7.31	9	119 400	•			: !		•
MEMA SVICE	HENAGGLUTIMIN.NEULANIMIDASE	SIMIAM VIRUS SUSON ATE CANINUX'FI)	=	<u> </u>	- F			:			
PIEMA SVSCP	HEATAGG LITTINIA-NE LILAMINIDASE	SIMIAN VIRUS & (ISCII ATC. CANIMIZCELE)	2.2	101	33.5		! -				
HEMA SVSLM	IENIAGGIUTHMANEURAMINIDASE			<u> </u>	110	į.	!	!!!!	:::	:	
PHEMA VACEC	HE NAGOLUTININ PRECIMENT	VACCINIA VIBUS (STRAIN CONUNITACION)	12:00	!	1	-		i	:	:	:
HENA VACCI	I EMADOL LITHIN PARCITASON	VACCINIA VINUS (STRAIN BID 3)	111111		!	1	!	Ī	İ	•	;
MELKA VACET	=	VACCINIA VIBUS (STRAIN TIAN TAN)	17.191	!	-	į.				i	İ
MEMA VACEV		VACCINIA VIRUS (SIRAIN W.R.)	101-11					ļ		1	1
HEMA VALV	IGMAGGLUTININ PRECINSOR	VARIOLA VIRUS	<u>=</u>		!	-	-			,	
MGXs ADES	HE KON ASSOCIATED PROTEIN PRECUISOR	INDIAN ADENOVIRIIS TYPE 1	1	9		-		Ì			!
MEXI ADEO!	2	ILIMAN ADENOVIRUS TYPE ;	27.44			1			1	!!!	
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PICKE ADEA!	E E	MONAN ADENOVISUS TYPE 4!	1	21.146	İ						
PIETS ABEN	 #	MOUSE ADENOVIRUS TYPE I	1	İ	1	1		1		-	
MEXT ABIO		INDIAN ADEMOVIALIS TYPE 1 AMD)		İ	1				1	 	1 1 1
HEX ADEC		CANNE ADEMOVIAUS TYPE 3	13.77								İ
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PIGG COWPX		COWPOX VAUS	517.133	38.4	919-609	İ			-	:	
PIIT ASTOR		AFRICAN SWINE FEVER VIRIIS (STRAIN BATIV)	13.0		1	-			İ		•
PIN ASFB!		CHICAN SWINE FEVER UPIUS (SIRAIN PATIV)	06:09						-	;	1
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PUSS ASTRE	LATE PROTEIN USAL PRECURSOR	AFRICAS SWINE PEVER VIRIS (STRAIN BATEV)	91.50	i	:						Ī
PITS ASTRI	EAKLY PROTEIN 1768	GRECAN SWINE PEVER VIRIIS ISTRAIN BANIN	2.		:						Ī
PIBAD SOCIA	INCLUSION BODY MATRIX PROFEIN	COMBEAN CIR. MOTIC LIOT FLE VIRUS	93:119	 !		:	-	:	!	:	:
PICIT EBY	PROBABLE PROCESSING AND TRANSPORT PROTEIN	EPSTERY BARR VIRUS (STRAIN DVS-1)	10110	E:E:E	1.2		!	!		İ	:
ZCIS HOWA	PROBABLE PROCESSING AND TRANSPORT PROTEIN	MALAM CYTONEGALOVINUS (STRAIN AD169)	26-136 36-136			İ				-	-
10 E	PROCESSING AND TRANSPORT PROTEIN	GAPES SDOLEX VIRUS (TYPE I / STRAIN 17)	2	=		2. E		İ	- - ! !		İ
ì	PROCESSING AND TRANSPORT PROTEIN	IGENES SECTEX VINUS (17PE I /STRAIN ANGRICOTTI)	£	3	2	131.168		ļ	İ		
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Ĺ	TRUBABLE PROCESSONG AND INAMSPORT PROTEIN	BOVING RELUESVINUS TYPE 2 (STRAIN BAIV)	2	=	!						İ
1	CENTRAL PROCESSING AND INAMEDIAL PROJECT	COUNTE FEBRUARIS 1 YPE I	*	=	2						
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THE PERSONS	TRUBABLE PROCESSING AND HAMBERS EXPERIN	AUTOM CTTONE GALOVIRUS (STRAIN SAITH)	=	20.22	=						
- 1	PROBABLE PROCESSING AND INAMSPORT PROFEIN	REUTONATES VIRTIS (STRAIN INDIANA-FUNKITAUSER / DECKTR)	20.5	11.71							
ALCIE VEND	TRAMSFORT PROTEIN	VAUCELIA-ZOSTER VIRUS (STRAIN DURIAS)	=======================================	619.634	33.74						
	DOGLINATE CALLY PROTEIN	GLOVES SWOLER VIRUS (TYPE I / STRAIN 17)	-							i İ	!
NO POL	VAVILLE	GENER SUCLEX VIRUS (TYPE 27 STRAIN HGS2)	713.739								
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PRIMS ISVAD	FMS TYROSING KINASE TRANSFORKIING PROTEIN	FELINE SARCOMA VIRUS (STRAIN MCDONOUGH)	\$1:13	143.263	414.450	100	701.801	136.177		İ	
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_	TILYNDDRE KINASE	QUINE IERPESVINUS TYPE I (STRAIN ADAP) AND (1501.ATE HVS25A)		134.101	107 17				Ì	Ì	-
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1		VAMILELLA-COSTER VIRILS (ACYCLOVIR-RESISTANT STRAIN 40A2)	97-216								
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- 1		Γ	197.316	İ	Ì	-			1	!	-
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	MUCLEUC AND PROTEIN	MEASTER VIPES (STRAIN TALL F.)	40.50						•		:
14. W. 16. V.	MACLECCAPSID PROTEIN	MEASILES VIRUS (STRAIN YAMINGATA. 1)	40.34	<u> </u>	l :	:		1	:	:	:
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3	MUCLEOCAPED PROTEIN	MONO'S VIRUS (STR 4IN ATTVALLARA V ACCINE)	136.170			İ	Ī	-			
3	MULEOCAPSID PROJECT	PROSPECT HILL VIRIS	1 7 2	311.3%	4.11	100					
¥ 3	MUCLEOCAPSID PROTEIN	INDIAN PALAINFLIENZA I VIRIIS (STRAIN CO)	2.50	101-103							ĺ
	MUCLEOCAPSID PROTEIN	HUMAN PARAINFLUENZA I VIRIUS (STRAIN WASHINGTON 1959)	15:50	107							!
Ι.	MUCLEOCANSID PROTEIN	BOVINE PARAINFILIENZA J VIRUS	161.114		İ		-	!	1	;	
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	MACLEOCATED PROTEIN	PURMALA VIBIG CONTRACTOR NAMED IN	ī	- 177	Ì	-			İ		
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.:	ACCEPTANCE OF THE PROPERTY OF	AUPT VALLEY FEVER VIRIIS (STRAIN ZIII S48 A112)	2							!	
_ 1.		SENDAL VILUS (STRAIN 2 / 1105T MUTANTS)		10-103		j 		1	<u> </u>	:	
		SENDAL VIRUS (STRAIN ENDERS)	43.50	1013							<u> </u>
PHCAP SUIDH	MUCLEOCAPSID PROTEIN	SENDA! VIBUS (STRAIN HARRIS)	5	1 191-91	-	<u>;</u>				Ī	
		SENDAI VIRUS (STRAIN Z)	100	101		-		-	1		
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	MEGATIVE FACTOR	HIGHAN BOATHOTHETICIENCY VIRITS TYPE 2 (ISOLATE HOD)	£ 0	<u>-</u>			Ī		İ	İ	Ī
٦		HUMAN BENADOFI ICIENCY VIRUS TYPE 2 (1501, ATE ST)	100			1	Ī	Ì			1
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-	GENOME POLYPROTEIN	BOVING ENTRICOLET (STRAIN VC.1.2)			100	Ī		Ì	Ì		Ī
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		DEPARTS VIRIN 14TE (VIRAIN IANIAILA)	141.00	11.016	1117-1119	1.4.14.1	1176 1 FW.	7. -		100	1
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	PA VPP CEN	POUL-AND-MOUTH DISEASE VIRUS (STRAIN A.)					-				-
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		IRPATHIS CYRUS INOLATE RK)	13:13	141.144	039 619	-	1111.111	341.3446	2836.3686	100	-
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		IEDATHIS EVIRUS (1501.A 1E IR. 11)	Τ		7			92.5	Ž	_	199
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7	MONETAL FIRST POLYPROPERS	POLICY TO STRAIN MAHON Y)	ŝ		_		_			İ	- 								
٦.		NEWS CHARLES AND THE THE VIEW (STRAIN TRINIDAD ONLY	W-107	2 2	1414	101.00	111111	1971-1974	1177 7144 2	1311-1066									
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	Pircfilli	All Virgon (No Becteriophages)		П		-	П		Г	Т	
THEBANE	ZAOTZIN	YIRUS	O NEAL	7	72.50	7	T STEP	ANTA-	AREA I	ABLAL	4R[41.
	NON-STRUCTURAL POLITICAL PROTECTS	TELLINE CALIFORNIA (STRAIN CTON TIV)		1	ŧ	200		1	!	:	:
PPOLY ICYTE	NON-STRUCTURAL POLYPROTEIN	DELINE CALICIVIETS (STRAIN FOR		115.515	1 200 616	134.351	131	1547.756	-	;	İ
PROUNTENBU	NON-STRUCTURAL POLYPROTEIN	INFATITIS E VINUS ISTRATIV BURNIAL	250.766	374.139	i		-	-	-		1
POLN IEVAR	NOW STRUCTURAL POLYPROTEIN	IGPATITIS E VISUS (STRAIN MEXICO)	330 744	1333.636	ļ	İ		!	i	Ì	:
	MON-STRUCTURAL FOLYPROTEIN	MEPATITIS E VINUS (STRAIN MY ANNUAL)	30.00	1274.1761	!	<u>-</u>					
	HOM-STRUCTURAL POLYPROTEIN	(CEPATITIS E CIRUS (FIRAN PARISTAN)	109.765	231.173	: !	•		:		!	
PPOLH MIDOV	MONSTRUCTURAL PALYPROTEIN	MIDDELBURG VIRUS	41.512	628.643			_			•	
DANON MON	MONSTAUCTURAL FOR YPROTEIN	D HYONG-HYOMS VIRUS (STRAIN GULU)	80.107	Š	-	19					:
A CAN	HON-STRIKCTURAL POLYPROJEJN	RABBIT LENGTHINGIC INSEASE VIRING	96.180	22.22	377.170	_	119.1	330 6.71	1		
	MON-STRUCTURAL POLYPROTEIN	RABBIT IBAKIRRIAGIC DISEASE VIRUS (STRAIN V.191)	13.135		_	-					
_	MONSTRUCTURAL POLYPROTEIN	ROSS ELVER VIEUS (STRAIN NE 1062)	19-106	3	2111.2128	3077-1017					i i
	MONSTRUCTURAL POLYPROTEIN	ROSS RIVER VIRIUS (STRAIN 741)	187.797								
¥	HOMET BUCTURAL POLYPROTEIN	RUBELLA VIRUS (STRAIN THE RIEN)	14.19	1			1100	174.11	1015-2057		
	NOWSTRUCTURAL POLYPROTEIN	SEMLIKI FOREST VIRIS	901-16	617.64)		317.71		!			
	NONSTRUCTURAL POLYPROTEIN		20 646	0511.0211		141.316.1					
	HONSTAUCTURAL POLYPROTEIN	SINDBIS VIAUS (STRAIN ILEST)	620.646	1123.1110		190.001	1912 2716	711 1711	<u>i</u> !		!
	ANA NEMLICASE POLYPROTEIN	ECGPLANT MOSAK VIAUS	106.133		<u>.</u> ! :		 ! !				:
	ANA REPLICASE POLYPROTEIN	ONORGS YELLOW MOSAIC VIRUS	101.111	276.176	!	<u>.</u>	:	;		,	
	THA LEFT LEASE FOR YPHOTEIN	TURNIP YELL OW MOSAIC VIRITS	111.111	110 910	2011	Ì	-		İ	:	!
	BMA BEN N'A CE NOS YOU OFF IN	TERMINE VELLOW MOCKAIN VIRING FRANCO AND	111111	110.01			1	:	:	-	
ANAL STORY	ALICCIAN NO STATEMENT	THEN YELLOW MOCAL VIEWS HOLD ATE I VAICE	117.11		100	:		:	:		
VALUE AND VALUE	STRIKETIMAL NO VPROTEIN	PASTORN FOLING BACEPILATITIS VIRING	16.30	211.230	9	İ	ĺ	İ	-	Ī	
100 6 88 604	CHAINTING AT EN VER CTERN	CASTER ENTERINE COLUMN	1			İ	Ì	İ		!	:
T	MANUAL TO CASTACATA	CASTERN EVOING ENTERTINE VINES				1	Ī		-		
Ĺ	STRUCTURAL POLYTROIEIN	VEREZUELAN EQUINE ENCEPHALITIS VIRUS (STRAIN TC-11)	1	276.763		-	İ			ļ	
7	STRUCTURAL FOLYPROTEIN	VENEZUELAN EQUINE ENCEPHALITIS VIRUS (STRAIN TRIMIDAD DON	7.	24.243	3	-	-			_	_
200	STRUCTURAL POLYPROTEIN	AVIAN INSECTIOUS BURSAL DISEASE VIRILE (STRAIN 15/70)	20	İ		-	Ī		!	:	
	STAUCTURAL POLYPROTEIN	AVIAN INTECTIOUS BUBSAL DISEASE VIRUS (STRAIN AUSTRALIAN OF	900-972				Ī	İ		i	-
DAGE COL	STRUCTURAL POLYPROTEIN	AVIAN INSECTIOUS BLINSAL DISEASE VIRUS (STRAIN CU.!)	600.033		-		-	:			
	STRUCTURAL POLYPROTEIN	AVIAM INTECTIOUS BURSAL DISEASE VIRUS (STRAIN MICTOR)	11:03		j	1					
	STRUCTURAL POLYFIOTEIN	AVIAN IMPECTIOUS BURSAL DISCASE VIREIS (STRAIN STC)	2		İ	7			-		-
TOTAL ON PART	STRUCTURAL FOLYPROTEIN	CATCACATORC VINCS (STRAIN COLO)	100		1		Ī	İ	-	!	
ŀ	STRICTURAL FOLTPROTEIN	POSS MAYER VIRID (STRAIN 143)			-	Ì				i	1
7	STRUCTURAL POLITICAL PRINTERS AND THE PR	TOREST A VINCENT STATE OF THE PROPERTY OF THE	100	1	· · ·	1			1	:	•
	STATE OF THE STATE	ACCEPTED TO CONTRACT OF STATE			<u> </u>	1	1				
	CHELLING AT BAN VERNING	THE PARTY AND THE PARTY NAMED IN		920	İ					İ	
ı		SELECT CONTRACTOR			100	İ	Ī	İ			
	TELEFRICAL POLYPROTEIN	GINDSIG VIBILS (SURINGE OF KILLING) STRAIN FOR NOVE 51.11					Ī	ĺ		Ī	
POLI SPOV	STRUCTURAL POLYPROTERY	SINDRIS VIRUS (STRAINS LIXSP AND HRLP)	11.51		Ī			Ì		Ī	Ī
	STRUCTURAL FOLYPROTEIN	WESTERN EQUINE ENCEPHALITIS VIRUS	15:91	166-604		İ				i	
	POL POLYPROTEIN	A VIAN ARTICUL DENDOMIEL IOSIS VIAUS	163.103		_					 	
3	POL POLYPROTEIN	BABOON ENDOCENCUS YIRUS (STRAIN M?)	526-544	199.174		1000-1001					
	POL POLYPROTEIN	BOVING DOADNODE/ICIENCY VIRUS (ISOLATE 106)	9-10	2	=						
- 1	POL POLYPROTEDS	BOVING MAUNON FICIENCY VIRUS (ISOLATE 17)	100	741-768	2						
ادِ	POL POLYPROTEIN	BOVING LEUKENDA VIRUS (AUSTRALIAN ISOLATE)	٠ <u>٠</u>								
- 1	1	BOVING LEUKEMIA VIRUS (IAPANESE ISOLATE BLY-1)	23.50								
•		CAPAINE ANTHRITIS ENCEPHALITIS VIRUS (STRAIN CORK)	11716	1							
POL CALVC	:	CALL FLOWER MOSAIC VIRUS (STRAIN CM. 1841)	2	ī	₹ -						
•		CAULD LOWER MOSAIC VIRUS (STRAIN OAT)	25.17	- 1	4	Ì					
		CALL DE OWER MOSAIC VINUS (STRAIN RBC)	2	ī	ī		Ì	ĺ		İ	
- 10112	EN3-122-167-107-107-107-107-107-107-107-107-107-10	CAUCHEUMER MOSALC VIRILS (SIRAIN STREET)	20.00	67.51			Ì	Ì	1	Ì	1
		CARNATION ETCICED RING VIRIES		T		Ì	Ì			-	
7	PUTATIVE POLYPROTEIN	CONDUCTION YELLOW MUTTI E VIRUS	20.02	19	1606-1633	1841-1848	Ì	ļ	Ī	ĺ	
ï	POL POLYPROTEIN	EQUITME THAT ECTIONS AMENITA VIBUS (CLOME 1)649	93-486		•			Ì	Ī	Ì	Ī
	POLYPROTEIN	FOUNDE IN FCTIONS ANT MIX VINUS (CLONE CLY)	433.436			Ì	Ì			Ī	Ī
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	POL POLYPROFEIN	EQUINT THE ETIOUS ANEMIA VIRUS (150) ATE WYDAING)	15:35	ī	ī	ī	+		ī	1	
1	POL POLYPROTEIN	FELINE CNIXKLENDUS VINUS ICT.	,	9(1.951	<u> </u>	:	:	!	:	:	•
PPOL PIVE	POL POLYPROTEIN	I EL INE INMINIMODICETCH NEY VIREIS (ISON, ATE PL. I ALUMA)	ī	33.73	:			:	:		
ŀ	POLYPROIEIN	FEI INE INCHINODELLICIENCY VIRUS (ISOLATE SAN DILGO)	1	:	-		! : i		i	i 1 -	
	POL POLYFROTEIN	FEI INE INDICHOUSEICIENCY VIRIS (ISOCATE TAIT)		;	31.55	30.15				Ī	1
PPOL FLAVO	ENZYMATIC POLYPROTEIN	FIGWORD MUSAIC VIRUS (STRAIN (144)	191.213	181 190						.	
	POL POLYPIOTEIN	FONAN SPUNARE FRIVIRUS									İ
PPOL DALV	POL POLYPROTEIN	GIBBON APE LFUXENIA VIRTIS		971.901	1018-1031					ĺ	-
	POL POLYPROTEIN	HUMAN F-CELL EFIXENIA VIRIJS TYPE I (STRAIN ATK)	330-346		<u> </u>			İ			:
PIOL HITLIC	POL POLYMOTEIN	HUMAN F.CELL FUKEMIA VIRIIS TYPE I (CARHINEAN ISOLATE)	330-344			.			i i		
	POL POLYPROYEIN	HAMAN T CEI L'LEURENIA VIRUS TYPE II	609-627	<u> </u> 	<u> </u> 	<u> </u>					
t t	POL POLYPROTEIN	HEMAN INDAINOISE FICTENCY VIALIS LYPE I (ARVZ/SF2 ISOLATE)	199		<u>-</u> -	İ		Ī			
ſ	POL POLYPROTEIN	HARAM BOHINGOEFICIENCY VIRUS TYPE I IBHIO ISOLATE	T	177.104	Ì	Ī				Ī	
1	POR POR VERDIERA	TANAM INC. DOORS INTERNATIVE TARES SESSEES ARES	ī			1				Ī	İ
ı		MARKET SCHOOL STATE OF THE SCHOOL STATE SCHOOL STATE SCHOOL SCHOOL STATE SCHOOL S		İ	İ	i					1
1	TOL PARTIEIN	HUMAN INUMUNIAR FILLENCY VIAUS 177E 1 (HAU ISULATI.)	ī	-	- <u>'</u>	-			1	-	
1	POL POLYPROTEIN	HUMAN DAMUNODEFICIENCY VINUS TYPE I (E.I.I ISOLATI)	=	10 110		-					!
PPOL HVIE	POL POLYPHOTEIN	HUMAN DAMINODELICIENCY VIRUS TYPE I (11 KB) ISOLATE)	100	 		-			ĺ		
Ĺ	POLICE PROPER	HEALAN BARINGSHICIENCY VIRIAS 1978 1 JIRCSP 1501 A751	2	İ	<u>:</u> 	İ					
1		HINAN BOAR MODELICIENCY VIRUS TYPE I DAAL ISOLATEL	1	İ	:	†		Ī			
12		INDIANA ISAM MANAGERIA (SAME) VIBING TOPE I ARALICOLATES		i	<u>-</u> 	Ì		Ī			Ī
1		THE PROPERTY OF THE PARTY OF THE PARTY OF THE	Ī	-	1	1	Ī	Ī			İ
	TOT TOT I WAS A STATE OF THE PARTY OF THE PA	HUMAN MANUACOURTICINA VIRUS 1176 1 (NEW TOTAL) 130CATE)	1		1	İ	Ì			1	
		HUMAR INTRIMEDIALIER TO VIRUS 117E I (MUR 130LA14)	Ī		-				j		
.		HUMAN INDURACIONS ICIENCY VIRUS LYPE I (DVI ISOLATE)	Ī		1						
		MUNAN MONTHUME INCIENCY VIRUS TYPE I (PVZZ ISOLATE)		817 879		 					i
1	POL POLYPROTEIN	IRINIAN BOARMODE! ICIENCY VIRUS TYPE I (AFAIAT ISOLATE)	200	<u>. </u>		-		İ		!	-
ı		INPARAN LAGRANDEFICIENCY VIRIJS TYPE I (STRAIN UCANDAN / 150	Ĺ	<u> </u>	-	i 			-		-
1		HENDAN BOARNODER KIENCY VIRIUS TYPE I (22/CDC-234 ISOLATE)	L	910 010	i	-				-	
PPOL IVIZE		III MAAN DOADWODEFICIENCY VIXIIS TYPE 1 (ZAIRE 4 150LATE)	Ī	-	İ	ì	Ī		ļ		
ı		HIRAM DOMINOUR HOLENCY VIRIUS 199E 3 (150), ATE BEN	Ĺ	207.014	-	-		İ	i		
i.		HIMAN INDAINOBERCIENCY VIRIS TYPE 1 (150) ATE CANSI	Ĺ		i	İ	Ī	-	-	İ	İ
İ		HIMAN BOADNODE ICIENCY VIRUS TYPE 2 (150), A TE D1941	L	025.052		-	Ī				
ł		HINAM DOMINODEFICIENCY VIRUS TYPE & HISOLATE DIDE TO	Ī		İ	+	Ī	Ī	Ì	-	-
1		IN THAN DOUNDE FICIENCY VIRUS TYPE 2 11501 ATE GIANA. 11	Ĭ	19.014	İ	ĺ	Ī				
1		IN LAN BOAR BOOK FILEBROY VIRILE TYPE 2 (150) ATE MILL 21	Ī	ī	718.18	İ	Ì	Ī			İ
1		INDIAN BARBANE LIENCY VIEW TYPE FIRM A TE BOOM	1	T	<u> </u>	İ				Ì	
PROUNTIE	HOL HOL VALOTEIN	IN BLAN BARA MODES ICIENCY VIBIA TYPE 7 INCH ATE WILLIAM	Ī	100	İ	İ	1	Ì			
1		IN BLAN MACHINE CITIENTS VIETA SVEET 11501 A PE 411	Ī	1	1	İ				İ	Ī
PIOL DILL	PUTATIVE FOL POLYPROTEIN	IGALISTER INTRACISTERNAL A PARTICLE	Ī	1	-122.037	İ	Ì		1	1	
ANG DES	PUTATIVE FOL FOLYPROTEIN	MOUSE DITLACISTERNAL A. PARTICLE	ī		Ť	1000	98. 99	Ī			Ī
L	PROBABILE NOT POLYPROTEIN	MOUSE INTRACISTERNAL A. PARTICLE	T		ī	Ť			Ì		Ĭ
VAN KAV	NA NO VPROTEIN	CHEEP PIR MONARY ANGUSTA VIOLENIE VIA ACCIED TO CHEEP AND	T	7					Ì	j	
L	POL POLYPROTEIN	MONE CELL FOCISE FOREITH AND PERFECT A VIEW AND A FERTINAL	ī	Т		1	Ī	Ī		İ	
	POL POL VPROTEDN	AKE KIRDE I EIRSMIA VIRIN	ì	151 344	İ	İ		Ī		İ	;
1	POL POL VPROJEDI	ANY MARINE LEGIC ENTRY VIRING		÷	21917	100	-	1		:	;
PPOL LA VCB	POL POL YPROTEIN	CAS OR E NOTIFICE LEINER LEINER LEINER	ī		_			Ī		i	;
	POL POL VPROTEIN	FREND MORNAGE IN FACE VIBING A COLLA TE 43.	Ī,	ŀ		1917	Ī	Ī	Ī	Ī	
	POL POLYMENT BY	PRINCIPLE CITE CALL CIDE CALL CALL CALL CALL CALL	Т	i				Ì			
	POL POL VPBOTE NA	THE NOTATION OF THE PARTY AND THE CASE AND DESCRIPTION OF THE PARTY OF	T	3			1	Ì	j	i	
	POL POL VPROTEIN	ACCIONEY MUCHAEL FOR FILLY VIRILE	ï	-	-				İ		!
PPOL NE VIID	POL POLYPROTEIN	RADIATION MITUME LEUKENIA VIRUS	100	;		100		İ	į	-	:::
	POL POLYPROTEIN	RADIATION MINUNE LEUKINIA VIRUS (STRAIN KAP) AND		•			İ	1		i	1
L	POL POLYMOIEN	AIOUSE MAKONARY TIMIOR VIRIUS (STRAIN BRE)	210	ī	!	İ	İ	Ì	Ī		
A	POL POLYPROTEIN	SUMAN MASON-PRIZER VIRUS	741.763	1	i	Ť	İ		!	:	
5	POL POLYPROTEIN	OVINE LENTIVIAUS (STRAIN SA ONIVY)	ī	199 4111 41	12 647	1901:100	İ	ĺ	i	!	!
	POL POLYPROTEIN	ROUS SARCOKIA VIRUS (STRAIN PRAGUE C)	1		ī			Ī			-
1	POLYPROTEDI	RICE TUNCAD BACILLIFORM VIRIIS (RTBV)		1036-1083						İ	Ī
Prof. R Tave	POLYMOTERN	AKE TOWING BACILLINGAL VIRUS (1501, ATE PHILIPPINES)	116-100	M. Init					<u>-</u>	İ	İ

	PROTEIN POLYMOTEIN	YRUS	-			_					
	POL POL VPECHEN										
		SAGAN SOAMY VALUE IT TO SEE IT	3	3	755	ABEAN	AB GA	AMEAS	ABEAI	AREAT	ARCA :
ĺ		SOUTH FOALTY VIETE STORE IN STRAIN THE	9		2	2					
		SERIAN SCHOOL SERVICE STATES OF STAT	2			978 401					
ł		THIS IN THE STATE OF THE STATE	9.913			-				-	
1		STATE OF THE PARTY (ACM) ISOLATE)	111.726	070-970				1		į	-
1	200	SIMILAN IMPRIMODE VICIENCY VIETS (150LATE AGM / CLONE CRITI)	524 EE							1	
ł		SIMIAN INDAMONT FICTENCY CIRCIS (TYO. 1 KI) ATES	124.741]	-
ŀ		CHING ANZEE INSAL MODE FICIENCY VIRIS			-						•
		SEMIAN INDIANACIA I PERSON CONTRACTOR TO PERSON STATEMENT		j				;			
POLIVE		THE PERSON NAMED IN COLUMN TO SERVICE THE PERSON NAMED IN COLUMN TO SE	60.00	97.					!		:
ĺ		STREET THE STREET WILLIAM TO STREET AS STREET	10.01	11 mm.	:	:	:				
ı	TOUR TOUR IN	SMITAN MONTHODE ICIENCY VIRIES IN SUN 1504 ATEN	100 001		1	!	1	i		1	į
i		SMAN DOG NOTE IN MINO VIEWS IN THE STATE OF THE PARTY OF			31	! !					
ł		CHANGE TO THE PARTY OF THE PART	141-170	12:19		_					
,		SIMILAN IMPROVODE ICIENCY VIRTIS (PRIMICIS ISOLATE)	146.373	18.54							
ı		SQUIMEL MONKEY RETROVINGS	140 340	1	:				-		
PPOL SMSAV		SIMIAN CARCINA VIBILE		:		. !					•
PPOL EDCINV	FRZYMATIC PALVPENYELS		2 2			!	!				
Ĺ	See Leading to the second seco	AND IN CORUS	3			*					
ł	TOL FOLLTRUIEIN	SIMLAN RETROVIATIO		!		İ					
	POL POLYPROTEIN	VISNA I SAMIONETTE JOHN TILL THE STATE OF TH			<u> </u>						
PPOC VILVI	POL POLITICISM		Ŕ	200	<u>\$</u>	:					İ
۱	120.045, 104.00	VISINA LEMINATURE (STRAIN (STATCHONE LVI. IKS))	41.507	3	18:				Ì	1	
ī		VISNA LENTIVIRUS (STRAIN 1916 / CLONE LVI. 18 43)	100								
_	LANGE STRUCTURAL PHOSPHOPROTEIN PP150	MUMAN CYTOMETAL DVIBILE (CITATION CONTO)				1					
_	TAKO STRUCTURAL DUNCSINIBATION	THE PERSON OF THE PERSON AND THE PER	2			-		į	!!	i	
1	STORY OF THE PAST	HUNCH CHICALOVIAUS (STRAIN AD169)	100		!						
-		HEAPES SUPLEX MAUS (TYPE 6 / STRAIN GS)		1				_		ļ	
_		INDIAN CYTOMETER AND STREET STREET									
_		THE PERSON OF TH	11:33							j	
•	The label to see the second se	THE CALICAL CALICALLY STRAIN TOWNED	101.333		<u> </u>			:			-
-		PLALAN CYTOMEGALOVINIIS (STRAIN AD169)	10.10			-	Ì		į		
VIEW CONTRA		MOUSE MANAZER TIRADE VIEWS AND BEST			-	•					
_	PAOTEN PRI	MONTH PARTY OF THE								į	i
		MOUSE MARTINEON VIRIS (STRAIN CA)	10.00			1	Ï	Ī			1
200		MOUSE MANDAGE TIMES (STRAIN CR)	1			Ī	Ī	Ī			
	The second secon	MOUSE MANDARY TIMOR VIRIS ISTEAM CE.	17.55	İ	i						
-		HARVEY MINING SARCOMA VIBIG								İ	
	TRANSFORMING PROTEINS PSI AND PSE	DALLING A PLANCALL MALES	2								
_	REPEAT ELEVENT PROTEIN	A STATE OF THE PARTY OF THE PAR	2						Ī	1	İ
•	A LANGE OF STREET STREET	CAMPULE 13 SONORENSIS VIRIIS	1			İ				-	
~	U AMPICIA RESISTANCE PROTEIN	CSTRAIN WAL AND ISTRAIN COPENIACIEN					İ				
_	AUTAMORCO RESISTANCE PROTEIN										
_	NAMES		***							İ	Ī
_	KEV MOTEIN	THE PROPERTY OF THE PARTY OF TH	2.17							Ì	
١	Photograph solding history and he had been to a ser-		45.77					Ì	Ì	Ì	
7		ANTICAM SWING FEVER VIRUS (ISOLATE NIALAWI LIL 201)	1	169.310	1917.00		Ī			İ	
7	INCHICATION INDICATOR	Ī									
╗	REMONECLE OF ENEDINC TASE	4 A D I A S	ī								
	IBONUCLEO I IDE REDUCTA SE		Ī	200							
Г	RIBORUELEOTOR RETAILTACE		٥					Ì	İ	ĺ	
MINISTRACTION OF THE PROPERTY	PIRONG BOTTOM BETAKEN ARE	LOUIS MECHANIST IN THE I STRAIN ABOVE	20.00	366-240	P648.849		İ		Ì	Ī	Ī
ī	STATE STATE	PERCESVIKUS SAIMIRI (STRAIN II)	136-151					Ī	Ī	1	
ī	BOWING REDUCTASE	VACCINGA VIBUS (STRAIN COPENIAGEN)	15.95	-	-				į	-	
-	RIBONICE ESTIDE REDUICTASE	VACCIDITA VIRUS ISTRAIN WRI		!	!:::			_			1
-	BONUCLEOTOB REDACTASE	VARIOLA VIRUS		į	İ				İ		i
~	BONTXLEOT DE REDUCTASE	VARIOR! A VOCES USES								İ	
ī		Charles and Control (SIRAN HINAS)	14.50	221-247	256.780			İ	Ì		1
į.		CALCIN BACK VIRUS (STRAIN 895.1)	36.23		1			İ			İ
ī		TENES SINGLEX VIRILS (1 YPE 1 / STRAIN 17)	Ī	1	İ				j	_	_
ī		ICEDES SOCH EX VIRILS (1 VPF 1 / STEAM WOOL									_ i
		TELEGRAPHY VINITE IN CASE STATE AND	1	2.67	2.01				<u> </u> 		
_			9	13.21							
ī		POLINE PERSONNEL CONTRACTOR						İ	İ	İ	
PRINCIPAL VICTOR		COUNTY OF THE STRAIN ARAP	Г	351.233			İ	Ì		-	!
1		IENESVILUS SAIMIRI (STRAIN !!)	11:11	İ		-	İ	İ			į
STATE TO SECOND			ī	111.311	1	-		Ì	Ì	-	
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NACO VACO	RIBONUCLEOTIDE REDUCTASE	VACCINIA VIRUS (STRAIN L.IVP	3							-	
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			134-206				İ		İ	ļ	
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MCCENE	P11CT1.219	All Viruse (No Berrertaphuger.)	_	-	г		Г	Г		Г	Γ
THERE	PROTEIN		NIA.	19 TY 191	BREAL AR	ARGAS OF	OBLAL	AFCA9-	ARIAL	ANVA	AREA
MURI VARV	RIBONACL FOTIDE REDUCTASE	DIROCA VIRUS	Ī	-	:	<u> </u>	- :	:		-	
OVZV CALL	MICHALLED TIDE REDUCTASE	MUCELLA COSTER VINOS (NIRAIN DURINA)		•	:	-					
AVEW ANDWE	CALL SERVICE PROTEIN RIPASE TRANSFORMING	IAM BOUS ASSOCIATION VIAIS FULL	1		12	-		:			
TANK VALLY	BAA POLASSOCIATED TANACCEPTIVE COLUMN	THE A CIPIES THE AND AND AND ADDRESS OF THE PRINCIPAL OF					-	Ī	!	-	
PERO! VACE	PANA PRINCIPLE BINA POL 143 ED POL VERPTIDE	CCIMA VINIS (SURAIN COPEMIACE N	T	04.170	8	71017	İ			Ì	
PAPOL VACCV	DNA DOLECTED INA POLYMONASE 143 KD POLYP	E VACCINIA VINUS (SI PAIN WA)	Ī	200	•		Ì	İ		-	
PRPGI VARV	DHA DURECTED LWA POLYNERASE 147 KD POLYP	MOLA VIRUS	İ	*	1	101.500	i I		:	!	:
PRJOJ CAPVK	C DNA DIRECTED RNA POLYNERATE ISI KD POLYPE CA	PRIPOXVIRUS (STRAIN KS-1)	13.79	2	,	_					
MAD COMPX	DWA-DIRECTED RNA POLYMERASE 111 KD POLYP	E COWPOX VIRUS	200	ž:	100 00	-	-	:	:	:	:
PRPOS VACCV	ONA DIRECTED ANA POLYNGRASE 111 KD POLYP	E VACCOMA VIBILS ISTRAIN WED AND ISTRAIN CUFFNIAGILM	2	2	-:			:	:	į	:
PRIOS VARV	DNA DIRECTED RNA POLYMERASE 111 KD POLYP	E VARIOLA VIRIES	20.00		ś	!				1	:
TAN VACE	ONA DESCRED ANA POLYNA FASE 19 KD POLYN	PIVACCINA VIRUS (STRAIN COPT 2014 of 14)		:		-	•		•		
	DAA GREETTED RAA POLYMERASE 19 KG POLYT	PACCINIA VINUS (STAZIN W.K.)	į		_	_				_	
1	CHANGE CILD AND PARTHERANE IN RIT FOLTON	AIOLA VIAUS	-		-	_	_				
1	CONT. CHEROTER SIZE TO START THE TANK THE POLICY OF THE PO	TANCTURE VINCE STATE OF THE STA		:		_:	•				
200	CHA CHARLETTE BAY BOY WAS IN A ST THE STATE OF THE STATE	DIOLA VIBILE			_	<u>.</u> .;	_	_		_	
PERSONAL PROPERTY.	SALE DE LA SELECTION VICE DE LA CONTRACTOR DEL CONTRACTOR DE LA CONTRACTOR DE LA CONTRACTOR DE LA CONTRACTOR	THE PLANT OF THE PARTY OF THE P	_	<u>:</u>	<u>:</u> !	+	Ī	•	:	-	:
	TOTAL STREET TOTAL BOY CONTINUES.	THE CALL AND THE COLUMN THE COLUMN THE CALL AND THE CALL		100		11.0	9111				
	THE PROPERTY OF THE PROPERTY O	·	3					_		_	
77	San Britishen Sus bee Sans it	Strain plant was the strain of							1	:	:
	AMA-UNIA CIED MAR POCI PICA SE	EQUINE ANITALIS TO SET TOTAL STATE S	ī		_		∹				
THE CHANGE	MAA-DIRECTED AMA FOLYMERANE SUITINE FO	INCHE VIALES (STRAIN INCHES INCHES)	 	E :			-				
		VIXUS (STAVIN		i	<u> </u>	. <u>.</u>	1	!			1
W WE	TANA DIRECTED DAY POR PARTASE SUBURIT PI	INTLUENZA A VIRUS (STRAIN AMELINGATIVA)	20.00	i	; 	1	-	-		::	-
ALCO LABOUR	ICA-DIALCTED ICA POLYMERASE SUBUNIT PI	1		: : :		<u> </u>	<u> </u>	-	İ		İ
PRIO LAGO	INA DIRECTED ENA POLITICIA SI DICINI PI	INPLUENZA A VIEUS (STRAIN ACCULLATAR YLANDYION)	74.76	:	-		1	1			:
THE PARTY	ANA DIRECTED LONG POLITICA AND STIBLING PL	INTURKA A VIEW (STEAM ALCUMALATION)		<u>:</u>	 	-		!	:	:	٠
	ANA-CHARLES HAN FOLTMENASE STRING FOR			<u> </u>	-	.		i	İ	-	:
I.	ENA SITE CHES BUY FOL WELL IT SIMILARY PI	ZI III		1	<u> </u> 	-1	1			!!	
10.00	BRA DARFORD BNA POLVAGBACE SIMILARIO		342.367	<u>:</u> 	!		-	İ	i	-	!
HIN ME	KHA DIRECTED RIVA POLYNGRASE SURINIT PI	THE CENTA VINIS CS RAIN AS ENINCHALVISCO 251	244.762	<u> </u>	1	!	-		-	- 	!
HIN ME	KNA DIRECTED KNA POLYNGKASE SIMINIT PI	IS IS IEAN	344.363	<u>:</u> 	-	<u> </u>	i	Ī	į	Ī	-
PUDITURES.	APA DIRECTED ANA POLYMERASE SIMUNIT PI	A VIII (S)	344.341	į	<u>i</u> :	<u>!</u> {	<u>:</u>	İ		İ	
HED! WES		A VIRUS (STRAIN	144 241			<u> </u>		İ		İ	
HAD! WHE		Z S S S	191.141								
MAN MAN	INA DIRECTED BAY POLYNGRASE SUBLINIT PI	VIRIS CARAN	36.36		1	-					
1 THE PERSON NAMED IN COLUMN 1	3 12	INCLUENCE A VINCE STANIA ASSESSMENT AND A STANIA ST		<u>:</u> į	<u> </u>	<u> </u>	i	i	j	-	
1011	MAN HOUSE THE BAY WAS A SUBJECT OF	A VIEW CONTRACTOR		1 - 277.77	1	<u> </u>	İ	Ì	Ī	Ì	Ī
PREDI LAWAL	INA DURECTED INA POLYNERASE SUBUNIT PI	A VIRUS (STANIN	144.767	<u> </u> 	<u> </u> 	<u> </u>		İ	-	Ť	
	INVA-DIRECTED INVA POLYME MASE SUBLINIT PI	A VIRING BIRAIN	100.00	<u> </u> 	<u> </u> 	H	i	İ	İ	İ	ļ
	AMA BURECTED ANA POLYNGRASE SIMINIT PI	DALUENZA A VIRUS (SIRAIN ASWINEJNING KONG/126/12)	1 1 1 1 1	<u>!</u> 	<u> </u> 	<u> </u>	T		-	i	-
	ANA DIRECTED RIVA POLYNGRASE SUBUNIT PI	A VIRUS (STRAIN	144.363	<u>i</u> 	<u>:</u> -	<u> </u>	1	İ	i	İ	1
	AMA-DIRECTED AMA POLYMERASE SUBLIMIT PI	A VIRUS (STRAIN	344 363		<u> </u> 	<u> </u>		<u>.</u>			
PRINT DONC	AMA-DURECTED ANA POLYNGRASE SUBUNIT PI	B VIRUS (STRAIN BLANN ARBORUING (COLD ADAPTED))	105 233		<u> </u> -	<u>_</u>		İ			
PRESI DOM	AMA BOLECTED BUA POLYMERASE SIMINIT PI	# VIRLIS ISTRAIN BYANN ARRORLING (WILD: TYPE)	305.222		<u> </u>	<u> </u>	<u>-</u>			İ	
TAN DOLE	RMA-DIRECTED ANA POLYMERASE SUBLINIT PI	B VIRUS (STRAIN BAFE/40)									
200	ANA CIRECTED ANA POLYMERASE SUBINITY	C VIRTIS (STRAIN C/11/50)	<u>-</u>	10.50							1
PR. 17.	ANA DIRECTED ANA POLYMERASE SUBUMIT PI		115.515						: .		:
	ANA DESCREDENTA FOLYMERASE SUBINITY	A A VIRIIS (STRAIN AFOWL PLACUE VIRUSROSTOCK//1)	- 15.75	<u> </u>	:	: ;	1	-		-	:
	ANA DIRECTED KNA POLYNERASE SIMINIT P?	A A VIRIS (SIRAIN ACCULIANARYLANDYDOUT)	18.81	<u> </u>	i :	<u> </u>	<u>:</u> 	-	!	i	Ī
_ 1	ANA-DIRECTED RNA POLYMERASE SUBINIT PI	A A VIRUS (SIRAIN AN QUINLA ONIX DALIAIS)	116.557	<u>' </u>		<u>!</u> 			j	İ	:
PLUT ME	RNA-DIRECTED RNA POCYNERASE SUBUNIT PI	A VIRUS (STRAIN A.E. NINGRAD) 14:51)	114.553								
PROFES INC.	ANALISE CEL ANA POL IMPRANE MINISTER	INTEREST A VARIOUS OF FAIN AN ENDINABLE SUPPLIES (1)	4	1	$\frac{1}{1}$	\dashv	1	1		1	

PCCLFC	PHETER	All Virgan (No Beststand)			ľ						
LEBANK	ZNOILIN		ARGAI	SELA?	ARTA	- ZY3#Y	101.4	ARIAG	A HI A S	THEY BE	AHEAS
100	RNA-DIRECTED RNA POLYNIE I ASE SIBIRIT PE	INTLUENZA A VIRIJS (SIRAIN AFINTALLAI OFRI AVITAVI)	134.537	Ϊ.		!	ı	ī	7		!
PROS IAPUE	티	INSTITEMEN A VIRIES (STRAIN ANDERTO RICONVIA)	114 517			i			!	:	<u>:</u>
	zi	INPLIENZA A VIRIS (STRAIN ARUDDY TURNSTONONIN VICESLY WITH	25.53			-					1 1
	2 iz	MALLENZA A VIRIS (STRAIR ASSIGNMENTS)	554		!	į	İ				
PALES IAWE		THE PARTY AND THE PARTY AND THE PARTY OF THE	3	-	-	İ		į			+
PLUT TABLE	Z	CONTRACTOR AND AND AND AND AND AND AND AND AND AND				i	İ	!			1
PREPT TAZHE	2	INFLUENZA A VIRIIS (SIRAIN ASWINGAIONG KONG) 19623	11.53		:		i	!	:	=	
16501 14211	2 2	INTLUENZA A VIRIIS (SIRAIN A/SWINE/10WA/15/10)	14.33	İ	:	Ī	!	:	!	:	i :
THE WITH		DOLUCENZA A VIRUS (STRAIN A/SWINT/TENNESSE EZG/7)	536.537			İ	İ		İ		:
		MOTUENZA B VIRUS (STRAIN BIANN ARBONING (COLD ABAPTEU)	1 1		İ	-	i i	İ		-	1
	BINIT PE	INFLUENZA B VIRUS (STRASH BJANN ABBORJING [WILD:TYPE])	1.5		İ		Ī				
PR. 27 (205)	ANA-DIRECTED ANA POLYMERASE SUBLINIT PZ	DOFLUENZA B VIR. IS (STRAIN BISINGAFORE/22/209)	13.54		<u>:</u> 	İ	İ	Ī	Ī	I	
NE P		INFLUENZA C VIRUS (STRAIN CAUSO)	406-435		İ	i I	Ī	:	:	!	
PREST IANK	ANA-DIRECTED NAA POLYKERASE SUBUKIT PI		210-314	21.560	İ	† 	ĺ				i
May Made	æ i	(STRAIN ABUDGERIGAR/ICIKKAIDO/1/7)	314-134			-				-	1
NACH INCH	RMA-DIRECTED RMA POLYMICA SE SUBUNIT P.	INFLUENZA A VIRUS (STRAIN ACHILLYMT)	219-334			-					
	-	INCLUENZA A VIRUS (STRAIN A/TOWL PLAGUE VIRUS/HOSTOCICUS)	1	<u>ا</u> ي							
1000	BUT NOTE THE BUT IN THE LAST SUBURILLY	DOLUENZA A VIRUS (STRAIN AGONL PLAGUE VIRUSAVEYDRIDGE)		3		<u> </u>		1			
	BUA DIRECTED BUY DO WAS ASSESSED.	STRAIN ACCULANARY LANDY 0477		3	j		j				
	TRUA SHEEFFEE BUY DA WAS ASSESSED IN THE		1	2		j			1		
1_	ANA DIRECTED BNA FOLVINGRASE CIMITALIS	100		2		Ì	Ī	Ì	i	-	
	RMA-DIRECTS DAYA POLINGERASE CININATES				-	İ	Ì	Ì		İ	
	ANA DIRECTED ENA POLYTICEASE STREET PI	THE PROPERTY OF THE PARTY OF TH	1	8		+	Ì				į
	RNA-DIRECTED BNA FOR VACEBASE STREET PE	DATE PARTY A MINISTER TANDED TANDED TO SELECT			İ	-	Ì	Ì		ļ	
PLANT LABOR	TANA DEBECTED ANA POLYNCE ASSESSED FOR			1		İ				Ī	
	15	1		19	<u>-</u> !	†	İ	1	-	i	
	ANA-DIRECTED RIVA FOL YMERASE SUBURILED	DOLUENZA A VIRUS (BRICAIN ALENINGRADI) 6:41/31)	219.234	303.360	İ		İ	Ì	1	İ	
-	RNA. DIRECTED RNA FOLTNERASE SUBLINIT FI	INFLUENZA A VIRUS (STRAIN ARKALL ARIMARW) ORKUSTONIS	200	98:	İ	ĺ	İ	Ì	Ì	Ì	Ī
	RNA-DIRECTED RNA POLYMERASE SUBINIT PI			3	<u> </u>	r	İ	Ī		İ	
VILLO WATE	THA DIRECTED BUY POLYMERASE SUBLINIT PI	INTLUENZA A VIBUS (STRAIN ANTMONS)	=			İ	Ī				
. 1-	ANA CHECHES ANA POL THERAND SUBLIMIT FO	INTUENZA A VIRIUS (STRATO APULETO RICOVIDA)	-	=	42.540					İ	i
	THE STREET STATE OF THE STREET STREET STREET	THE THEORY A VIEW SHE SHE AND THE STREET AND THE SHE SHE SHE SHE SHE SHE SHE SHE SHE S		3!							
	ANA. DIRECTED RIVA POLYNGRASE SUBLINIT PI	INCLUENTA A VISUS (STRAIN ASINGAPORE/1/5)			İ	İ	İ	Ì			į
	=	INFLIENZA A VIRUS ISTRAIN ANTURKEYA IINNE SOTASSINOS	100	2	İ		İ			İ	
	=:	INGLUENZA A VIRLIS ISTRAIN AVICTORIANIS	11:11	23.560		İ	İ	Ì			Ī
THE PARTY	= ::	PALLENZA A VIRUS (STRAIN AVVILSON SNITHVILL	219.374	99				1	Ì	ĺ	
, may 1	RAN-CHARLES IN POLITICALES SUBJECTS STEELS	INTLUENZA A VIFUS (STRAIN ASWINEAUWALLY)O	216-236	341-360					İ		
7712		INTUENCA A VICUS (STRAIN ASWINGTENNESSEE/1477)	<u> </u>	3							
PRAIN BREAD	ANA MARCHED BNA POLYMERASE SCHOOL FOR	THE LUCKER BY VIEWS (STEATH WARM ARBOW) NO TOLO ADAPT TO	Ĩ	2.5	j	j	İ				
PULL DICAL		Ť	2 1	200		j	j	İ		Ì	
HELD BACK	ANA DIRECTED ANA POLYMERASE SUBUNIT PJ	DALLENZA C VINUS (STRAIN CIPSO)	T		İ	İ		Ì	Ī		
PREED THOON	RHA DOLECTED RNA POL SUBURIT PI	Ť	I			T	\dagger	Ì	Ì	İ	
PALVA CYNES	ANA-DOLECTED ANA POLYMENASE		Т	100		402.1507	11.10	(41.1961)	24.3140	1074.7863	277.117
PARPA CYMDO	ANA-DOLECTED RINA POLYNGAASE	ACMINE HEPATITIS VIRUS (STRAIN DEFECTIVE HIM)	Т	Ť	Ť	_	÷	<u></u>		• •	
PROA CYME	MAN-DIRECTED ANA POLYNGRASE		11.9.1	100	-	÷	461-1480	120.131	783.1804	165.2167	11.3184
100 mg	1470-1484		<u> </u>	⋍	Ť	_	+-	<u></u>			
1	ANALAKE CIED RAN POLITICEANE	BELUNE VIRUS	104.613		111.1397 21	131			İ	Ì	Ī
CONT.	AND THE PARTY OF THE PARTY OF		1	:	_	_			İ	<u>.</u> !	
FLUE CVPS	ANA DESCRIPTION FOR YAGE LASS	The state of the s	=	•		20	1694 272			<u> </u>	1
HUND CAPA	ANA-DIRECTED ANA POLYMERASE	-	T		İ	1		Ī			
PARIN BYS	RHA-DIRECTED INA POLYNGRASE	AVIAN INTECTIOUS BLONCINIIS VINUS (STRAIN BEAUDETTE)	Ţ	110.361		111111111111111111111111111111111111111	444.1434	1	İ	Ì	
PART STV10	RMA-DIRECTED RMA PCH, YMF, RASE	-	Τ	ī	T		Ì			İ	
					1	1		1	1		7

4710770	1000000										
		All Virbacs (No Dactertophages)			l i						Γ
MANUAL PROPERTY.	TOWN THE PARTY OF		ARTA L	AH7.52	SHIA)	APCAK	AMEA !	- f Valie	China 2	AKPA	- Y E
700		PONTAM WITH A VILLE	3			2	117.1178	1141.14,6	1411.144	Mr. Jane	Part 2017
	AND THE REAL PROPERTY OF THE PASSES	I. UDI.A VIRUS	-	_							!
	KIT THE KASE	HANTAAN VIRUS (STRAIN 16 118)	151-168	131	119.461	301.158	2017-1105		i i	 - -	! :
	ANA MALTHERASE BETA SUBUNIT	HIMAN RESPIRATORY SYNCYTIAL VIRUS	÷:								-
Y IOCA	KAA POLYNEKASE BITA SUBUNIT	PUMAN RESPIRATORY SYNCYTIAL VIRUS (STRAIN AZI	2:	11111106	100	1633-1633	1761.0161	1101-1101			
TOOL WAR	MANDURECTED RINA POLYND RASE.	MARBURG VIRUS (SIRAIN NUSOKE)	15.30	46.169			267.10	\$46.569	97 16	1907.00	10.101
			1711-171	1970-3017	1011-2014						-
NAST AND	MARRIORG VIRUS (51% 41% FOFF)	15-10	64.169		-	546.469	. ž	1042-1067	100	677.16%	
			1115.111	1001-1011	1102.04		233.246	1	!		:
A PART	ANA POLYNERASE BETA SITBLINIT	MEASLES VIRIS (STRAIN EIMINISTON)	116.711	11.633	103.103		239.1104	50.150	2018.2041		
PRIN, MANON	AMA POLYNCEASE BETA SUBLINIT	MUNDS VINUS (STRAIN MIYALIARA VACCINE)	14	16:135	95.59		8			1216	Ī
PRIM, NOVE	RYA POLYNGEASE SETA SIMONIT	MEWCASTLE DISEASE VINUS (STRATS BEALD)ETTE CASS	104.334	19	13	is Is					
PARPL PIZIT	ILMA POLYPICELASE BETA SINBUNIT	HUDGAN PARAMALLENZA I VIRIIS ISTRAIN TOSTIDAL	200	168.70	_	1	201	2100			
PREST, PUM	ANA POLYNORASE BETA SIMILARE	TO DAZAN DAN DANA LINE A LINE SECTION AND AND AND AND AND AND AND AND AND AN		ī	i		_				
PREPI PURE	ANA PARACTED BUT ANS NASERACE	TOP OF THE PERSON OF THE PERSO		ī			_	7068-2084	111.2114		
17117 1 14 14	AND DESCRIPTION OF THE PROPERTY AND PROPERTY	TOURS THE STATE THE LINE LINES IN THE LINES	13:184	7	si	8	000-3110				
	ATT THE PRINCIPLE OF IN SUBJECT TO SERVICE OF INSTRUMENT O	AAJUES VIRUS (STRAIN PV)	266-216			=	402.151.7				ĺ
	ANA PULTMERASE BETA SUBURIT	AABIES VIRUS (STRAIN SAUDIO)	266-216	Г	Г	-	403.1517	121.20			
	MA-DIRECTED HAS POLYMERASE	AUCE DWARF VIRUS	100	533.366	1 (84 OB)	361-166	1	-			
	KNA DIRECTED ANA POLYNERASE	AUT VALLEY FEVER VIRIIS (STRAIN 2)1.548 AII 2)	1000	7-	ī	!		Ī			
PRINT SECTION	KHA POLYMERASE BETA SIMUNIT	SENDAL VIRUS (STRAIN 2 / HOST MUTANTS)	3	10	194.311	144.11	11.00	401.175		25.22.201	
	ANA POLYNCHASE BETA SUBLINIT	SENDAL VILUS (S) RAIN ENTIFIES)	12.5	117.799	ī	ie	777	100			Ī
PAUM, SENDS	KNA POLYKERASE BETA SCHONIT	SENDAL VIRUS (STRAIN Z)	1	7	i			ŀ			
	ANA DIRECTED RIVA POLYNGRASE	SECUL VIRUS IS TRAIN 10:365			ī	1					
PLEM SVSWR	ANA POLYNOLASE BETA SUBUSHI	STACKAN STRUCK ASTRUMENT WELL		_	1	ķ		5017:103			
PALL SYNV	BHA POLYMERASE BETA SIMERIT	SALCHER VELLOW DEP VIEW			ī	-	2	21.5	3117.2137		
PERM TENVE	ENA CORPORATION AND VALUE AND	Free and the second residence and second sec	200	_	_	-	161:131	116.911	1484-1510	1336-1343	
$\overline{}$	BAA POLYACE A CE	THE PROPERTY COMES AND TO SERVICE AND THE PROPERTY OF THE PROP		eΙ	-:		2678-2703				
PLED VEVE	BNA POLYMENT TO BETA C. IN. A. P.	POLYCRAP A PROPERTY OF THE PRO	1		ΞĪ	2000	2060-20E1				İ
_	BNA PCH VAGE ASS BOTA COMPANY	VIEW AND STATE OF THE STATE OF		46.51	_		000.1001				ĺ
-	BNA BCI VARBACE BETA SINITAR	CASE OF THE PROPERTY OF THE PAR		16.53	976-1982	1010-2101					
_	ENA PRECITED BUY DO SAME AND	TESCULAR SIGNATION VIRUS (STRAIN SAN JUAN)									
WAYNE BANKE	MITATION BUT MEETING BUT IN	AFTECHNORUM LEAD SPOT VIAUS	376-249	036-1054	5511.201	173-1401				ĺ	
	MITANUS BUT PORPORES BUT BO	EST WESTERN TELLOWS VIRUS (ISOLATE FL. I)	٦	╗		-					
MUA DATE	MINISTRAL BAS DEPTHEN BUT BOT	MAKE THE COM DWARF VIRUS (ISOLATE ALAVIS)	٦	-	2.2						
	HIPASKA BULK HIREPIEN BULK	SALLET TELLUM DWARP VIRUS (ISOLATE PAV)	Ì	7	105.912						
	SECRETARIA DATA PAREFERD BALL BOX	BARLEY TELLOW DWALL VIRUS (ISOLATE P.PAV)	•	361-416	\$05.513		Ī	İ		Ī	
	MANAGEMENT AND					1111	Ī				
	PROPERTY NAMED AND AND AND AND AND AND AND AND AND AN	CLACK CHARLES WAS THE PRESANCE VINUS (WATERNIELON STRAIN	П	Ī	=	333-1534				Ī	
Ī	PROBABILITY NATIONAL PARTY OF THE PARTY OF T	CONCRETE MICHORIS VIAUS	ا	1	410.484					Ì	İ
_	ALTANICE BUA. DISEPPED BUA SOL	The Land Mandail VIII of the Control	٦	200	470.044						
PART VALVE	BUT IN WAR ARE	INFELLIOUS FAMILIES IN CHECKOSIS VIRUS (SEXOTYPE JASPER)		į							I
_	ENA POR VEREA CO	CHARLES CHURCHERING III S'IRUS (STRAIN ADISTRONG)	Ī	107.611	699.682 0	1001.110	1334-1251	170.170	1033.3099		
T	PROPABILITINA DISECTED BINA BOT	MAINE THE CHANGE REPORTS THE STREET WE	2	ī							
L	NA DORECTED BAY POLYAGEASE	INTERPORT INTERPORTED IN	ī	2	8						
Т	PUTATIVE RMA. BOLECTED RNA POL	POTATO LEAD OUT VINE STEAM IS			Т	7.6	j				
	PUTATIVE KNA BELECTED RNA FOL	POTATOLEAROIL VALIS ATTENTION WACENINGTON	T			1	Ì				
T	PLIATIVE RNA-DOLECTED RNA FOL	PEPPER MILID MOTTH E VIBILE (COMMAN	T	ī	÷			j			
	PUTATIVE RAY DOLECTED INA POL	BED IT OVER METROTIC MONTH CORING	Ī	╗	1 8 1 8 1 8 1 8 1 8 1 8 1 8 1 8 1 8 1 8	100					
	NA-DIRECTED BAY POLYNORASI	BEOVERIG CTABLE AND MACHINETIC	B	-	İ	i		i			
PILLIO LEON.	KHA DIRECTED RNA POLYNERASE	REOVING CTYPE 17 CIP AND AMON	*	1		İ		-			
PRING ROTER	NA - DIRECTED RINA POL SUBIDNIT VPI	BOVONG BOTAVIBIR ATIA PER				Ī	1				
PRING ROTSU	LIVE SOLECTED THAT FOL STREET VI	BOVING ROTAVIBITE ACTION IN	İ		ļ		_	200			
PARED ROING	KNA DURCTED INA FOL SIGNATI VPI	PORCINE ROLAVILIS (CROLLY C. STRAIN COWDEN)	Ī	7	-			1007.1046		İ	
_	RMA-DIRECTED INA POL SIBIDNIT VFI	POACINE ROTAVIRUS (31 RAIN COTTFRIED)	Ī	Ŧ	ī	Ì			7	-	
ī	RINA-DOZECTED RMA POL SUBLÍMIT VFI	SIMIAN IT ROTAVIAUS ISTRAIN SAIL)	1	-	1	i	Ţ		2	1027.1049	
I	PROBABLE RMA-DERECTED RMA POL	SOUTHERN REAL VINUS	ī	7	١.	ī	Т		23.146	<u> </u>	1
PRANO TACY	RHA FOLYMERASE		Ī	ī	ĪΞ	100	Ŀ	7	İ	<u> </u>	1
]			-1		1	1]

PCCENE	Pricture	All Victors We Institute								•	
THE HAME	PROTEIN	VIAUS			7	-					Γ
Ų	PUTATIVE RHA-DIRECTED RHA FOL	TOWATO BUSHY STIDYT VIRILIS (STRAIM CLIEBE V)		4	3	7	7	17710	1 7787	ANKAL	ARKAS
Mano 1cv	PUTATIVE MA-DIRECTED RNA FOL	TURNIP CATHALE VIRUS				-					
5	PUTATIVE RNA DIRECTED ENA POL	TOBACCO MILD CREEN MOSAIC VIRUS TIME STRANTIN	110			1					
PARTO TAY	PUTATIVE ANA DIRECTED HAS POL	TOBACCO MOSAIC WILLS (VIEGARE)				-					
PRESO TAVICE	PUTATIVE RHA-DIRECTED RHA FOL	TOBACCO MOSAIC VIRUS (STRAIN KOREAN)	100								
PREMO TANTO	PUTATIVE ANA BILLECTED ANA POL	TOBACCO MOSAIC VIRUS ISTRAIN TONIATION	20,734	100		1111111				j	-
METO TAVA	RNA-DIRECTED INA POLYMERASE	TOBACCO MECROSIS VIALIS (STAAIN A)							·	:	
DAY ONE	ANA-DIRECTED BNA FOLYMERASE	TODACCO NECROSIS VIRIN (STRAIN (1)	١	:	:	:	:			_	
A COA	RNA POLYMERASE ALPHA SUDUMIT	CHANDIPURA YIRUS (STRAIN ISSISIA)	1	İ	!						_
	RNA POLYMERASE ALPITA SUBIRAT	MUNDS WAUS (STRAIN SOL.1)	11.11			ŀ					
	RWA POLYMERASE ALMIA SUBLIMIT	HUMUNE VIRUS (STRAIN EMDERS)	313.316		Ì	-				İ	
No.	DAY POLYMERASE ALPHA SIBIRUI	MADOS VIEUS ISTRAIN SUYAJIARA VACCINE	1		Ī						
PEUT NOVA		NEWCASTLE DISEASE VIRUS ISTRAIN AUSTRALIA CULTURIANT									
75.7 TO	RNA POLYMERASE ALMIA SUBUNIT	DEWCASTLE DISEACT VIBIGACIBANAMINATINA			!	-	-				
PREST PUET	RNA POLYNERASE ALPHA SLIDONIT	MINAM PARADRI RIVE - COMING				1					_
PILLEP WINT	RNA POLYNELASE ALPIN SUBJECT	TO BLAND PARA INC. 15 NOT A STATE OF ST	216-70			•					
PLEASE PROPER	KNA POR VACERACIO AL PRIA STRUBALI	INVESTIGATION OF THE PROPERTY	216.743							Ì	İ
PERSON PROPERTY.	ANA POLYMERASE ALPHA CINITAR	LENGTH DATA HAR LENGTH AND CONTROL OF THE CONTROL O	39.30						Ī		
PARTY PRINT	BIVA POLI VACEDACE AT MILA CITATATA	MARCHINE LUENCA 4B VIRUS (STRAIN 6E. 1)))	230-343							ĺ	
Т	BUA BOX WAS AND AT BUT OF BUILDING	FACT VINOS	130-161			-				İ	
T	BUA NOW WASTE AND AT MAJE STREET, WASTE	MARIES VINUS (STRAIN AVOI)	10:33							İ	Ī
т	BAA BY WAR ACE AT BUA CITCHING	MARIES VIRUS (STRAIN CVS.11)	1.33							Ì	Ī
STATE STATE	THE COURT OF THE ALTER SUBJECT OF	HABIES VIRUS (STRAIN ERAL AND (STRAIN PM)	12.0	116.311		Ţ.		Ì		t	Ī
T	NATIONAL PROPERTY OF ALL PROPE	INVIES VIIUS (STEATH PV)	=	316-337						İ	Ī
Т	THE STATE OF THE S	RADIES WRUS (SPRAIN SAD BIS)	=	316.337	ĺ				Ì	1	
Ţ	ANA PULTERAL DE ALPIGA BURILINIT	SIMIAN YRUS S (STRAIN W.)	12.12	12.30		ŀ	I		Ì		
7	ANA PULTIBLIA SE ALIMA SUBURIT	VESICIALAR STOMATITIS VIRUS ISENDITIBLE NEW IERSEY / STRAIN OC	018.181			Ī			İ		
7		AJ ALCAM SWIDE FEVER VIRUS (STRAIN BASIV)	135-361			1		Ī	j		
_	SUPEROXIDE DISMATTANE LIKE PROTEIN	VACCINEA VIRUS (STRAIN COPEMIAGEN)	9742		T	T			1	Ì	
	SUPERDUMP DESMUTASE LIKE PROTEIN	VACCOMA VIRUS (STRAIN WR)	09-61		Ī				1	1	
7	SUPEROXIDE DISMATASE LIKE PROTEIN	VAUOLA VIRUS	19.40			1			1	j	
	SATISFOLDING	AMSACTA MODRE I ENTONOPOXVIRUS	50.74	627-648	İ	Ī		Ī	İ	i	
_	STREET TREETINGS		17.30		İ	1			Ì		1
-	SCOUR)		61-13	117.34)	İ			T	Ť	İ	
200	SWIGH PAULETIN		13:50		Ì	Ī		Ī	Ť		Ī
-	LAKUE I AMI IUEN	SE VIRUS	354-366		Ì	Ī		1	1	İ	
-	LANGE I ANTIGEN	POLYOMAYIRUS BK (STAAIN AS)	201-134	139.441	Ī		Ī		İ	İ	Ī
Name of the last	And a second	POLYOMA VIRUS BIX	201.114	139-444				Ī	İ	1	Ţ
~	LABOR TANFICEN		385-600				Ī	Ī	Ì	$\frac{1}{1}$	1
1	Alick T Attroop		43-49	10.56				Ī	T		
	LAIGH Y APPLICEN	POLYOMAN VILLS AC	101-123	(38-44)				Ī		\dagger	<u> </u>
	LAIGH ANTICEN		43-49	\$16.542				Ī		\dagger	
+=	CAIGE LAYTORN	1	36.391						-	l	
	LAIGE TANTICEN	MOUSE POLYGMA VIELE (STEAM COMMOND SELLI)	374.380		j						l
×	AJGE T ANTIGEN	T									ĺ
7	LANGE T ANTIGEN	Ī	100 700	╗							
	MIDDLE T ANTIGEN	HAMSTER FOLYOMA VIRUS			İ						
_	WALL I ANTIGEN	T		Í	İ	Ť	1	1			
-	SMALL I ANTIGEN		41.68	Ì	İ			1			
_		Ī	1	17.10	†	Ť	1	1	i		
TAIR RVAC	HAMS ACTIVATION TIANS LEG PROTEIN	WEDROSIS VIAUS			T	Ť	†		1	1	
Т			47717			l	Ì			1	1
Т	TAKE ACTIVATION TRANSPER PROTEIN	ACOSIS VIAUS	319-414				T	T	\dagger	+	-
Т	TANK ACTIVATING TRANS LEG PROTEIN	BOYNG MARKORE REPORT VIRUS (150LATE 104)	\$.5					T	\dagger	t	Ī
	MANG ACTIVATORS TRANS BEG PROTEIN	T	6.5		j	Ī					Ī
П	TRANS.ACTIVATING TRANS REG PROTEIN	HUMAN PART LEINENG VINICAVER INTERNATION	21.210								Ī
		7	012:24		1	1					Ī
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1	PROTUR	VIRUS	Alich	ABEAL	ARIAL	O HEAV	AHEA!	A BEALD	A87A2	ABLAI	SKYS
		HUMAN INDICINIDEFICIENCY VIRUS TYPE I (STRAIN UGANDAN / ISO	7		1	1					
7100		PELIDE LEUTEMIA VIRUS	٦		-	Ī				Í	
THE MAN	PROBABLE TECCHEMIT PHOSPIRMENT IN	EQUINE PEATES VINUS 177% I (STRAIN ABAP)		Ì	1	1	1		1	1	
1 SALE	ILUDGAMI PROTEIN	EUGINE INJURATION TO I (SIRAIN RENTUCATA)	T	T	Ť		÷		_	Ī	
		EVER IN DAUG (STRAIN BY)-1)	٦	Ť	-	-	Ť	-	⇁	∺	
A PART OF THE PART	TACOMALIE WALCE (ELCOMEN) TROTEIN	TRUNCA CT TOWARDALIMINOS (STACK ADION)			100-100	2	60		304-1336		122
		HEALT SOUTH A VICTOR IN STRAIN	T	i	ď	÷			İ		
	LACE IELANGE IN TAXABLIN	HENCES SIMPLEA VINUS (1772 07 SINAIR US)	Т	7			320-1328			İ	
WEND HOWE	LAKGE TECHNOTER	EQUING HEILDESVIRUS TYPE I (STRAIN ARAP)	٦	Ť	<u> </u>		9	20.20	╛	_	
PEGD HEWSA	PROBABLE LARGE TEGLAGNIT PROTEIN	HEAVESVENUS SALMINI (STRAIN 11)	┪	14:33	1001.100	121-H31	153.1174		1503-1535	1401.1622	101.1015
							П	_	_	_	
MICH WW	LARGE TECHDONY PROTEIN	VARICELLA-ZOSTER VIRUS (STRAIN DUMAS)		115-14	111.111	101-123	020-568	101).1034	1360-1376	1633-1697	1316.1801
			3006-3829	23 705 23 07 13	104-3717	ŀ	Γ		İ		
PTEAM ADEC!	DNA TELVONAL PROTEIN	HUDAAN ADENOVIRUS TYPE 2	1	397.616				İ	İ	İ	l
1 .	DMA TELMONAL PROTECU	MENAN ADENOVIRUS TYPE S	Γ	10101		Ť	Ī		Ì	İ	Ī
L	DNA YELLMAI PROTEIN	IN BLAN AREMINIST TYPE 3	Ī	100 045	Ì	1	Ī	Ī	İ	Ì	Ī
	Mar Tenanal Menyeru	Without a heart of the 14	T	Т	444 644	1	1	T	Ì	İ	Ī
	PALL PARAMETERS IN	Attack to the second se	Ī,	Т		Ì	Ī	1	1	1	
	THE PERSON NAMED IN	A BOLAN SWINE VENEN VIEW (STANSANDAS)	Ī	2	İ	-	1	1	1		
200	DAY TOPOSOMERANE II	AURICAM INTRIPEVER VIRUS (ISOLATE MALAW) LIL 701)	٦	20 - TOP	1	7					
VILY HOPA	HYPOTHETICAL PROTEIN TREES	MUMAN CYTOME GALOVIRUS (STRAIN AD149)	136-165	j		ا				j	
AVD.	REI. TICANSFORMONG PROTEIN	AVIAN LETICULOENDOTICE LIOSIS VIAUS	¥-74								
PTYSY VZVD	THYSODYLATE SYNTHASE	VANCELLA-ZOSTER VIRUS (STRAM DUMAS)	41:14			Γ.					
PULLE HEVAL	POSSURIE GANCICLOVIA KINASE	HEAPES SOCIET VIRUS (TYPE 47 STRAIN UCANDA-1103)	11700		-	Ī					
PURE HISTORY	PROTEIN 21.	HEAPES SUMPLEX VIAUS (1 YPE 4 / STRAIN UGANDA-1102)	2	İ	İ	Ī		İ			Ī
HINGS LOVA	TOP AT INTRAM TO ANALES A CE DESCRIBERA	ALTOCAL PAIA CALLEGERATE MAICH SAN POLYTIC DE COLONIA			İ	Ī		Ì	İ	1	
MAN LOSAVA	LIVERTHEY PART PROTEIN IN 1	HARAN PARACAL COURT RESERVATOR		İ	Ì	T		-		i	-
	-	CONTRACTOR CONTRACTOR		İ		+		1		i	-
AND MANY	-	CONTRACT CALCULATION STRAIN ACTION		İ	İ	Ì		Ī	İ	Ì	
	-			+		1		Ì	İ	İ	
A CALCON MICHAEL	MYPOTHE TICAL PROTEIN ULB	HURACA ETTOREGALONINOS (STRAIN ADION)	2	İ	1		j		j	j	Ì
	VICTOR PROTEIN U.A	HENTES SHATLER VINUS (TYTE I / STRAIN IT)		Ì		1				j	Ī
	VALUE OF RESIDENCE	EQUING MEANES VINOS 1 TPE 1 (3 I MAIN ABAY)	•	İ	1	1					
PLEASE PROVIN	VICTOR GENE 43 PROJECT	(PLACES YEAR) (STRAIN (1)	3								
	THE STATE OF THE S	LEASTER WALLS (SILVING BY) II	Ī		1						
1	MINDING TAULEN OF	SUPPLIES CALLIVINGS (STUATE ADDING)	╗	6.4	1	j					
	MOTERA UL?	HEAVES SDOLES VIRUS (TYPE I / STRAIN I 1)	8	j	1						
70.00 E	CEME 33 PROTEIN	EQUING MEANESVIALIS TYPE I (STRAIN ABAP)	? =	İ	1	Í	j				
		HEAVESVOLUS SADVILL (STRAIN !!)									
20.00	GENEL ST PROTECT	VAUCELLA-20STER VIRUS (STRAIN DUNAS)	1	20.00		j					
	MOTEN UL	HEAVES SOUREX VIAUS (TYPE 1/STILADA 11)	7	3.73							
MEN VIVO	CENE 12 PROTEIN	VAUCELLA-ZOSTER VINUS (STILAIN DUNIAS)		393-616	_						
ME BOVIE	CRESCH OF REPLICATION BINEDIN PROTEIN	HEAPES SOURCEX VIAUS (TYPE 1/STRAIN 11)									Ė
_	ORKON OF REPLECATION BOODED FROTTON	EQUIPE HEXPESYTAUS TYPE I (STRAIN ABAP)		٦							
200	ORIGIN OF REALIZATION BINDING PROTEIN	VAUCELLA-ZOSTER VIDUS (STUAN DUMAS)	٦	164.190	484-508						
A COL	MINORE INCAL PROTEIN UL!	HOMEN CYTONE GALOVILUS (STILAIN AD164)	231-347								
AT IN MONA	MYPOTHETICAL PROTEIN UL!!	HUMAN CYTOMEGAL OVIRUS (STRAIN AD189)	(49-46)						-		
PULIS HOSIVA	HYPOTHETICAL PROTEIN UL 14	HUMAN CYTONEGAL OVERUS (STRAIN AD 189)	310-199					Ī			
PULIT HISVIE	HYPOTHETICAL ULIA PROTERI	HERPES SOUREX VIXUS (TYPE I / STILAIM II)	\$ 1 2 1							r	
FUCTO HEVER	HYPOTHETICAL CIENTS 44 PROTEIN	EQUING HELLYCLUS TYPE I (STLAIN ABAP)	100011		l			İ			İ
PULLE MAY!	PROTEIN UC 16	HENNES SOURCE VINUS (1 YPE I / STEATH IT)	113-49		l	T	ľ	Ī			Ī
PULIT HIS VED	CENE 40 PROTEIN	EQUID GENERALIS TYPE I (STRAIN ABAP)	39-43	ī	114.139	ľ		Ī		Ī	ĺ
PULIS HEVSA	CEME 33 PROTEIN	HERPESYTHUS SATAIN (STRAIN 11)	П	L		Γ		T		T	
PULIS VZVD	GENE 44 PROTEIN	VANCEL LA ZOSTER VILUS (STRAIN DURIAS)	63-10	111.111	İ			İ	Ì	İ	Ī
FUCES EBV	PAGTEST SQU!	EPSTEIN-BAUN VIRUS (STRAIN BOS-8)	117.101		<u> </u>		İ	İ		Ť	Ī
PULLIS MCNOVA	INTOTAL PROTEIN UL!	HUMAN CYTOMEGALOVINUS (STRAIN AD 169)	10·01				Ī			İ	
PULIT HISVII	PROTEIN UL.17	HERPES SCHLEX VIRUS (TYPE 1 / STRAIN 17)						T	İ		Ī
ALL BOTA	CENE 33 PROTEIN	HEAPESVIXUS SALMIDI (STRAIN II)		348.330							Γ
PULIS HONA	HYPOTHETICAL PROTEIN UL 19	HUMAN CYTCHEGAL OVIRUS (STILATH AD184)	10-10							Ī	Γ

	PULIS VAVO		YAUNG (No Briteriaphogra) YAUNG (No Briteriaphogra)	V	THE STATE OF	П	\Box	77187	AREAt	П	AREAI	17,117
Heart Hall Hea	PLE 18 VIVE	_	PSEUDOLABES VRIUS (STRANKAL)	ABEA	TYNY	П	П	ABGA	AREA	Т	AREAI	ANDA
WASTER TO WAST	ONE OF THE		THE PARTY OF THE P			I	t	1			2	
PRODUCTOR PROD	VILLE HOLVY			Z.	_					T		
PRODUCTAL			THE STATE OF THE VIEWS (STRAIN DUNCAS)	201-124	L		1					
MATCHEST MATCHEST		PROTEIN (#3)	THE CALIBORIAL OVIRUS (STILATA AD164)	100			1					
CONTRIBUTION CONT	ML2 H3VII	PROFILIA 18 41	PULATES SOOTE EX VINUS (1 YPE 1/ STRAIN 17)	1	110 111	<u> </u>	1					
	PULL RIVE		HEAPES SOCHEX VIAUS (TYPE 1/STRAIN IDEM)	1		1	1					
	MEN VEVE	Τ	EQUING HEAPESVILUS TYPE I (STICKIN ABAP)	1013	100	107 92	-					ŀ
	JULIE HOSAVA	T	VAUCELLA LOSTERIYMUS (STRAIN DUNAS)	10.01	1					Ī		
	PULS EBV	7	HEBLAN CYTONEGAL DVIRUS (STRAIN ADISS)	1			1					
	HILLS HOWA	т	EVSTEIN-BANK VIRUS (STRAIN BOS.1)	1		1						
PROPRETEUR R PROPRETEUR PROPRET	TAPE PER	Т	INDICAN CYTOMEGAL OVIRUS (STRABA AD 169)									
THE PROPERTY THE			MERPES SOCHEX VIRUS (PYPE 1/STRAIN 17)	3						Ī		
		THE PER ULT HOMOLOG	INFECTIOUS LAFTHCOIPACHTIE WATER AND STATES THE PROPERTY OF THE PERSON O				L			T		
VIOLENTIAL STATES VIOL	A STORY	INPOTIGATION IN 15	INDIAN CYTOMORE AND	2 - 1 M					Ī	Ī	1	
WINDS THE STREET STREET FOR THE	1841	VILLON PROTEIN UL 35	PERSONAL STREET, CALLON (AT IACA)	484.500			-					ļ
VIOLENCE FOR THE TRANSFER VIOLENCE FOR THE TOTAL AND THE STATE	ULUS HISVED	IVIRION PROTEIN La 31	TOTAL SIMPLEA VINUS (TVPC 1/STRAIN 1)	101-91	İ				•		!	
HE DEPONDED PRESENCE	UL15 HSVSA	VINCH CRAFT to secretary	ECUME IRENT SYNUS 1977: 1 (STRAIN After)	10.0	677		~			_		
	W-1015	AND THE PERSON OF THE PERSON O	PERPESVINUS SAIMIN (STRAIN II)									
The control of the		THE PROPERTY	INGECTIOUS LAINTACOLEACHER THE VIBIL CONTROLLE	î	9					İ		
The property, and the property of the proper		HTPOTHETHCAL PROTEIN LE 37	DEDGAN CYTONOGAL DONNING THE AND	12 281	316-336		-			†	1	
	E S HOLVA		HIBLAN PATABOA CARINA STRAIN ADION	307-324	406-307	L	-			1	1	
HOUSE BELLE HOUSE BELLE HOUSE BELLE HOUSE BELLE HOUSE BELLE	TO HOLY	ı	Interest Action 2017 (STRAIN ADIO)	239-266			1		Ì	1		
	ULJI EBV	I	PRINCIPLE CALLOVINOS (STRAIN ADISO)	77.			1	Ì	1			
	ULI HCMVA	HYPOTHETICAL PROTECULAL	CESTEPPEDALIC VILUS (STRAIN UP). 8)	23.74			1	1	-1		_	
UNIVERSITY UNI	UCH HSVI	PROTEDUTY	MUNICAL CYTOMEGALOVIAUS (STRAIN AD169)	416.419	157							
STATE STAT	C. Haves	CENT SERVICES	MEANES SWOLEX MAUS (TYPE 1/STACK)	7170								
		CONTRACTOR OF THE PROPERTY OF	POUNT MEADES VIAUS TYPE I (STRAIN ASIA)						-	İ	İ	
VALUELLA-CORDITION VALUELA	1	CHANGE OF THE COLUMN	HEAVESVIALS SABATU (STRAIN III)		601					İ	İ	
WOON EVALUATION OF ACCOUNT IN THE STATE OF ACCOUNTS AND	L		VAUCELLA-ZOSTEA VIRUS GITEATH DI MARE		2							
	200	PROBABLE MANCE DAY OF YCOPROTEIN ULIT	MEAPES EDIONEX VIRUS CTYPE 1/ STRA NO 13							\dagger	t	Ī
PROPRETICAL POTENTIAL PARTICULAR STATES BLOOKED PART		PLACE ENVELOPE OF YCOPROTEIN 300	EQUINA VENINUS TYPE LISTA AND AND		364.583		_		İ	Ì	Ť	Ī
			VANCELLA-POSTUR VINUS (STRAFFINALE)	20					T		1	
WINDOW TOOLS ILLAND TOOLS		CANDIEDY COUNTED REC HOMOLOG UL)		337-534				İ	İ	l	1	Ī
		HTPOTHETICAL PROTEIN (A.14							t	t	1	
CHAPTER CANONIC CANO	1	VOUCH PLOTEIN U.LA		1	297-321		-		t		\dagger	Ī
VALON ROLE IN THE PARTY VALUE LANGE AND	Т	VICON CENE 28 PLOTEIN						-	İ	$\frac{1}{1}$	Ť	Ī
WATCH STATE WALCH CONTENT	7	UEAB 67 PROTEIN		3					İ	+	1	1
PROTECTAL FOOTBY U.S. FIGALNA CYTOGGGALOVRATS (STALM ADIES) 116-161	_	VALOW CENT 24 PROTEIN		201.279				 				
HOUSEN BLOATEN ULM ULM HOUSEN ULM	-	MYPOTHERICAL PROTECN UL 33						f		1		
FLOTER ULT)	Ť	ATTOTAL PROTEIN ULN		٦		131.348		-	\dagger		1	
CENSES IN PROTECTION CALCALLY STATEMENT 131-31 13	Ť	TRUITIN BOLL!		7		Г			t	1	1	T
COUNTY C	Т	ALCI TELIN UL.)				Г	914:1004		t	1	1	Ī
CONTRIBUTION CONT	7	COM DIVISION		╗		Г	Г	Т	Ť	2,01	1	
INTOPIERICAL PROTECN VALCELLA ZUSTER VINUS STANIN BUNAS) 1-10 104-114 105-10	┱	CENT 63 PROTEIN		Ť	Г	ī	Г	Τ	Ť	1	1	
INFORESTICAL PROTECTION 166-111 166-112 115-114 166-112 115-114 166-112 115-114 166-112 115-114 166-112 115-114 166-112 115-114 166-112 115-114 166-112 115-114 166-112 115-114 166-112 115-114 166-112 115-114 166-112 115-114 166-112 115-114 166-112 115-114	7	CENE 21 PROTEIN				ī	Τ		†	+	1	Ī
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INVOINGETICAL PROTECT LATER LATER AND INCOMES AND IN	7	PPOTHETICAL PROTEIN LEJIS		904-923	İ		T	ī	T	7	٦	9
INTOTACTICAL MOTERN U.d. INTOTACTICAL MOTERN U.d. ILL-114	7	MYOTHETICAL PROTEIN IE.10		027-64				t	t	1	1	
USE OR NEW PROTECTION	7	PROTECT MOTERICAL						\dagger	1			
ORDER 1 PERMINAN PROTEIN COUNTY	7	COURAGE PROTEDUZAS			100		T	\dagger	+		1	
	_[JENE 17 MENDRANG PROTEIN			Г	Ť	1		+		1	
		JENG IS MEMBRANE PROTEIN			Ť	Ť			1			
ROTEM ULAT 15-44		ROTEIN ULAS		T	í	T	Ť					Ī
PROTECTION 10-34 10-34 13-34		ROTESTUCA		T	i	Т	Ť	8	<u> </u> 			
	NIAS SVIM	NOTE OF UCAS		1	İ	İ	\dagger	1	1			Ī
VIDION PROTEIN U.A.? IEENTS SIDELEX VIDER (179E 17 STALIN F) 604.435 604.435 VIDION PROTEIN U.A.? REPES SIDELEX VIDER (179E 17 STALIN F) 604.435 60 TAED ALTHAN TRANS-REDUCING PROTEIN 804.435 604.435 60 TAED ALTHAN TRANS-REDUCING PROTEIN 604.435 604.435 61 K.D. ALTHAN TRANS-REDUCING PROTEIN 604.435 604.435		ROTEM UL 49		3	l	T		1	1			
VINDON PROTEIN ULTI WEIDES SIDELE VINDS (179E / 5 STAIN 1) WO ALD ALTAL TRANS PROTEIN BOYDE WINDS (179E / 5 STAIN 1) WITH ALANS PROTEING PROTEIN BOYDE WINDS 177E 1 IS STAIN 13) WITH TRANS PROTEING PROTEIN BOYDE WINDS 177E 1 IS STAIN 13.) WHICH TRANS PROTEING PROTEIN BOYDE WINDS 177E 1	1 HSVII	THOM PROTEIN ULAS		Т	ī	T	T		-		_	Ī
89 I DA ALMA TRANSENDATEND PROTEIN BOYNG HELTENTENTRY I ISTANT PL. 1) 11 EO AL PILA TRANSENDUCING PROTEIN ROAM HELDESVARUS TYPE I STRANT PL. 1)		MINON PROTEIN (8.4)		Т	T	T	7	*	1			Ī
97 KO AL MIA TRANS REDICING PROTEIN (COMPUTED STAND) 178 (STRANM 19.3)		6 7 KD ALPHA TRANS-BIDICENG PROTEIN		527-00	İ	T	+		1			
and a supplied to the supplied		TKD ALMIA TICANS INDUCING PROFEIN		61.103	l	T	\dagger	1	1			
				100-00		t		+				

PCCEME	PISCHALIF	All Virgas (Na Bacierias baces)				-			
Г		YZKUS	AREAI	AREA J AREA 3	C) AREA!	A KANA	ANEA & AREA	TARRAS P	VARA 6
Г			107-408	Ι	Т	Τ	Т	Τ	
HULLI VZVO	ALMA TRANS-INDUCTING FACTOR 91 8 KD PROTEIN		41-31	601-627	<u> </u>		-		Ī
Г	HYPOTHETICAL BRIEF PROFESS	EPSTEIN-BARA VIRUS (STRAIN BOS.S)	116-158		<u> </u>	-	<u> </u> 		
	IYPOTKETIČAL PROTEIN IA 19	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	248-364	531.543					
	TEGULENT PROTEIN ULA	HEADES SINDLEX VIAUS (TYPE 1/STRAIN 17)	236-253	}			-		Ī
П	HYPOTHE TIGAL GENE 44 PROTEIN	HOLFES YINUS SAIMOU (STRAIN !!)	111.153						
	TOTEN UIS	HUNKAH CYTOME GALOVIRUS (STRAIN AD 189)	94-119				<u> </u> -		
	PROTEIN ULSI	HERDES SIMPLEX VIAUS (TYPE I / STRAIN II)	49.46				<u> </u> 		
_		EQUINT BERNESVIRES 1 YPE 4 (STRAIN 1942)	12:12	:			-		_
ī		PORTED TO SELECT A PROPERTY AND A CAMPAN AND A	14.4		•				_
MEST VAVO	CENE 7 PROTEIN	VARICELLA ZOSTER VIRTIS ISTRAIN DUNAS	500	:	†				İ
г	PEDBARE B DALA BS PLICATION PROTEON BYLE!	FPCTS PLEASE VISITA (STRAFF BOLE)	37.77		1	†			
		MERSE BACH EX CIRCLE 1996 1 / STEAM 19	1	1979	 	+	1		
Т	KAIX BEST ELISINAL SEASON IN 15				1	1			
	THE PER PERSON AND PROPERTY OF THE	COUNTY MEAN CONTINUE STATE TO STATE THE STATE OF THE STAT	12-1	ī		1		i	_
T	MA METERA INCHESION DESI		2	113.159 114.113	- · ·	_			
X		HURTHS SAIMING (STRAIN 17)	47.40	(P. O.)	-	_	_		
┪	PROBABLE DNA REPLICATION CENE & PROTEIN	VARICELLA-ZOSTER VIRUS (STRAIN DUMAS)	446 466	645-670					
	PROTEIN ULSI	HUNGAN CYTONE GAL DVIRUS (STRATIN AD149)	1173.168		-				
		HEAVES SUMPLEX VIAUS (TYPE & / STRAIN UDANDA. 1102)	3.5						
	HYPOTHETICAL PROTEIN (IL 60	HUMAN CYTOMEGALOVIRUS (STRAIN ADIAS)	13014						
PULAS HOMVA IN		JAMAN CYTOMEGALOVIAUS (STRAIN AD169)	63.14	11.70				1	
PLAS HOMY H		HEMAN CYTOMEGAL OVIRUS (STRAIN AD IGE)	17.167						
PULTS HONVA	UL 70	HABAAN CYTOMOGAL OVIBLIS (STRAIN AD 169)	324.245	406.410 466.414	14 A36.446	10.101			-
PLLY HOLVA		HIDAAN CYTOMEGAL OVIELS ISTRAIN ADIAN	34.96	t	T			I	
Т	KYNOTHETICAL BLAST PROTEIN	FORTS PLEASED VALUE (470 AFT BOLD)			 	1			
1	WAS STORY AND A STORY OF SECURITY	Lieutectual in California (1975)			<u> </u>		1		
T.	TOTAL STATE OF STATE	PERCENTED SAMPLED (STACK)	21-73						
	TO COLUMN THE PARTY OF THE PART	HUMAN CTTONEOALOVINOS (STRAIN AD199)			- 				
	CACATE PIPAL BECKER 18 18	HANDAR CYTOMEDALOVINOS (STAATM ADTOV)	R	407-418					
	CANTERDAY ESSENTING	HUNGAR LY I CHECALOVINOS (STACIN AD189)	2	20.50 20.50	$\frac{\cdot}{1}$				
	A CONTRACTOR OF THE PROPERTY O	HANNEY CT CONCOAL CVINGS (3 LANG AD 187)	S. C.						
	Cherry Charles Defend Inches	KUMAN CT LUNE UALUVIRUS (STRAIN ADIEN)	8		7				
	TANKS OF THE STANKS OF THE PARTY OF THE PART	FUNCTION EDUCATION (STRAIN TOWNE)	9118		٠				
15	DOMONIA MANAGEMENT IN CANAGEME		717	7	Т				
1		INCREMENT TO DESCRIPTION (STRAIN ADTER)	1	109-133 606-628	£	123.78			
Т		MENDE CHEIK SAMMI (CHEIK)	121 122	101.101			1		
L	HYPOTHETICAL PROTEIN UR AR	HENLY CATCHERS OF SECTION	T	Т		1	1		1
Т		HERRICE COMPLEX VIRING CTYPE 4 / CTR A full I CA LIA A. (101)		1	1	1	1		
_		HUMAN CYTONEGALOVIRUS (STRAIN AD149)	3		-		1		
г		KEAPES SOURCEX VIRUS (TYPE 6/STRAIN UCANDA-1102)	145		-	+			Ī
YAY C	4	HUMAN CYTOMEGAL DYNUUS (STRAM) AD169)	16.99				<u> </u>		
	KYPOTIÆTICAL PROTEIN M.	HEADES SALDLEX VIRUS (TYPE 67 STRAIN USANDA-1103)	100	100					Ī
NO.		HUMAN CYTOLOGOALOVICUS (STIANDY AD169)	\$ 10						Ī
		EPSTED-BANK VINUS (STRAIN BPS-4)	30.335			-			
	,	HISAM CYTOMEGALOVIAUS (STRAIN ADISS)	308-526		-				
٦		HERDES SOULEX VIRUS (TYPE 6 / STRAIN UGANDA-1102)	6.30	330-346					
7	24 PROTEIN	HERPESYTEUS SADKINI (STRAIN 11)							
7		HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	208-223	341.567					
7	PROTEIN ULIES	HIBITAN CYTCHEGAL OVINUS (STRAIN AD169)	164-183						
_		HUMAN CYTCHEGALOVIRUS (STRAIN ADIM)					-		
-		HUMAN CYTOMEGALOVIAUS (STRAIN AD166)	\$	433-450					
MEAN MONTH		HUNCAN CYTOMEGAL OVIRUS (STRADY AD169)	3:1						
-	HTTOTIGETICAL PROJECT ULTI	HUNCAN CYTOMOGOAL OVINUS (STRAM AD169)	1793						
_	CHARLES AND THE PARTY OF THE PA	AUPLAN CT I UPLE DALLOVERUS (STRAIN AD109)	31.						
	CONTRACTOR DESIGNATION OF THE	ADMINISTRACT CONTRACTOR (STRAIN ADMIN)	13:18						
VAPOR I		MANAGE CONTROLLED AND CONTROLLED AND AND CONTROLLED	R	Ī	+		1	1	
			100	$\left \right $		1	-		7

PCGERE		10 84									
THE NAME	PROTEIN	All vacate into tierteriophages!			Г.	Г	Г	l		Ī	
PULD? HCMVA	HYPOTHETICAL PROTEIN ULIST	INDIANA CYTOLIS GAL DANIELE ASTERNO ABILET	4	AREAL	<u> १४४४</u>	V FVZHV	AREA!	AKEAS	AREA!	AREA	ANEA 9
PUNG FOWFI	URACEL-DWA CZ YCOSYLASE	FOWLYOX VIRIS (STRATE P. 1)	7	†		7				Г	Ī
PUND HSVED	URACIL-DHA GLYCOSYLASE	EOUNE HERNESVIEW TYPE PETERIN ARABA		†		+					Γ
PUMO VACCE	UNACIL-DNA OL FCOS YLASE	VACCINIA VIRIIS (STRAIN COSTALACIES)	2		1						
PUMO VACEV	LIMACEL-DWA OL YCOSYLASE	VACCINIA VIAUS (S FLAIN WE)	10.7			1					
ZNO VARV	UNACEL-DINA GLYCOSYLASE	VARIOLA VIRUS		†		1	1				1
200	URACEL-BNA GLYCOS YLASE	VANCELLA ZOSTEJĮVIRUS (STRAJN DIDAAS)	11.21	1	+	1		1			
A SA	CENE 44 PROTEIN	EQUINE HERDES VIRUS TYPE I (STAKIN ABAP)	-	İ	\dagger	T	$\frac{1}{1}$	1		٦	
	USI PROTEIN	EQUINE HERPESVINUS TYPE I ISTRAIN KINTIKKY A)		j	1	Ì		1		:	:
	PROTEIN UST HOMOLOG	PSEUDORABIES VIRUS (STRATIN NIA. J)	1	İ	-			-			
VANO GROV	HOLL I PROTEIN	STUNKIN CYTOMEGALOVIRUS (STIKAIN ADIGS)		ļ		+		1		Ì	
NO SECTION	PUTATIVE GLYCOPROTEIN USS	HEADES SINGLEX VIRUS (TYPE 1 / STRAIN 17)				1	1	1			
7283 HEV3	PUTATIVE CLYCOPROTEIN USS	HEAPES MADLEX VINUS (TYPE 2)	2 2		1	1	+	1	Ī		
PUSOB HCMVA	HYPOTHETICAL PROFEIN HALFS	HUMAN CYTOMEGAL OVINING ASTRAMA ANIMAN		1	+	1					
PUSIT HOAVA	HYPOTHETICAL PROTECNIDALFI	HUBAAN CYTOMOTOL GVIRTIE AFTER A FILER	3	†		1					
PUSIT HICHAY	HYPOTHETICAL PROTEIN HYLFF	HUDAN CYTOMOTIAL AVISTRE REPORTS AND									
PUSID HOLVY	HYPOTHETICAL PROTEIN HW. F3	HAMAN CYTOMOTORI DVINITE PETERIN ADMINI	2	Ť		-					
MUSH HOLIVA	INTOTAL PLOTEN HALF		?	Ę.		•	_			-	
PUBIT NOWA	•	MAINTENANCE CONTROL OF THE PRINCE OF THE PRI	31.76			7		-			
PUSIO HOLYA	•		38.40	999-17		-					Ī
MUSTIN HIGHWA	+	_	2	37.52				:	:	i	
AUSTIN HOLVA		MALAN CARACTAL CARACTAL CARACTAL CONTRACTAL CARACTACTAL CARACTAL CARACTAL CARACTAL CARACTAL CARACTAL CARACTAL CARACTACTAL CARACTACTAL CARACTACTACTACTACTACTACTACTACTACTACTACTACTA	20	_				-	İ	İ	
PUSJI HOVVA		HALLING SCHOOL OF THE STATE OF	130-142	178-703	214-213		-		-		Ī
PLESS LICENA	SARIY VINIT BAN DO CELLINA P.	INCHARACT I CHECAL CIVIROS (STRAIN ADIAS)	44.67	139-112				İ	İ		Ī
HRIT BOWL	TANDUNCTURE OF THE PROPERTY OF	HUMAN CYTOMEGALOVINUS (STRAIN AD 169)	170-743		 	F		l	ļ	1	1
HRIS LINA	WARANCE IN THE PARTY IN THE PAR	HUMAN CTICHECOLOVIAUS (STRAIN AD169)	916.246		-	-		İ	Ì	İ	
HR31 HOAVI	A DECISION OF THE STATE OF THE	HUMAN CYTOMEGALOVINUS (STRAIN AD169)	152.575		-	1		T	T	Ť	Ī
AUSTI MANA	ACTION AND REPORTED TO A STATE OF THE PARTY	HUMAN CYTOMEDALOVIALIS (STRAIN AD169)	34-48	391491	-	-			Ì	\dagger	Ī
PUSS HOAVA	KYPOTNETICAL PROTERS GARRA	PICHAM CTIONELOVING (STAIN TOWNE)	36-49	140-140		T		t	İ	T	
MISTO HOLIVA	AVPOVATOR IN THE PROPERTY IN THE PARTY OF THE	SHORT CALL CALL CALL CALL CALL CALL CALL CAL	146-269		_ 	-	-	t		İ	Ī
PURIT HONDA	KYDYTKITY' PENSEN BARY	JIUMAN CTIONEDALOVIRUS (STRAIN AD169)	163:138	208.313				Ì	T	T	Ī
VE X LSV	7 ED PROFESS		41-59			-	-			T	
PVOTE MANY	7 KD PROTECT	41	7				-		 	T	Ī
Τ	PLD PROTEIN	(DYIAN)	20-49			-	-				Ī
PVOTE PVX	7 KD PROTEDI	The state of the s	7						İ	Ì	Ī
Ľ	TKD PROTEIN	100	7				-		f	T	Ī
Т	US 121-1 PROTEIN		7								
T	135 KD PROTEIN	36 18 18 5 18	2	<u> </u>						İ	Ī
PVISK PVICE	13 KB PROTEIN		4.4						-		
PVINK TRVPL	IN ED PROTEIN		M								
DAVAM INIVE	IELICASE	T	10.00	1	-						
PVILLE MEMY	(4 KD PROTEDI	BALLY STRUE MOTAL VILLE MELLY	707-107	1914	013-1037	<u> </u>					
_	IE KO PROTIEM	T	25.52	i i		+					
VIM VACCV	PROTECN B19		114-113	12.13	+	+		1	1		
-	IA MUTEDA	VOLUS	022-450	115.227	+	\dagger	+	†	1	1	
Ī,	I A PROJECT		147.569		+	\dagger	+	+			
1	A PROTEIN	LI YAUS	344-363		1	\dagger	+	1	†	1	1
MAN CHAN	IAMOREN	STILLINGTON	775.600			+	+	+	1	1	İ
Ť	IA MOTEON		8		+	\dagger		1		1	
	IA PROTEIN	CUCUMBER MOSAIC VINUS (STRAIN Q)	114.79		+	+	1	+	1	1	
Ĩ.	A PROTECT		(13-48)	103.606	+	\dagger	+	\dagger	+	†	Ī
PATE HOUSE	STATE MACHEN		Т		+	\dagger	+	\dagger	†	\dagger	T
Ť	I IN LANGE		Γ	193.207		\dagger	+	+	†	1	
+	National Section 1			103:201	-	-	-	t	+	1	
VATE PERV	19 6 ED PROTEIN	SEAN WESTERN YELLOWS VOIUS (ISOSATE PL.1)		134-157		\vdash	-	1	\dagger	\dagger	T
Т	1A PROTEIN				-		-	-	\dagger	t	T
			135.303	759.777		L	-	-	-	\mid	
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	ATTURE OF THE PROPERTY OF THE	All Virgari (No Sectoriopheges)	*****		1					
100		COMPER AND CACHE LICE TO BE COMPER	ı	T		Т	Т	Ī	_	
100	7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7	TOTAL AND THE PROPERTY COMMISSION OF THE PARTY COMMISS	1		1	1	:			
AVI VI	TA TRUEIN	COMPTO ASSERTING VINES		:	-	!	-	:	Ī	-
PVJOK IRVIC	THEOTROIEM	INDALLO AATTI E VIRIO (SI INDIE ILM)		 	1			Ì		l
VIII TORISY	NI 7 KD PROTEIN	TOBACCO SINCAK VIRIA (SITAA)	A.				1		j	
PV162 AS/87	KISAZ PROTEIN	APACAM SWINE PENER VINOS (SIRAIN BATIV)		 			1	1		1
733	LIS 173 PROTEIN	AFICAM SWING PEVER VIRUS (SFILADA LISSY)		1			İ	1	İ	.
VIII 450.5	LIS 311 PROTEIN	A RUCAN SWINE PENT N VIRUS (STRAIN LISST)		1	!			_		
ı	COWPLA CALCACITI MOTTLE VIRUS		3							1
_	14 PROTEIN	CUCUMBER MOSAIC VIRUS (STRAIN FMY)	26.23		-					
1	3A PROTEIN	CUCLAMBER MOSAIC VIRUS (STRATIVIA)	216-239							
ı	SA PROTEIN	CINCUMBER MOSAIC VIRUS (STRAIN O)	116.339							
PWA CAW	IA MOTEON	CUCUMBER MOSAIC VINUS (STRAIN Q)	214-213					İ	t	
AND THA	CHACINGRID LAGGARE WATER OF TRAIN W		214.338	 -			İ	ļ	r	Ī
100	TA LEGITORY	A CALAN PLACE PRINCIPLE BEALD SHAPE CIBILS AND			-		İ	1		
- N. V.	T EXTREM	A TICK INVECTIOUS BROWNINGS THAT IS THE TENDER TO			+		j		İ	Ì
	JA PROTEIN	A VIAN IN ECTIONS BRONCHITIS VIRUS (STRAIN MAI)	27.							
PVJA BVTJ	SA PROTEIN	AVIAN DEECTIOUS BRONCHITIS VIRUS (STRAIN PORTUGAL) 122/12)	=======================================	_	-					
PV3A BAUS	JA PROTEIN	A VIAN DIFECTIOUS BRONCHITIS VIRUS (STRAIN UNITS)	2		-		Ì	ĺ	İ	
l	14 Horkin	HOMATO ALPERMY VIRING	10%.164				İ		İ	
POLINE BRIDE	CONTRACTOR OF THE PROPERTY OF	DABLE V CORDE LEGGAL CORDS	1		1	İ	İ		1	
	THE PROPERTY	DALLE SINGE MOSAIC VINUS		1	+		j		i	
PVMK BWYVE	PROTEINES	CAMINE ENTELUC CORONAVIRUS (STRAIN R.) II)	97.116						T	
PVYOR TYNYA	H KD PROTEDY	TURNIP YELLOW MOSAIC YITUS (AUSTRALIAN ISOLATE)	S-2							
PWKK ALVAL	NO PLOTEIN	TALFALFA MOSAIC VIRUS (STRADY 425 / ISOLATE LEIDEM)	\$		<u> </u>				İ	Ī
PVAGS VACCO	PROTEIN A4	VACCINIA VIRUS ISTRAIN COPEMIAGEN	33,344	<u> </u>			İ	İ	İ	Ī
UNITED STATES	11	CLAMBA CHAIR AND AND			ŀ		İ	Ì	1	
		TALCETA THOS (STEAM WA)			+		1	İ	İ	
A 100 A	TIONE IN A	VACULA VIRUS	1	1	•		Ì			
PVACCC	PROTECU AS	VACCIDIA VIRUS (STRAIN COPENIAGEN)	*						_	
	PROTESTA	VARIOLA VIRUS			_					
PVAII VACCC	PROTECHAIL	VACCINIA VIRUS (STRAIN COFEMINAGEN)		-						
	PROTECHALI	VARIOLA VIRUS	23.44 141.140	100-111						
	PROTEINAL	VACCINIA VIAUS (STRAIN COPENIIAGEN)	19.63		ŀ			İ		
PVAIR VARV	PROTEIN A14	VALUOLA VALUS	19-91		•					
	PROTEINAIG	VACCINIA YIRUS (STRAIN COPEMIAČEN)	191-161							
PVAIS VARV	PROTEINAL	VARIOLA VIRUS	146.34							
_	SE KED ABORTIVE LATE PROTECN	VACCIMA YIRUS (STRAIN COPEMIAGEM)	439.443					<u>!</u>	İ	
Т	IS ICO ABOATIVE LATE PROTEIN	VACCOMA VIRUS (STRAIN WR)	439-443	_			İ		İ	Ì
_	34 KD ABOATIVE LATE PROTEIN	VALIDLA VIAUS	Г				l		l	Ī
1	PROTEIN AND	VACCINIA VIRUS (STRAIN COPE MILIGEN)	107.131 183.200				l		T	Ī
PVAN VALV	PROTEDUAN	VALIDLA VIRUS	I							Ī
VALS VALV	PROTEONAL	VARIOLA VIRUS	Γ					İ	t	Ì
VAN VAPO	PROTEIN A31	VACCINA VIBIR (CITAIN WILL AND ICTRANCEDISTING					İ	Ì	T	Ì
VALUE VALUE	PROFFICE AND	VARIOR A VIRIS					İ	1	1	
CANAL VALVE	PACHE DA A 15	CAPTONA VARIACIONAL VID. AND COM AND CORRESPONDENCE NO.	20, 20,					1	İ	Ī
2010	11 7 7 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1		121					1	1	
2010	AND	VAPORIA VIBILIA CATA POPENIA CENT	200				İ	Ì	İ	Ī
ים זנו מזאים	PACTED A 14 DAY CAREAGE	CAPPENS CREEK COM AND	77.17	 -			Ì	t	İ	
VAN VANC	PACIFIC A15	VACCIDED VIEWS (STRAIN COSEMIANEM	T	_				t	1	Ī
TOTAL DITTO	SEATHER THE	TOACHAN CHAIR SEE WATER	2 3				1		1	Ī
	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1			-		Ì				
1	CEASEL STREET	VALLIFIA VIRUS (SIRAIN COTENIALEN)	R							
1	THOUSEN AND PRECORDER	VALLINIA VIRUS (STRAIN COLL MINOER)								
AVV.	PROTEIN A41 PRECURSOR	VACCINIA VILLE (STRAIN WIL)	167-71				_			
YAA! VAIV	PROTEIN A4! PRECURSOR	VARIOLA VILUS								
PVA1 VACC	PROTEIN A41	IVACCOMA VOLUS (STRAIN COPENIAGEN)								
PVA1 VACEV	PROTEIN A47	VACCINIA (STRAIN WR)		•						
744	PROTEIN A47	VAUOLA VIRUS	19.79 201.226	_						
WAJ VACE	PROTEIN ASS	IVACCINIA VIRUS ISTRAÍN COPEMIAGEN)	ŀ	_						
	MOTER ASS	VACCIMIA VIRUS (STRAIN W.R.)	20,240							
	ALI FROTEIN	JORET CUILY TOF VIRUS	56-75		I		_			

	ATTION A	All Virgon (No Bectertophoges)		ľ	-	Ī	ſ			İ	
	CAUTE	VIAVS	AKKAI	AREAS	AREA 3 A	ARENI	ARCAS	ARFAG	\$ 748Y		1000
	- 1	CASSAVA LATENT VIALIS (STRAIN WEST RENYAN IN)	Γ	;	Г	ī	Т				700
	┪	CASSAVA LATENT VIELD (STRAIN NEW RIAN)	-		;	:					
	ALI PROTEIN	DEET CURLY TOP VINUS	1	:	:	:	•				-
NAL G	AL) PROTEIN	CASSAVA LATENT VIRUS (STRAIN WEST KENYAN 240)		İ	İ	I	Ī			1	
WAL 0.W	ALS PROTED	CASSAVA LATENT VIRUS (STRADY HIGERIAN)	13.93		t	Ī				Ì	
7	ALS PROTEIN	TOWATO YELL OW LEAF COIL VINUS (STRATH MARMANDE)	10.00	Ì	+			1			
C C	AL) PROTEIN	TOMATO YELLOW LIAP CURL VIRUS	1	İ	<u> </u>	Ì					-
VAT CANVC	AMID TRANSMISKIN PROTEIN	CAUCHLOWER MOSKIC VIRUS (STRAIN CH. 1841)	135 36	 	!	Ī	i	ļ	;	- : :	
NA SAME	APHID TRANSMISSION PROTEIN	CAUL BLOWER MOSAIC VIRUS (STRAIN DAY)	191	İ	1	1	Ī		Ī	Ì	
3	APHED TRANSPESSION PROTEIN	CALL DEDWER MOSAIC VIRUS (STRAIN BBC)	1111	İ		T	1				
2	APHID TRANSLUSION PROTEIN	CAULDIOWER MOSAIC VINUS (STRAIN NYSISI)		Ì	1	-					
PVAT CALVY	APHED THANSAISSION PROTEIN	CALL OF LOWER MOSAIC VINUS IS PRAIN PULLY		1		1		1			
PVAT CARVE	APHID TRANSMISSION PROTEIN	CAULIFOWER MOSAIF VIRIS CTRAIN CTRAINS		1		1					
PVAT CLAN		CALE LELOWER LANCA IN CHESTE (175 2 IN COLOR)	100			1					
WAT CEEV	AMED TRANSMISSION PROTEIN	CABBATTON NOTICE BEST 100 101 10	9								
PVAT PLAND	APATO HANGAGISION PROTEIN	ICHORAT LANCE COLOR SERVICES	9							İ	
PVBCI VACCE	PROTEIN	VACCINI MESON, VICTO (STRUCK DAS)	13:13			-					
DAYYO COMPA	PEOTEN #1	ACCOUR VIAUS (STRAIN COPENIAGEN)	155-170		-	-		Ī	T		
200		VACCORA VIRUS (STRAIN WR)	041-351	-	-		Ī			İ	
1		VACINGA VILLE (STRAIN COPENHAGEN)			-	İ			Ì	Ì	
		VACCINIA VINUS (STRAIN WIR)	15.5	İ	\mid	Ť	Ì	I		1	
A		VAUGLA VIRUS	40.5		ł	1			1	1	
AVEG VACG	PRECURSOR	VACCORIA VIRUS (STRAIN LCIGHO)	341.331		t	T			Ì		İ
74CC	MECURSOR	VACCINDA VIRUS (STRADA COPENNAGEN)	111.111	T	1	İ	1	1			Ī
LACO VACO	PRECURSOR	ACCOUR VINUS (STRAIN LISTER)		1	1	İ					
PVBOS VACEV	PRECURSOR	ACCINIA VINIS (STRATA WE)		+	-	-					
PVBOS VACEV		VACCIDOA VIDITA CITATA MAIL AND COTO AND CONTRACTOR			1	-					
PVB19 VACCE		AACTINIA VIDIN (618 AND CONTAINS OF THE				1					ĺ
WELL VACEV		VACTORIA CONTRACTOR CONTRACTOR								ļ	
PVB IS VARV		AND A VALUE AND THE									
PVB IT VACCE	MOTERIALIS	VACCINIA VIBILITY DATE POST SALVENTA	2			-				†	
PVIII) VACCV		ACCIDE VINE CONTRACTOR	37:170								Ī
WALL CLVK	BLI PROTEIN	ASSANAT ASSET WASTE ASTA AN INCRES WELL ASSAULT				-				-	
PVBLI CLVN	BL! PROTEIN	CASSAVA TATEM CIBILS AND WEST STATEMENT				-					
ł	BLI PROTEIN	SOURCE DAY CHAIR COLLEGE	34:5		1						
PVBRI ALLAW	BAS PROTEIN	ABITE TO LANGAGE STORY AND THESE STATES	20.00								Ī
PVBB! BOAV	BALL PROTEIN	FAN OO DEN LANGE WITH		1						ŀ	Ī
PVERI PYNV	MI PASTEM	OTATO VELL DIE LINEAUT VEHIE AGGESTE GEGETTER AT	3								
PVIAL ELEV	BRI PROTEIN	SOURCH LEAD CINE VISIT									Ī
PVC01 VACCC	PROTECT	ACCINIA VINUS ISTRAIN COPENHACIEN		+	1						
PVCBI VACEV	PROTEINCE	VACCINIA VIELIS (STRAIN WR)	2 2			<u> </u>					
PVC01 VARV	PROTEIN CI	VANOLA VIAUS				1					Ī
PVCE SPVICA	INTOTABLICAL MOTERN CO	SHOPE FUNCKA VIRUS (STRAIN RASZA)		1		1		1			
PVC93 EPVKA	G-PROTEIN COUPLED RECEPTOR HOMOLOGICS	HOPE FIBROALA VIRUS (STRAIDS RASZA)	Ţ	100	+	1					
A VACOC		VACCEDIA VIRUS (STRADI COPENIAGEN)	L	+	1	†	1	1	1	1	
		VACCOGA VILUS (STRAIN WA)	10.E		+	t	T		1		
17.11	MINUTELLAL PROTRINCE	SHOPE FIBROMA VIRUS (STRAIN KASZA)	Ę	-	 	Ť	T	T	İ	i	
2000		SHOPE FUBROMA WRUS (STRAIN KASZA)	8.52	1	+	t	İ	t	Ì		
	TRUIEN CY	VACCODA VIRUS (STRAIN COPENIAGEN)	65.50	<u> </u> 	+	╁	1	1	1	1	
200		VACCINIA VIRUS (STRAIN WR)	55.53	+	+	t	1	1	İ	1	
AVIVA OILA		SHOPE PERCHAN VIRUS (STRAIN KASZA)	101.50	-	+	t	T	t	İ	1	1
PVCIS VACCV		VACCOMA VILUS (STRAIN COPENIZACEN)	17.77		H	t	t	t	T	+	Ī
PVC16 VARV		ACCIMIA VIRUS (STRAIN WR)	47-44		ŀ	t	İ	T	t	1	Ī
PUCIT VACAT	969	VALIDIA VIRUS	4		_	t	t	T		\dagger	Ī
VCI VACO		VACCIMIA VICUS (STRAIN COPEMBAGEN)	41-44			t	T	ļ	\dagger	\dagger	
PVC31 VACCE		ACCURA VIRUS (STRAIN COPENSAGEN)	101-336				T	T	t	1	Ì
PVCA EBV	MAJOR CAPSID PROFEIN	VACLARIA VICTOR (STRUM COPENHAGEN)		П				t	t		T
		FILTHWAY VINIT (SIRVIN BYS.4)	148-173	164-31(10)	1012.1095	H			f		T
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Pecent	19115-31314	AM Vignature and Management and American			ŀ	ľ				İ	
THERABIL	ZKOTEIN	YINUS	Alicki			78.74		4 610 4	ABEA 3	4004	****
ACA HONY	MAJOR CAPSID FROTEIN	HUMAN CYTOMEGALOVINUS ISTRAIN ADION	661.684	20.00	1	1	i	1		ī	-
100 HEAT	MAJOR CAPSID PROTEIN	HEADES SIMPLEX VIAUS (TYPE 1/STRAIN 11)	313.303	1	1111111	İ				<u> </u>	Ī
7.C. 25.V.	MAJOR CAPSID PROTEIN	EQUINE HERPCSVIRUS TYPE I (STRAIN ANALY)	32.55	_	ī	1				İ	
ACC MALE	MAJOR CAPSID PROTEIN	ICENPESVIRUS SAIMIRI (STRAIN II)	30.70		11.17	04.1.1000				-	
	MAKON CASUM PROJECT	VARIABLE A STREET STREET STREET	3	7							•
PVCO3 NPVAC	DNA. BRIDDING PROTEIN	A (MOCHANIA CALIMBAICA MICHARD DOLVIEDIORI CIRIL			2 2	Ì				- 	
PVD01 VACCC	PROTEINDS	VACCINIA VIRUS (STRAIN COPINIACIN)	2 2			Ī	-				1
PVD6) VACCV	PROTEIN DS	VACCINIA VIAUS (SIRAIN WR)	91.71							1	
PVD0) VARV	PROTEIN DI	VARIOLA VIRUS	2.39		1	ŀ				İ	
PVD05 FORFI	41 6 KD PROTEIN	FOWLYOX VINUS (STRAIN PP.1)	246.365	113.33	-	Ī	Ī			İ	
PVD05 SPVICA	PROTEDUDA DA	SHOPE FURIONA VIRUS (STRAIN KASZA)	12.3	1	İ	T	Ī			Ť	Ī
PVD65 VACCC	PAOTEIN DI	VACCINIA VIRUS (STRAIN COPENIAGEN)	36.06	56.35	115.134	Ī.				1	1
PVD05 VACCV	PLOTEIN DS	VACCINIA VIAUS (STRAIN WR)	36,160	3.13	115.116	ŀ				İ	
PVD05 VARV	PROTEIN DS	VALIOLA VIRUS	330-340	T	-	Ť				İ	
PYDEP CALVC	DNA-BINGING PROTEIN	CAULIFLOWER MOSAIC VIRUS ISTRAIN CALIBRIT	1	Ī	<u> </u>	1		İ		İ	
PVDBP CLAVO	DNA-BINDING PROTEIN	CAULTILOWER MOSAIC VIRUS (STEATH DAI)			Ì	1				Ì	
PVDEP CAMVE	DHA BINDING PROTEIN	CAULIFLOWER MOSAIC VIRUS (STRAIN DRC)			<u> </u> 	Ī				j	
PVD6P CAMM		CALL PLOWER MOSAIC VILUS (SHIAD) MYSISS)	1			1				İ	
PVDBP CAMVS		CAULIFLOWER MOSAIC VIRUS (STRAIN STRASBOUNG)	7.		+	†				1	
١,	PROTEBLES	VACCINGA VIRUS (STRAIN COPEMIAGEN)	2	144,116	140.000		Ī			İ	
PVECT VACEV	PROTEST ES	VACCINIA VIAUS (STACIN WR)	Ī	Ť	-	T	Ī				
	MOTERNES	VALIDLA VIDUS	Τ	155.160	\$40.415	1	Ī			İ	Ī
JVESS VACCC	PAOTECNUS	VACCORIA VIBLIS (STRAD) COPENDIAGEN)	Ļ	Т		Ì	Ī			İ	
	PROTEINES	VACCINTA VIXUS (STRAIN DADEN I)	134.330	Ī	\dagger	+	T				
	PROTEIN ES	VACCOMA VIALUS (STRAIN WR)	324 339		t	T	Ī	Ī		T	T
- 1	PROTEINES	VANOLA VIRUS	174.330	Ì		ŀ	Ī	Ī		T	Ī
JAZON NOZA	PAOTEN EL	EMIAGENI	18965	Ī		T	Ī	Ī		Ť	Ī
_	PROTECHES	VACCINGA VIRUS (STRAIN WR)	410-411			l					Ī
_	PROTEIN EA		Г	167011		-					Ī
-	THOUSEN TO	VACCIMIA VIBUS (STRAIN COPENILACEN)	154-130			-					
PURE UNIO			24.376								
_	PROBABLE EL MOTENA 1	1	N	Ì		1					
-	BARLY 10 5 KB PROTERS	ALTOGORACIA PARTICIPATION OF THE PARTICIPATION OF T				j					
MEI BAN	El Roteix	T	Т								
Ť	El Motera	~			1	j					
	El Paolitis	COTTONIAL EALBIT (SHOPE) PAPIL COLIAVIRIES (STRAIN RAWLAS)	Т		<u> </u>	Ť	Ī		1		
П	MINORIE	7	E			İ	Ì	1	1	1	
٦	EI PROTEDI		T		l	İ	T	Ī	Ī	Ì	Ī
Mai Mai	EI PROTEIN	SUMAN PAPILLONA VIBUS TYPE II	Г	11:11	146.364	T	Ì		Ī		Ī
Ť	E MOTEN		33.25				Ì	Ī	T	İ	
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Τ	El PROTEIN		X		-						
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	El Photesi		2								
	El Phoresi		╗		1	1				<u>-</u>	
T	II PLOTED				1		j				
Г	El Profess	RIGING PAPELLOMAN INUS TYPE I	7		<u> </u>	1			İ		
	PROBABLE ESPROTEIN	US IS TRAIN KANSASI		İ	1		i	1		1	-
П	EPROPER	1	900	İ	+	t	Ì	Ī	i	j	
П	LI PROTEIN		91.18	İ			Ì	1	1	İ	
	EJ PROTEIN		20.00	İ	-	\dagger	Ť	1		†	1
PVEJ IOVIA	Charles		314.30		<u> </u>		İ	Ť	İ		Ī
	E PROTES		311.534					Ì	T		Ī
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100	THE STATE OF THE S	PROPERTY OF THE PARTY IN THE IS	20.707							
	E2 PROTEIN	HEMAN PAPII LONIA VIÁUS 1 VPE 19	917	-		F	<u> </u> -		Ì	ĺ
	E2 MOTEIN	HUMAN PAPIL CONTAVINOS TYPE 43	1000		<u> </u>	-	 			Ī
2	ET PROTEIN	THEN LAW PARTICISTATION PRINT TO THE TO THE TANK			<u> </u>	<u> </u>				
	E MOTEIN,	SHALL PARTICIPATIONS TYPE AND	11.79	<u> </u>	1		1		- 	
	PROBABLE ES PROFILM	DELL PAPILLONIAVIIUS		<u> </u>	-			-	!	
1 VES 100 VI	ESPROTEN	PYCHY CHAPACT PAPER LINE COURT TO THE	1	-	•	:	_		-	
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	TACKS INTO THE PROPERTY	TARMAN FAFE (MAY INC.)	14:34 14:34				_			
	PRUBABLE 24 PROTEIN	PERSON PAPILLIDAIA VIII IS 17 PE 41	-	<u> </u>		-	<u> </u>		Ì	
	PROBABLE EA PROTEIN	HANGAN PAPIL LOMANIAUS TYPE SI	19:55	<u> </u>		-	 			
١.	PROBABLE EN PROPESA	AUCSUS PAPILI CANAVINITE TO BE		+	<u> </u>	1				
DVESA HPVIII	PECSAGE EST PROPEN	HARANDA PARTICIPATE STATE TO STATE S		<u> </u>		j				
	Period and direct period		-							•
		HENNE TAPE CONTAVENCE INT.	14.43			•				
	ED PROTEIN	BOVING PARILICALAVIRUS TVPI: 1, AND 1171: 2	7.7	_		•	_			-
	PROGRAMS ES PROTEIN	HAMAN PAPILI CALAVIBILE TYPE II		1		<u> </u> -				
	PROBABLE ES PROTEIN	HABITAN BANK BRATA WATER SOME ST		_			_			
67A	POND A BLANCHEN		2			_)
ĺ		TILDOWN FATTLE UNITARY INTER 41	5				<u> </u>			Ī
ı	PROBABLE ES PROTEIN		=		<u> </u>	<u> </u>	<u> </u>	1		ï
_	PROBABLE ES PROJESA	INMAN PAPILLONIAVIRIES INFI SII			:	_			_	
_	PROBABLE ES PROTECIA	MICHIGAN PAPHI CALLAVIANT IN THE STATE OF TH		:	· ·	:	:	:		-
PVES BPV	EA PLOTEIN	BOUNDS DATE: CALL CALL STORY		1	_					1
14 P. 15 P. 1	EA DECHES		11-12	_		_	<u> </u>		İ	
		COTTONTAIL RABBIT (SHOPE) PAPILLONIAVIRUS (SHAIN KAKSAS)	17:9	<u> </u>	<u> </u>	<u> </u> -	 -	-	İ	i
		MONAN PAPEL CONTAVINUS TYPE I		l		 	 		Ì	
		HABITAN PAPILI DATA VIBITA TVSE 14		1	<u> </u>	-				
ı		## MAZE SAME PACE CITE SEEP 11		<u> </u>	<u> </u> -	ļ	į			
ı	TA DEMINER	MARKET MARKET STATE OF THE ALL		_	-	_		:	:	i :
17.0		HUDIAM PARLICIMA VIRUS TYPE 35	2.5	<u> </u> 	<u> </u>	!	;	:	į	:
		HUMAN PAPELCOMA VIRUS TYPE SI	2.5	<u> </u>		 -	<u> </u>		İ	
		HUMAN PANILONIA VIRUS TYPE 11	1	<u> </u> 	 		 	Ī	Ì	
1		INCALAN PAPILLOMAVIAUS TYPE 30		l		-	1	1		
^	EAMOTER	MECROMYS MINEUTUS PAPIL LOMAVIRUS	17.1	Ţ		-	 			-
		COTTONIAL BABBIT (SHOPE) PARILL CANADAM CENTAL DE LA CANADAM	Ī	<u> </u> 			 	-		
PVET HOVES	(1) PROTECU	INTERIOR PARTITION AND THE PUBLIC PUB							!	<u> </u>
1 PV	FFEOTFIN					_	_		İ	
PVIT DVG	MANAGER								İ	
PVET LIBVI	S MOTOR		10.11						İ	
100 Carlot	CHECKS AND COUNTY		74.105	L		<u> </u>			İ	
1000	CALL I M LO PAULEM	AUTOGRAPHA CALIFORNICA MUCLEAR POLYHEDRÖSIS VIRUS		2					1	
	VICAL EXPLOREING FACTOR	Γ	1411	160 677.444	3				Ì	Ì
A	ENVILOPE PROTEIN		Τ	Ť					Ì	
ADA DIVI	ENVELOPE CLYCOPROTEDY PRECURSOR	NAWI 31 IVA II	T		1					
VDV LAV	PROBABILE ENVELOPE PROTEIN		Ī							
A TAT A CAN	NISTANCE ENVIRONMENT IN THE PROPERTY OF THE PR			Į.		-	$\frac{1}{1}$			
PVD/V	MACHOR DAVELORS PROTEST				+		1			
PVENV MCVI	PACADA IDAVEL DIFE PAGTEIN	MOLLUSCUM CONTACTOSTAL VIRUS SUM FYRE 3	T							
PVENY THOCK	THANTONE OF ACOMODIED MECHASON	Ī		Т		1				
Г	ECON. I SITE PROTECT ETM	1	1		 -					
Т	14 K.D. LLA KYAL LUS LATANA DE OTERNA DES CHINACAS	1	12:103							Ī
PVF65 VACO	N KO MAKOR LIGITARIANE PROTEIN PARCING COM	VAPORAL VIRIALITY IN CORPUS CONTROL VIRIALITY	20,705							Ī
т	M. P.S. MANY LANGES AND DESCRIPTION DESCRIPTIONS		280-309				L		İ	
Т	14 P. LALING LIGHT AND BEAUTIFUL BEAUTIFUL OF		301.306	_		<u> </u>				Ī
т	PER MEN AND THE PERSON OF THE		100-105	<u> </u>		 -				Ī
		VALUMIA VIAUS (STRATIV COPENITAGEN), AND (STRAIN L.IVP)	36.300	<u> </u> 		 -			Ì	Ī
2017	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	VACCIPITA VIEUS (STRAIN WR)	14:300	<u> </u>		-		Ì	İ	Ī
		VAUOLA VIIUS	26.38 26.38	<u> </u> 				1	Ì	Ī
77.7	TAULUS III	S (STRAIN COPENIAGEN)	111.10	<u> </u>			1	Ţ	İ	
	TRUITMENT I	VALIGLA VIRUS	711.19	-			-			Ī
	CAULEIN F13	VACCINDA VIRUS (STRAIN COPEINIAGEIN)	1	-	-		-	İ		
				ł	$\left \cdot \right $	$\left\{ \right.$		1	1	7

Percent.	P12 F72 P19	All Virgan (Na Bosterianhores)			-	-	-	-	+	t	
¥	PROTEIN	CAUS	AREAL	ABEA1	AREA! AB	ABEAN A	ARIA AR	ARTA 6 AH	AHEA3 A	APEAI	1111
٥	PROTEINFIS	VACCINIA VIRUS (STRAIM L.IVP)	2	:			1	<u> </u>	!	,	
PVFIS VAAV	PROTEINFIS	VARIOLA VINUS	31.51				_	-		-	
PVFPI JOWEV	PROFESHIP	OWLPOX VIRUS	297.113								
PVPP3 SOUPV	PACIENT FF	FOWLPOX VAUS	111-104								
WHI CLW	PROFESSION	- APRIDOXVIRUS (STRAIN KS-1)	166-151								
PVFFF TOWEV	PROTECNIFOR	FOWLPOX VIRUS	63-70							İ	
PWIN CAVK	CHAMOTEM .	CAPAIPOXVIRUS (STILATN KS-1)	51-34								
PYFUS CHUNZ	16 KB FUSION PROTURK	ORU VIRUS (STRAIN MŽI)	Ŧ					_		_	
PVPUS VACCO		YACCINIA VIRUS (STRAIN WR 65-14)	13.54		_						
PVC41 MSVES	PEOTEN	EQUING HEAPES VIEUS TYPE I (STRAIN ABAP)	261 - 193 193	_					<u>-</u>	<u>'</u> 	
PWZBI KKWI		CTALUMED HE RESENTUS I	216-313	317.319	319-015	_			l		
L.		VACCEMA VIRUS (STRAIN COPEMHAGEN)	364.338	T	-	†			T	İ	
Ļ	PROFEDUO	VACCORIA VIRUS (STRAIN WR)	Т	313.314		1	L		t	T	Ī
1	PASSEDIGI	VALICIA VIRUS	Г	116.305		†	<u> </u>	<u> </u>	<u>-</u> !	-	:
SALE POLA	NAMES OF THE PARTY OF THE PROPERTY.	VARICEL A. POCTER VIELS ATTENDED IN MASS		İ	<u> </u> 	i	<u> </u>	<u>i</u> 1	<u>:</u>	!	!
		VACTORA VIDIR (CTRAIN COREMIACEN)	1		ļ	†	+	<u> </u>	1	Ì	Ī
		CARLOT A MAIN			+	†		+	1	İ	Ī
т	THOUGH OF	VANCES VINCE		İ	1	†		$\frac{1}{1}$	t	1	Ī
	100 COLUMN 100 COLUMN	CABINE A WALLE			+	1		+	\dagger	1	Ī
	ALCO SE	ULPHAN WEIR ATTAIN CARENALIERS		Ť		†			\dagger	T	Ī
	SECRETARY OF	MACHINE AND CONTRACTOR CONTRACTOR				†		+	1	†	Ī
Т	TACHEST OF THE SECTION OF THE SECTIO	THE STATE OF THE S			t	†		+	1	1	
	MITOINE IN COME INCREMENT TO THE	CIALUMU MENTERATION I	17.50		+	1	1	+	1		1
Т	MATERIAL COM IN MEMBERS TRUITING	REINFURGER FRIENDS I		****		t			1	1	Ì
		EXCENTION SAME (STEAT !!)			1	+			1		
NO! ION!	NACTE OF STREET	CTALUAD MARKASYING I	101-123	91100	+			+		1	
IN CO.	J'r HOSELF	EXAMINATED VINDS				+	+	1	1	1	Ī
1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	MATCHE IN AL CARE IS PROJECT	CAPTES VACUO SADAGO (STRAIR 11)	24-02	1	$\frac{1}{1}$	†	+	+	1	+	
Ę		LINES FOR CHANGE FOR TANABLE				†		1		\dagger	Ī
Т	# FILT	ISPECIAL ASSA VISITE COVINCIAL DE			+	t		+	\dagger	T	T
PWGS DRVII	WHO THE STATES	CTACINED JORDY SVIETS 1	100.131			t	1	ł	\dagger	\dagger	Ī
FVGS LRVS		CATUALIS 18 EMESVIEUS 1	114.333	T		+		\dagger	t	\dagger	
IMBN JIDA		ICTALUNIO RESPONDOS I	13:15:	T		l		l			Ì
Т		HEAPESVAUS SALMIN (STOAM II)	201-236			t	-		l		Ī
Γ	HYPOTHETICAL CENE 35 PROFEIN	ICTALUAIS HE IN ESTABLIST	133:163	915:10		r			-		Ī
	HYPOTHER RICAL CENTERS PROTEIN	EDPESYIRUS SADAIN (STRAPH II)	14.40			-		L			
7	AVYONALYICAL CEMENTO PROTEIN	ICTAL UNID HE DPE SYINUS I	į			1					
Ŧ	NATIONAL MANAGEMENT OF MULLINGS	K. IALUMU PERUSATURUS I			1	İ					
CATA CIONA	CATAS AS PROSTEIN	ANGLELA-COSTER VIRUS (STRAIT DURINS)	201	, ,	1	1		+		1	
STATE STATE	DOSCHELL I FROM AND SIN FINANCE	HAVE THE PRESENT OF THE PARTY O				†		+	+	\dagger	1
INHI STONE	AVYOTHETICAL CLEME 19 PROPEDI	CTALINED TO BE SYLVE !	T	976.000	1011.101	T	+	+	\dagger	\dagger	ĺ
PVOM HIVI	HYPOTHETICAL CENT 40 PROTEIN	CTALUAD MANYSVINUS I	Т	Т		\dagger		+	\dagger	\dagger	
PVGAT HSVII		CTALLIALD RECOVERYS!	<u> </u>	Т	344-360			+		$\frac{1}{1}$	Ī
PVGAI MSVII		ICTALUMD HEIDESVIRUS I	Г	153.178	311.345 511.	\$11.538		-	-		Ī
PVOM HISMI	-	CTALUND RENPESVRUS I	*	980-607	937.963 134	1344-1230		-			Γ
I INSH TYPNA		ICTALUND KENTESYAUS I	[71.9]			r		-	-		
PVGIO HISVEA	PROS TRANSCRUPTION ACTIVATOR EDRUI	HELDESYDIUS SADVINI (STRAIN II)	5.16	30.03		h		-			
PVGSI HSVIS	HYP COVE SI MEMBRANE PROTEIN	CTALLIALD HE APPEAUNT I	Ž	M-103							
PVGS HSVI	HITTORIO INCAL CAPAB 31 PROTEIN	ICTALUNUD MERVESVINUS I	174-131	i	-	j			+		
PVOS MSVII	INTO THE TICAL COMESS PROTEIN	CTALUMED HE RESVINUS !	2	2	100.300						
VOS HSYSA	HATFOLDE INCAL DEPEND PRIOTEIN	POLICE SATING (STILATIV II)	8		-	1		1			
PVOM PISVI	STRUCTURE OF THE STRUCT	RCIALUM DI MESVINUS I			7				1		
SONG DOOL	WISCONS TO LEGENDA AND SHOULD AND SHOULD BE SH	CTALIBITION OF CURING 1	T	Т	111111	10.01		†	1	1	1
Т	CONE SPROPEDI	PROPLASMA VIBILS 4	1			Ì	+	+	\dagger	l	Ī
PVOZO UKVII	HAND HOLDER AL CENE AD PROPER	7. A. 1. 4. 10 17 17 17 17 17 17 17 17 17 17 17 17 17	T		1	†	+	+	\dagger	+	T
1]		1	1	1	1	1	1	7

MCENE	PIICTIZIP	All Virges (No Becieriophoges)	П	П	П	гт	П				
INVESTI	PROTEIN	VIRUS			3	7	3	1000	Т	т-	1
PVG61 HSVI	HYPOTHETICAL DENE 61 PROTEIN	ICTALUATO PERCES VIRUS I	Ī,			$\left\{ \right.$				\dagger	
NOV.	HYPOTHETICAL GENE & PROTEIN		Т			I			†	r	
	NATIONAL CEPT OF TACKET		Т	135.17	2.53	165.53	1347.1134	1347.1369		ŀ	
1000	INVESTMENTAL CENTERS AT PROTEIN	KETALURID HEADESVIRUS I	Γ	Т	Т	332.745	•	_	1315-1341	Ī	,
MINES SOVI	CORNEL A PROTECTA	SPIROPLASMA VIRUS SPVI-RSAZ B	23.63								
PUNK MAVI	KAYPONOTHE AL DENE TO PROTEIN	ICTALUAD HEAVES WALLS 1	164.709							-	
PVOTI HEVEL	HYPOTHETICAL USES 71 PROTEIN	HERPESVIRUS SAIMINI (STRAIN II)	П	П					: :		
PVOH HBVII	Т	KCTALUNID HERPESVIRUS I	495-471	535-561	120-144	1252-1269					
PVOM HSVSA	г	HERPESVIRUS SAIMING (STRAIN 11)	124-151								
PVOP EPVIR	CENE 9 PACTEDA	SPECPLASKA VIKUS SPVI-RIAZ B	_				7	_	7		
PVOPI IBVB	J. PROTEIN	AVIAN INFECTIOUS BRONCHITIS VIRUS (STRAIN BEAUDETTE)	_	1856-1877	2100-2177	2210-2226	1788-2806	1973-2990	3071.3090	3120-3145	1174.1199
			3601.3625			-			!	!	:
PYCHO HOYA	_	HIDMAN CYTOMEGALOVIRUS (STRAIN ADIM)	137.178	Ì		1				1	
PVOLI CVPLI	EL OLYCOMOTEIN MECURSOR	PORCINE RESPIRATORY CORONAVIAUS (STRAIN BE) 3700AUNITIS) IS	2	1							
PVOL1 CVIII	ES CE VOOPEDIEIN PRECUBSOR	BOYING CORDMAYINUS (STRAIN F15)	1	╗	٦	264-279	401-104	239.1280		1	
POL CHE	E2 CLYCOMOTEDN PLECUTSON	BOVING COROMAYIAUS (STRAIN L9)	_	T	٦	921939	101.04	1259-1280			
WOLD CWILL	T	BOVDES CONCONAVIRUS (STRAIN LY-131)	16-33	П	٦	14.73 17.	991-1017	239-1280			
PVOL3 CVBN	Г	BOVING CORONAVIRUS (STRAIN MEBUS)	2		П	20.18 8	135-1360				
אסרו נאוס	ES CLYCOMOTEIN MECURSON	BOVINE CORONAVIAUS (STRAIN QUEDEC)			╗	264.275	\$1017	1259-1280		1	
VAC CAN	r	BOVING CORONAVIRUS (STRAIN VACCINE)				991-1017	1359-1280				
107	T	HUMAN CORONAVIRUS (STRAIN 229E)	768-794	1	11151134						
PVC CVM	T	MUBBE CORONAVILLE MIV (STILAIN WILD TYPE 4)	111-56		1267-1290	1317-1338					
WOLL COMA	t	INCIDENTE CONCINA VIXILIS BOTY (STRAIN ASP)	111.86	CL6-176	1021-5121	1265-1286					
WOLL CALLE	т	MURLING CONCOMAVIRUS MAY (STITAIN INDAY / VARIANT CL-1)	111-50	1	1267-1290	1317-1338					
MO 5 CWLD	1	INCIRUME CORONAVIRUS MAY (STRAIN MAX)	111-56	П	16[1-91] 6911-9211	1176-1197					
VOL3 CVP1	1	PORCENI TRANSMISSIBLE GASTROENTENTIS CORONAVIRUS (STRAI	64-13		9 9-003	1031-1064	1254-1297				
PVG13 CVM4	ES CE PCOPILOTEDI PRECURSOR	PORCEMI TILANSHISSIBLE CASTROENTERITIS CORONAVIAUS (STRAI	3	П	╗	9	1031-104	74-130		1	
PVOL3 CVPM	Т	PORCONE TRANSMESSIBLE CASTROENTERITIS CORONAVIRUS (STRAI	3	7	Т	791-114	_	277-1793			
*4013 CAN	EJ CLYCOPROTEIN PRECURSOR	PORCING TILANSMISSIBLE CASTROGRAFENTIS COXONAVIRUS (STRAI			416-906	1	1001-1002	CA21-2/2			ĺ
200		TOTAL LINE ALLEGATION I CONTINUE TO THE STATE OF THE STAT		T	1	100				T	Ī
NG 7		PORCHE RESPURATION TO CONCINUS (STRAIN ANN)		T	019707	10.00	1016-1062	1373, 1364		1	
	-	INSTITUTE THE PARENTAL DESTROYER WHITE CONTRACTOR AND THE CONTRACTOR A	1	1	1377, 1300					T	Ī
	-	A VIAN BOTECTIONS BEONCHITIS VIEWS (STEAD) 6/12)	T	-	797 177	1026-1001	1384-1111			T	
1	P. O. VONDE OFFICIAL PRECIDENCE	AVIAN BEECTIOUS BRONCHITIS VIRUS (STRAIN BEAUDETTE)	Γ	Т	25.04	1015-1080					
200	P2 CE VOOPECITSIN PERCENTION	AVIAN BRECTIOUS BRONCHITIS VIXUS (STRAIN D274) (196-219	(09-19)	181.181	1054-1081					
PVOLE BVDS	Es de Ycomothus MECLASOR	AVAN DESCRIQUE BEONCHITIS VIRUS (STEAN DAISS)	П	П							
FVOL1 BVK	Г	AVIAN INFECTIOUS BRONCHITIS VIRUS (STRAIN KB1521)			110-196	1055-1060					
PVCL3 IBVN	П	AVIAN BEECTIOUS BRONCHITIS VIRUS (STRAIN MAI)		378-398	307-406	770-796	1055-1080				
FVOL1 BWUI	П	AWAN DRECTIOUS BRONCHITIS VIXUS (STRAIN UK/12)/82)	178-201							1	1
7401	EL CLYCOPIOTEDA	AVIAN BREETRIUS BRUNCHITIS VIRUS (STRAIN UKVERDE)		Ī						T	
2 2 2 2 2	T	PPSTEDNIA AND VICTOR (STRAINS AS)	132-753							T	
PVG B HOVA	1	HUNKAN CYTONEGAL DVTRUS (STRAIN AD144)	Γ	T	150-777					T	
PVOL HOVE	+-	ROMAN CYTOMEGALOVIKUS (STIAJIY TOWNE)	336-539	101.133	146-156					-	
PVCLB HSVII	CALYCOPROTEIN B PRECURSOR	HENDES SIMPLEX VIRUS (TYPE 1/STRATH 17)	83-104								
PVCLB HSVIP	GLYCOPACTEDY IS PRECURSOR	HENDES SDOLEX VIRUS (TYPE I / STRAIN F)	12:103								
PVGL B HSVIK	CLYCOPROTEIN B PRECURSOR	HERDES SINOLEX VIRUS (TYPE I / STRAIN KOS)	82.163								
PVGLE HSVIP		NEADES SOUTH YOUS (TYPE I / STRAIN PATTON)	93:04								
PVG B HSV2	П	HERPES SINGLEX VINUS (TYPE 2/STRAIN 1)1)	74.90							1	
PVOLD HSV2H		HERPES SEATLEX VIAUS (TYPE 2 / STRAIN HGS2)	8							1	
PVCLB HSV2S	CLYCOPHOTESM B PRECURSOR	PRINCIPLE STATE OF CHAIR AND THE AND STATE OF THE STATE O		77						1	Ī
PVG S NSV	Т	BOUND IS BEEN WINDS I THE BUSINESS CONTROL TO STANDARD CONTROL TO	76.77	, in the					Ì	†	
WOLL HSV8	Т	BOUTE IS APPLYING TYPE JISTRAIN BAND LIDOVINE MANAMILLITIS	279.76	745.767						Ì	Ī
TON S IUNA	1	BOSTNO TO RPS STIPLY TYPE I ISTRAIN COOPERS	693.710								Ī

1945	16187-11519	All Virges (No Botterlophages)	П	П	П	П				
TILL KANG	PROTEIN	77.0%	4	1	AKEAJ AKEAK		4	Т	1	
PWGLE HSVE	GLYCOPROTEIN B PRECINSOR	EQUIND HELPES VIAUS TYPE (ISOLATE HYSISA) (EHV-1)		1] 	}			l	
PANSH STOM	CLYCOPADTERN B PRECURSOR	EQUIPE HEAVESVIRUS TYPE I (STRAIN ABI)	7/00/2/2	t						Ī
PYCLE HEVEA	CLYCOPACTED B MECUASOR	EQUING KENPESVIRUS TYPE I (STRAIN AB!)	736-753	1		+			+	
PVCI LISVE	CALYCOPROTEIN B MECHASOR	EQUING HELLPES VIRUS TYPE I (STRAIN ABAP)	130-73	1		+			+	T
	IN VOOR OTEN B PRECISEOR	EQUINE RELIPES VIRUS TYPE I (STRAIN KENTUCKY D)	736-753					1		T
400	CE Versenotrina in MECLINICAL	MAREK'S DISEASE IE IVESVIRUS (STRAIN NB-18)		┪						
1000	Col Without Help In March Col.	PERPESVINUS SALMINI (STRAIN II)	483-506 58		01-716	-				
	AN UNMAN MAN INC. THE PARTY IN CASE	NO SCHOOLS LAN WACOTRACHEITIS VIRUS (STRAIN 632)	256-275 55		740-758				1	
	At Charles And Mark to Con-	MARCHANIS LARVAGOTICACHEITIS VIRUS (STRAIN SA-2)	366-285 60	Г	750-768					
	CATCUTAGE PRECUESOR	PARAMETER AND VACATE ACTIVITY OF STRAIN THORNE VIEW	Γ	101-631	150-764	ļ.				
WELL ILIN	GLYCONOTEIN B MECUROOR	THE PERSON NAMED AND ASSESSED.	Т	T	738.765		L			
	CLYCOPROTEDY B PRECURSOR	MUMBER OF LUMBUALOVINGS (SPROMIN SMITH)	Τ.	T						Ī
PVG. B MAN	GLYCOPROTEIN OU MECURSON	PSEUDORABIES VIRUS (STRAIN INDIANA-FUNKITAUSER / HECKER)	27.62				 		+	Ī
100 M	PU VINDER OFFICE IN THE SECURE SOUL	VALICELLA-205TER VIRUS (STRAIN DUNAS)	338							
	AT UNKLE K-T- NJ P. T- NJ P. T- NJ P. T- NJ	HARDES SINCE BY VIEUS (TYPE 1 / STEATH 17)	3.22	467.483						
NAC.	ULTURAL FRANCISCA	THE BASE DAYS IN CITE OF CASE 1 / RYDAIN MOS!	11.23	467.493					_	
DVGC HSVIK	CLYCOPROTEIN C PRECURSOR	CUTES SUBTLEA VIRUS (1178 1/ 31 MAIN MOS)	T							
PVOLC HSV2	CLYCOPIOTEDIC PRECURSOR	PERPES SIMPLEX VIRUS (TYPE 1)					:	;	_	1
	A LAXABASE PROPERTY BOOK	LEBERG SIMMER VIRIES CTYPE 2 / STRAIN 3331	436-459			-			-	:
WGC 18V2	ULTUTALISM C MELONOM	TAKEN THE PROPERTY OF STREET AND STREET BY	20.00		<u> </u>		-			
PVCIC HSVBC	OLYCOPROTEIN CAILPALCUASOR	BOATCH INCOME TO THE PARTY OF THE PARTY OF THE PARTY.	277.746	-					- 	
PVCLC HSVEA	CLYCOMOTED C MECURSOR	EQUING MELOPENIKUS TYPE 4 (STANIN 1912)		t		+			ļ	
PWELL HEVER	GLYCOPAOTEIN C PRECURSON	EQUOTE HEAPES VIRUS TYPE I (STRAIN ABAY) AND INTRAIN KIND IN							İ	
A 150 PM	CHARLEST AND WASHINGTON CANAS MECHASOR	MAREK'S DISEASE HERPESVIRUS (STRAIN HC-1)	199-421	_					1	
	Capa at a series of the series	LANDERS AND AND POST COLLEGE AND AND AND AND AND AND AND AND AND AND	127-66							
MAC JONES	SECTE TORY OF TOWNS IN COLUMN	ALL DESCRIPTION OF THE PROPERTY OF THE PARTY CAN	194.420							
I VOLC IS WAD	SECRETORY OF VIOLENCIES OF 17-45 PREC	MALE S USEASE REACTS VIRUS (STRAIN OA)		t			-			
PVSI Z PV4	SUCRETORY OF YOURSTEIN CASS 45 PRECURSOR	MARK'S DISEASE HERPESVIRUS (STRAIN MID!)	٦					!!!		Ī
10 to 10 to	And verses of the Partition of	PSEUDORABIES VIRUS (STRAIN INDIANA-FUNKIIAUNER / INECKI-R)		446-472			1			
		CABINET I A PORTER VIRING (STEAM DEMAS)	431-449	-	_					
200	O. YCOTROTED UPV	THE PERSON NAMED IN COLUMN TWO IS NOT THE PERSON NAMED IN COLUMN TWO IS NOT THE PERSON NAMED IN COLUMN TWO IS NOT THE PERSON NAMED IN COLUMN TWO IS NOT THE PERSON NAMED IN COLUMN TWO IS NOT THE PERSON NAMED IN COLUMN TWO IS NOT THE PERSON NAMED IN COLUMN TWO IS NOT THE PERSON NAMED IN COLUMN TWO IS NOT THE PERSON NAMED IN COLUMN TWO IS NOT THE PERSON NAMED IN COLUMN TWO IS NOT THE PERSON NAMED IN COLUMN TWO IS NOT THE PERSON NAMED IN COLUMN TWO IS NOT THE PERSON NAMED IN COLUMN TWO IS NOT THE PERSON NAMED IN COLUMN TWO IS NAMED IN COLUMN TWO IS NAMED IN COLUMN TWO IS NAMED IN COLUMN TWO IS NAMED IN COLUMN TWO IS NAMED IN COLUMN TWO IS NAMED IN COLUMN TWO IS NAMED IN COLUMN TWO IS NAMED IN COLUMN TWO IS NAMED IN COLUMN TWO IS NAMED IN COLUMN TWO IS NAMED IN COLUMN TWO IS NAMED IN COLUMN TWO IS NAMED IN COLUMN TWO IS NAM		l			-			
MOLC VEW	OLYCOPLOTED OPV	VAUCELLA-20STER VIRUS (STRAIM SCUTT)		t		-	-		-	
PACE D MEVE	CALVERSALE DI MALCUASOR	HERDES SOCHEX VINUS (TYPE I / STRAIN IT, AND (TYPE I / STRAIN		1					†	Ī
	CI VIONECTION DIMECLA SOR	HEAVES SOURCEX VIRUS (TYPE 2)							1	Ī
	Col brook Avenue half in the	GRAPES SLOPCEX VIAUS (TYPE 1 / STRAIN 17)	104-130	113-11						
	AL COMMENCE OF BUILDING	VARIORITA 2037ER VIDIUS (STRADN DOBLAS)								
	CL. YCUTHOLIGIA II THE CANADA	ANGESTS SECTION AND VINE VINE VIRIAL VIRIALITY OF ANY ASSOCIA	303.331	187.287	483.504		L			
	INDIGORIOL YCCOMOTERN PRECURSOR	BOTTLE REPORT STREET WAS STRONG WITH A PARTY OF THE PARTY	Τ	Т	15.71		L			
	PUSION OF VCOPHOTED PRECURSOR	BOVING RESPUENTION STRUCTURE VINCOLOGICALINA CONTRACENT	Ť	T	741,00		-		İ	
PWC) HALVY	FUSION OF VCOMBITION PRECURSOR	BOVING RESPONDED STRUCTINE VIRUS (STRAIN RIGH)	1	T	2				Ì	
	HINDALCE WOOMBITTIN PERCENTOR	CANDED DISTEMPER VIRUS (STRAIN ONDERSTEMOORT)	336-361		362-389		$\frac{1}{4}$			
	MINISTER OF UNCOMMENDED IN BUT IN COMMEN	MELLAN RESPERATORY SYNCYTIAL VIRUS (SUBGROUP B / STRAIN IIS	125-221	365-210	104-506					
VQ. 18V	-1	CHAPAC BREEK AND V CONFORTAL MINISTER (CTS AND A2)	105-225	Г	484.506	L				
WOU HOSVA		HUMAN MESTICAL STREET S	306.336	Ţ	464.504		-			
TASK DAY	PUBLISH OF PROPRIETER PRECUISOR	HUNCAR PENTALORE STRUCTURE TRACE (SOUNDER N. STRONG		Т				I		
TAX THE PLANS	PERSON OF WOOMSOMED PRECURSOR	HONDAN RESPIRATORY SYNCYTIAL VIRUS (STRAIN RSS-2)	7	Т	2]	1	
1777	FIRM OF Vicesorian PLECUASOR	MEASURE VINUS (STRAIN EDMONSTON) WA (STRAIN HALLE)	124-145 2		631-477		-			Ì
	SCARL CARREST CONTRACT OF THE PARTY OF THE P	MEASURS VIRUS (STRAIN IP.) CA)	227-248 2	289-305	087-50		-			
3	-	LANGUAGE CARRIED FOTO AND	224.245 12	286-302	451-477	_	-			
		T 10 to the 1 to 10 to 1	6.36	336.365	46.467	L	-			
TOTAL PORT		MUMPS VIEWS (31 MAIN 300-1)	Ţ	t			-			
TOTAL TONG		ACINOS VIRLIS (STRAIN POTANAMA VACCINE)	T							
SALVE TO SALVE	•	MONOS (STRAIN RW)	276-292	446-467					7	
	_	ACTIONS VIELDS (STRAIN SEL)	5-20	176-292	446-467					
	_	CONCACTOR PACE AND VARIATION AND ANGER ALIA. VICTORIANZI	273.210	-	-					
WOL 10V	_	NEW AND LINE DISEASE AND ACTOR AND	351 388	T						Γ
MON COM	PUSION OLYCOPADTEM PRECURSOR	NEWCASTLE DISEASE VAIOS (3) PAIN READURE 1.5 Cm.)		İ			+	Ţ		
DWG CENT	PUSION OF YCOPIGHTON PLECUASOR	KEWCASTLE DISEASE VILUS (STIAIN HERA))	1 P	1					1	
TACK PARTY	т	NEWCASTLE DISEASE VIRUS (STILAIN BI-HITCHDIELAT)	273-289				 -			
1747	TRICKALI DE VICTORIONISTE PRECIDENCE.	NEWCASTLE DISEASE VIRUS (STRAIN LASM)	277.289							
	т	NOWPACT B DICEASE VIRILS (CTEAN MIYADERAS)	273.289							
202	FUSION CL. TCOPILOTE IN PARLUNSON	CANCELLE DESCRIPTION OF A PARTIE AND A DECREE AND A DECREE	311.380	Ī		L				
SVOT POVE	PUSION OF YCOPHOTHER PRECUISOR	REMICASILE DISEASE VINOS (SINGER COESTIGORA)		İ						
MON TON	-	NEWCASTLE DISEASE VIRUS (STRAIN TEXAS)		1				Ī		I
WC YOUR		NEWCASTLE DISEASE VIRUS (STRAIN TEXAS G 8 /48)	****	1			+		İ	Ī
Wed New	r	NEWCASTLE DISEASE VIRUS (STRAIN ULSTEINA?)	T	1	100		1	1	Ì	
VACABLE BANK	t	PHOCINE DISTEMBER VIRUS	269-285	305-126	67.38) 531-538		-		1	1
	1									

The second	l	A. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1.										
		PHA ULIF	All Virgin (To Bertanophoges)	T			-1	7	- 1	Т	Т	
XBX	¥	PUSION CLYCOPROTEIN PRECURSOR	HUMAN PARAINT (TENZA) VIRIUS (STRAIN C19)		Ţ	Т		77.98	o d		4	
WOLL FEE	豆	FUSION GLYCOPROTEIN PRECURSOR	HUMAN PARAINFLUENZA 3 VIRUS (PIV-3)	15				T				
PVGL) HIMO	HIN	FUSION OLYCOPROTEIN PRECURSOR	HIMAN PARAINFLUENZA 2 VIRUS (STRAIN GRECK)	430-471								Ī
POLL NING	HAT	FUSION CLYCOPROTEIN PRECURSOR	HUMAN PARAINT LUENZA 2 VIRUS (STRAIN TOSIIIRA)	П								
	5	PUSION GLYCOPROTEIN PRECURSOR	BOVINE PARAINFLUENZA 3 VIRUS	92								
	2	FUSION OLYCOPROTEIN PRECURSOR	MUMAN PARAMF LUENZA 3 VIRUS (STRAIN NII! 47285)	٦	٦	45) 474						
		PUSION OF TOURIST IN PLECUASOR	INDEATEST VICUS (STRAIN KABETE O)	T	Т							
PVG (B)	500	PUSACH OF VONDERCHED PRECISE OR	SERVING VIETE (STEAM 2 / HOST ACT PANTS)	187 077	147-711		-		Ī			
WGU TEND	100	FUSION CLYCOPROTEIN PRECURSOR	SENDAI VIRUS ISTRAIN FUSITINII)	460-41	T	Í	1			-	!	
TVCI TODA	100	PUSION CLYCOPROTEIN PRECURSOR	SENDAI WALUS ISTRAIN HALLUS	460-481			F					
TVOL! LDM	90	PUSION OLYCOPROTEIN PRECURSOR	SENDAJ VIRUS (STRAIN HV))	460-48	Ì	T			T			
2	100	PUSION CLYCOPROTEIN PRECURSOR	SENDAL VIRUS (STRAIN Z)	466-48			Ī					
Way W	ž	PUSION CLYCOPROTEIN PRECURSOR	SDAAH VIRUS 41	453-476			Ī					
Wall Sw	S.	PUSION GLYCOPROTEIN PRECURSOR	SEMIAN VEXUS 5 (STRAIN W.)	Ι	19799		1					
WOUT THIS		FUSION GLYCOPROTEIN PRECURSOR	TURKEY RHINDTRACHEITIS VIRUS	Ī	452-474		-					Ī
PVCLO BBN	L	SPIKE OLYCOPROTEDN PRECURSOR	INFECTIOUS HEMATOPOLETIC NECROSIS VIRUS (STRAIN ROUND BUT	17.99		Ī	-		Ī			I
VOLO EN		SPIKE OLYCOPROTEIN PRECURSOR	RABIES VIRUS (STRATH ERA)		Ī		-					
PVOLO LASVY		SPIKE OLYCOPROTEIN PRECURSOR	RABIES VIRUS (STRAIN HEP-FLURY)	Г	14-14				Ī			
PVCLO LABVE		SPIKE CLYCOPROTEIN PRECURSOR	INDLES VIAUS (STRAIN PV)	454-474			1					
PVOLO LABVE		ISPIKE CLYCOPROTEDI PLECURSOR	ALBERS VIRUS (STILATIN SAD BIS)	454-474								
PVCLO_LABVI	Z W	SPIRE CLYCOPROTEIN PRECURSOR	RABIES VIRUS (STRAIN STREET)	454.474					Γ			Ī
VOLO TITO	TATIV	INVIOR SUBMINE OF YCOMOTEIN G	TUNKEY BUNOTRACHEITIS VIKUS	199-216					ľ			
PVOLO VIBVO	WBW	SPIKE CLYCOPROTEIN PRECURSOR	WILL HEMOREHAGIC SEPTICEMIA VIRUS (STRAIN 07.71)	406-428					Γ			
PVCCJI HOSAVA	HOWA	CLYCOMOTEIN H MECURSON	HRALAN CYTOLEGALOVIRUS (STRAIN AD169)	111.237	265.382	\$74.596	691-112					
Š	KOVT	CLYCOPROTEIN H PRECUASOR	HUMAN CYTOMEGALOVIRUS (STRAIN TOWNE)	1	364.388	473-597 6	116-069					
PVOLJE HBV11	HVII	OLYCOPROTEIN H PRECURSOR	HEADERS SINCELEX VIRUS (TYPE 17 STRAIN 17)		Г	603-627						
WOLL HOVIE	ZVII.	OLYCOPIOTED'N PRECURSOR	KENNES SIMMLEX VIRUS (TYPE I / STRAIN HIEM)		44)-467	121-101						
NO.	DWS.	OLYCOPROTEIN MPRECURSOR	HEAVES SINCEEX VIRUS (TYPE 6/STRAIN GS)	1								
PVQ I HVV	2	GLYCOMOTER H PRECURSOR	EQUINE HERPESYIAUS TYPE 4 (STRAIN 1942)	Π	614-516							
		CA. Y. COPROTEIN IN PRECORSOR	LEGULAGE REPRESVIKUS TYPE (STRAIN ABAPANA (ISOLATE HVS2SA)	T	207-873	1	7					
	1	OLYCOPROJECT RECORDOR	MENCES VICES SAMPLING (STRAIN 11)	T		1	•			-		
		DELICOTROLLERA TI PRECIONALIA	MONTH CATACONICATION (STRAIN SMILL)	00.000	1	1	1	1				
	J	In the second se	LINESPECE BROSE DE LINES CALVARE L'ARTE ANTICE	201	1	1						
100	T	Of recording to the control of the c	EXHANCE SOUTHER VANDA (1 TTG 17 STRAIN 17)	3	1							
	Τ	Octobronian I reconsor	INVESTMENT A PARTIE VALUE OF A PARTIE AND THE LAND.		1		1		1			
PVOLET LEBES	1	IN POLYPROTEIN PREPIREDA	INDIANA VIIII GELMISTON	T.	167.333	1						
VOLUME)	Т	IN POLYPROTECH PRECURSOR	BUNYAWAUS LA CROSSE RSOLATE L'34)	Τ	Т	196.711	1156.1744	1187.1416			1	Ī
PVOLICE BUSINESS	т		BUNYAVIRUS SHOWSHOE HARE	Ī	Γ	Т		1387, 1410	Ī			Ī
WOLK DAY	-		BUNYAMWERA VIRUS	<u>_</u>	ş	T	-					Ī
WOLK! DUGBY		IM POLYPROTEIN PRECURSOR	DUCING VINUS	Г	Г						Ī	
WOLL KANTE		M POLYPROTEIN PRECURSOR	KANTAAN VIIUS (STRAIN B.1)		Ť	_	999-1019					
PVOLM MANTH		M POLYPROTEDN PRECURSOR	HAMTAAN YIRUS (STILAIN HOIO)		914-349	0001-0001					Ī	
MOUNT HAVE	_	M POLYPROTEIN PRECURSOR	HANTAAN VIAUS (STRAIN LEE)	187613 0	614-319	1001-1001						
TWO TOWN	_	M POLYPROTED/ PRECURSOR	HANTAAN VOUS (STRAID 16-118)	2	П	1201-1001						
NO. N	2	M FOL YPROTEIN PRECURSOR	DOPATIENS NECROTIC SPOT VIRUS (INSV)	٦	264-293	348-367 5	181-181	197-511				
A PAGE	4	M POLYPROTEIN PRECURSOR	PROSPECT ROLL VIXUS	٦	-1							
		M FOLTPROTEIN FRECUNSOR	PUMIA TORO PREEDOVINUS	٦	1	1275-1702						
NO.		M FOL TPROTEIN PRECURSOR	INUMALA VIKUS (STRAM HALLINAS BI)		╗	٦						
NO.	,	M POLYPHOTEIN PRECURSON	PUDMALA VICUS (STRATH SOTRAND)	Ţ	٦	٦	643-1117					
	٦.	M POLYPROTEIN PRECURSOR	RET VALLEY FEVER VIAUS	I	П	Ħ						
7	т	M POLITYRUS EUR PRELUKSON.	KAPI VALLET PEVER VUIUS (STRAIN ZIL)46 MIZ)	T	Ŧ	7	2					
	Т	M POLITICAL PLANTACIONES CALIFORNIA CALIFORN	SELVE VIKUS (STRAIM BELTY)	Т	217-200	816-006	1018					
N N	7	M POLYPROTEIN PRICINGOL	SECOND VICES (STRAIN SELE)	125.00	Т	7	000-1000	1				
	3	M POLYPROTEIN PRECINSOR	CARLINGA VALIS	Τ	Т	36 841	-1		1	1	1	1
	1			1	7	7	1	1 A	1		1	

	PCCIONE	PISCHUZIP	All Viruser (No Besteriophages)	Т	Т		774	4 4 4 4	ABFAG	ARFA 9	ARFAILA	ARFA 9
A CHARGE OF CONTRIBUTION COORDINATION CONTRIBUTION CONTRIB	FILEHAME	PROTEIN	YIRUS	T	Т	-	1-	r		_	П	
ACCREMENT OF THE PROPERTY	PVGLF BEV	PEPLONER CLYCOPROTEIN PRECURSOR	BEANG VICES OF THE TYPE I VETT AND ABLES	Г	Г		-					
COUNTY C	PVGCX HSVES	7	ELICITIES TRACES TO SELECT THE CONTRACT TO SELECT TRACES AND SECURITIES AND SECUR			T	-					
ACCESSION OF PROPERTY 1915	YOU HEVE	т	ECHANGE LEGISTICS TYPE 1 (STEATH KENTUCKY D)									
ACCORDIGATE NUMBER PROCESSES ACCORDIGATION	PVG.X HSVEL	GLYCUMULEIN OA	PEFITIONAMIES VIRUS (STRAIN RICE)	149-176								-
ACCESSION OF PROFISER STATEMENT 13.1 13.15 13.	2000	_	JUNIA ARENAVIRUS	13.38								
CONTRIBUTION OF THE PROPERTY INCLUSION CONTRIBUTION OF THE PROPERTY INCLUSION CONTRIBUTION OF THE PROPERTY INCLUSION CONTRIBUTION OF THE PROPERTY INCLUSION CONTRIBUTION OF THE PROPERTY INCLUSION CONTRIBUTION OF THE PROPERTY INCLUSION CONTRIBUTION OF THE PROPERTY INCLUSION CONTRIBUTION OF THE PROPERTY INCLUSION CONTRIBUTION OF THE PROPERTY INCLUSION CONTRIBUTION OF THE PROPERTY INCLUSION OF THE PROPERTY INCLUSION OF THE PROPERTY INCLUSION OF THE PROPERTY INCLUSION OF THE PROPERTY INCLUSION OF THE PROPERTY INCLUSION OF THE PROPERTY INCLUSION OF THE PROPERTY INCLUSION OF THE PROPERTY INCLUSION OF THE PROPERTY INCLUSION OF THE PROPERTY INCLUSION OF THE PROPERTY INCLUSION OF THE PROPERTY INCLUSION OF THE PROPERTY INCLUSION OF THE PROPERTY INCLUSION OF THE PROPERTY INCLUSION OF THE PROPERTY INCLUSION OF THE PROPERTY INCLUSION OF THE PROPERTY INCLUSION OF THE PROPERTY INCL	TOTAL OF THE	т.	LASSA VIRUS (STILATA GA191)		П	2017	1		1			l
CHARGESTERN POLYMETHE PACKETON CONTROL	TOTAL ARMS	т-	LASSA VIRUS (STILAIN JOSIAH)		٦	27.440			1		1	
CONTINUED FOR PROTECTION CONTINUED CONTINUED TO THE STATE OF THE STA	TAN ARA	7	LYNDHOCYTIC CHORIOMENINGITIS VIKUS (STILAIN ARKISTRONG)	12-35						1	1	
CONTRINGENERAL PRICERS 19-15 19-	WORLY TOWN	CALVEDPROFILM FOLYPROTEIN PARCURSOR	LYMMOCYTIC CHONOMENINGITIS VIRUS (STRAIN WE)	13.35	3	Ì		1	1	1	1	
CANCESTER PATRICIPS FILELIZES 12-24 12-14 11-1	SULT VICTOR	CO VICTORIOTE N. M. VPA DITEIN PRECUESOR	MOPELA VIAUS	12-33	425-447		-					ļ
CONTRINCTOR TAYLOGUES TAXABLE VURS TAXABLE VU	THE CHAPTER		PICHENDE ALENAVIRUS	12.31	441-466							
GUNCONTERP DAY PROTECTOR TACADER WILLS STRANT NY 11-11		т	TACAUDE VIBUS	13.38			-					
ACCORDING PCC PROFILE PCC PCC PCC PCC PCC PCC PCC PCC PCC PC		т.	PACARIBE VIRUS (STRAIN VS)	12.31			1					
CONSIGN OFFICERS 111-111 111-1	1 N 1 N 1 N 1 N 1 N 1 N 1 N 1 N 1 N 1 N		TACARIBE VIRUS (STRAIN V7)	12:31								
CONTRIL NOTICE CONTRIL MOSTAC VALUE	1		TACALIBE VIAUS (STRAIN TRVL 115%)	12-38			-					İ
Trigge RYPTIGES Trigger BALLY VARIS TRIANS BELGINGALNI (EDESTITIS) 11-14 11-	No.		COWPEA MOSALC VIRUS	141-161			1	1165-1114				١
UNIVERSITE SEGREGARY AFFICIATION OF STITEMBARDAY WILES STANDARY IN STREAMS AND AFFICIALS OF STITEMBARDAY WILES STANDARY IN STREAMS AND AFFICIAL STANDARY AFFICIAL OF STANDARY AFFICI	2 1 2 W/V	CLENCAGE POL VPROTECN M	COWPEA MOSALC VIRUS	311-333	741.764		-		1		1	1
WASSALE STOCKAGOTOR OF STATEMENT OF STATEM	WATER VALUE	PROMÁBI B MEMBRANE ANTICEN GP220	EPSTEINLBAKK VIRUS (STRAIN 895-8) (HUNIAN HERVESVIRUS 4)	657-681			7					
PRODESTE PROMERTED FURTHER ADAY VIRIS (STALM) BED (UNIVANI IE PREVINES) 151-54	A Legis	BANNET THE CIL MCOPROTEIN GPAN	EPSTEIN-BARR VIRUS (STRAIN BOS-B) (HUMAN HERPESVIRUS 4)	854-878			-					
FITCHCHOLD GE/COMPORINT RECURSOR 1902.41 1913.41 1914.11		PROPERTY MEMORANE ANTICEN CP15	EPSTEIN-BARK VIRUS (STRAIN 895-8) (HUNIAN HERPESVIRUS 4)	11-19							1	
		STATISTICS VANDOUTS IN DRIED IN SOR	ISBOLA VIRUS	34.52	Г	653-675	•					
INCEPTION OF CONTROL PARTICLES PARTI	200	т	MARBURG VIRUS (STRAIN MUSOKE)	538-562	129-109							
NACESSAY VOLUS STRAIN CONFERENCES 18-21 16-121 16-		Т	MARRIED VIRUS (STRAIN POPP)	531-562	603-627		•					
NOTEST TOTAL TOT	MON PAR	т	VACCINIA VIETE ISTRAIN COPENHACEN	36-92	103.121							
ACCESSAL VARIES VACCESAL VALIES V	1	т	VACCINIA VIRUS (STRAIN WR)	76-93	121-501							
LYTE PROPERTY VACCESSA VENUS (STALIN WR) Web	2000	т	VARIOLA VIRUS	76-92	121-501		1					
LATE ROTEIN HT	TO THE PARTY OF TH	т	VACCINIA VIJUS (STRAIN WR)	10.97								
FIGEWARE RELECTER FORTHWAYER FELECTER FORTHWAYER FROM 1911-104 1911	AVA AVA	Т	VANOLA VIRUS	70-03								
PADAZES FELICASE PADAZE PROPRATED 150-151 PADAZE PROPRATED 150-1	VACT POR	PROBABLE HELICASE	FOXTAIL MOSAIC VIAUS	183-208			-					
FIGURE 19-135 1	PWEL NA	PROBABLE POLICASE	PAPAYA MOSAIC POTEXYTRUS	133-164			1				Ì	
PROTEIN	PVIDI VACCE	PROTEIN II	VACCINIA VOLUS (STRAIN COPENHAGEN)	50-62		Î					Ī	
HOTEM 1	PVIOL VARV	PROTEINI	VAUCA VIIUS	201-201							T	
MOTERN 19 VALUCA VRUS STACIN WAY 194-225 194	PVIOS VACCE	PROTEIN 13	(VACCINIA VIJUS (STRAIN CUPENHAGEN)	10.01			Ī				Ī	
PROTEIN	AND AVCCA	PROTEIN	VACUALA VINCE (STRAIN WR)	184.220						Ī		
PROTEIN # VALUELA VIRIS VALUELA VIRIS PROTEIN # PROTEIN	VARV	PROTEIN	SOACHARA VARIE (CTEANA WE)	104-128	133-135							
HOUTEN	200	TAU I BATT 10	VARIOLA VIRUS	106-178	133-155							
HOTEN HOTEN VACCHIA VEUS (STRAIN VR) 13.4 144.3	1	H No. 10	VACCINIA VIRUS (STRAIN COPENHAGEN)	13-34	344-367							
PROTEIN	7 77 10/14	PROTEIN 17	VACCINIA VIRUS (STRAIN WR)	13:34	344-367							
PUTATIVE BIA FELICASE VACCINIA VIDUS (STRAIN VO.) 198-212 418-213	PURI VARV	PLOTEIN !?	VAUGLA VIRUS	13.54 11.34	34.367							
PHTATIVE RAY RELICALE II	PVM VACOC	T	VACCINIA YIXUS (STILAIN COPENHAGEN)		?		1					
PUTATIVE RAY ROLLGARE VALOCA VOID VALO	PVIDE VACEV	П	VACCINIA VIRUS (STRAIN WR)	212							1	
15 TO DAGEDATE_LALLY PROTECT TO DAGEDATE_LALLY PROTECT 18 TO DAGEDATE_LALLY PROTECT	PVIOR VARV	П	VAUCA VICE	7 2 2							Ì	
S. K. D. D. D. C. L.	PVIET HCMVA		CERTAIN SECOND OF THE SECOND AND LOST	3 1	3		T					
45 TO DESCRIATE ALLA PROTEIN 2 14.13 TO DESCRIATE ALLA PROTEIN 2 14.13 TO DESCRIATE ALLA PROTEIN 3 15.14.13 TO DESCRIATE ALLA PROTEIN 3 15.15.15 TO DESCRIATE ALLA PROTEIN 3 15.15.15 TO DESCRIATE ALLA PROTEIN 3 15.15.15 TO DESCRIATE ALLA PROTEIN 3 15.15.15 TO DESCRIATE ALLA PROTEIN 3 15.15.15 TO DESCRIATE ALLA PROTEIN 3 15.15.15 TO DESCRIATE ALLA PROTEIN 3 15.15.15 TO DESCRIATE ALLA PROTEIN 3 15.15.15 TO DESCRIATE ALLA PROTEIN 3 15.15.15 TO DESCRIATE ALLA PROTEIN 3 15.15.15 TO DESCRIPTION 3 15.15.15 TO DESCRIPTION 3 15.15.15 TO DESCRIPTION 3 15.15 TO DESCRIPTION 3 15.15 TO DESCRIPTION 3 15.15 TO DESCRIPTION 3 15.15 TO DESCRIPTION 3 15.15 TO DESCRIPTION 3 15.15 TO DESCRIPTION 3 15.15 TO DESCRIPTION 3 15.15 TO DESCRIPTION 3 15.15 TO DESCRIPTION 3 15.15 TO DESCRIPTION 3 15.15 TO DESCRIPTION 3 15.15 TO DESCRIPTION 3 15.15 TO DESCRIPTION 3 15.15 TO DESCRIPTION 3 15.15 TO DESCRIPTION 3 15.15 TO DESCRIPTION 3 15.15 TO DESCRIPTION 3 15.15 TO DE	VE HOW		TOPICAL CT COMPLOY INC. (21 IANA) TO MAC.)		100,000		Ī					İ
45 DAGEDATE PART FOURTH 1 MUNDE CYTOREGALOVEUS (STAME SMITH) 50 KD BAGEDATE LALLY PROTEIN 1 MUNDE CYTOREGALOVEUS (STAME SMITH) 50 KD BAGEDATE LALLY PROTEIN 1 50 KD BAGEDATE LALLY PROTEIN 2 50 KD BAGEDATE LALLY PROTEIN 2 50 KD BAGEDATE LALLY PROTEIN 3 50 KD BAGEDATE BATCH ALLY BAGEDATE BATCH 3 50 KD BAGEDATE BATCH ALLY BAGEDATE BATCH 3 50 KD BAGEDATE BATCH ALLY BAGEDATE BATCH 3 50 KD BAGEDATE BATCH ALLY BAGEDATE BATCH 3 50 KD BAGEDATE BATCH ALLY BAGEDATE BATCH 3 50 KD BAGEDATE BATCH ALLY BAGEDATE BATCH 3 50 KD BAGEDATE BATCH ALLY BAGEDATE BATCH 3 50 KD BAGEDATE BATCH ALLY BAGEDATE BATCH 3 50 KD BAGEDATE BATCH ALLY BAGEDATE BATCH 3 50 KD BACH ALLY BACKH ALLY BACKH ALLY BACKH 3 50 KD BACKH ALLY BAC	PVE3 HCMVA	П	HUMBAN CT LONECAL CY UKUS (STRAUM AUTON)	171	107-111							
DAGEDIATE EALLY PROTEIN 1 WALLAN CYTOMEGIALOVRUS (STRAIN TOWNE) 4-33	PVES HONY	Т	TOTAL CONTRACTOR OCCUPANTO CONTRACTOR CONTRA	251.272							Ī	
DAGEDATE ALLY PROFESS TEXTES VALUE STACKS 155.40	NEW MON	Т	MONTE OF LONGOND FOOD STRAIN TOWNED	14.33								١
PROBRATE ENGLA RATIOGALMARIA CALIFORNICA NUCLEAR POLYMEDROSIS VIRUS 100-116 213-250 PRUB BRYECKAL MEDICALE ROTER BBAS PRÉTENHAL VENDRALVE PROTEIN RESTANDAR PROTEIN 133-132 203-222 PROBABLE BYTEGRAL MEDICAL MEDICAL PROTEIN READEL STANDAR PROTEIN READEL STANDAR PROTEIN 101-10 210-10 PROBABLE BYTEGRAL PROBEIN READEL STANDAR PROTEIN 161-10 210-210 143-172 PROBABLE BYTEGRAL PROTEIN READEL STANDAR PROTEIN READEL STANDAR PROTEIN 143-172 244-172 247-275 PRECORAL BYTEGRAL PROTEIN READEL STANDAR PROTEIN READEL STANDAR PROTEIN 16-101 113-311		Т	LEGINES VINITE & A TALIET (STEAD) 11)	65.10								
MAGESTAL MEMORIAN 15-100 15-100 15-100 15-100 15-101 10-101 15-100	WEO HSVSA	7	ATTION AND CALIFORNICA NINCLEAR POLYMEDROSIS VIRUS	100-116	173.290							
FIGURALE BRIEGAL REMOMANTE PROTEIN HADAAN CYTÓMGOLL ÖVRÖNDING (STRÁIN AD149) 68-66 190-217 PROBABLE BRIEGALA EMBRANTE ROTEIN REMOMBANTE BRIEGAL EMBRANTE ROTEIN 191-10 143-172 247-255 301-231 PROBABLE BRIEGALA EMBRANTE ROTEIN REMESONAL EMBRANTE ROTEIN 161-101 113-331 143-172 247-255 301-231	PVEN NOVA	SECTION SECTION SECTION AND PROPERTY BEST	EPSTEIN-BANK VIKUS (STRAIN 895-8)	75.100	135-152	222-02						
PEGGALLE BYTEGALL NEMBRANE PROTEIN NELVES SINCLEX VIIUS (TYPE I STRAIN I?) 81-110 310-370 FACGALLE BYTEGALL NEMBRANE MOTEIN EQUING NEAPESVINUS TYPE I (STRAIN AB4?) 24-49 91-130 143-172 247-345 301-321 DYTEGALL MEMBRANE PROTEIN HEAPESVINUS SAMIRÜ (STRAIN I.)	A LANGE	PROBABILE DITECTAL KENDRANE PROTEIL	HUMAN CYTCHEGALOVIRUS (STRAIN AD169)	68.89	190-217							
PACEALIE INTEGRAL DEPENDANE PROTEIN EQUING NEXPESTRUS TYPE I (STAAIN ABAP) 2449 91-130 145-172 247-283 JUL-231 DATEGRAL MEMBRANE PROTEIN	VDO HSVII	+	REAPES SINCHEX VIRUS (TYPE 1/STEAM 17)	97.180	150-170	Т	Т				1	
DYTEGRAL MENDIANE PROTERM (FEDERATING SAMIN) (78-101	TVD HSVE	1	EQUING HELD ESVINUS TYPE I (STRAIN ABAP)	24.49	93-120	Т	Т	26:100			1	
	ASVSH CONVE	٢	HELDESYTRUS SAMITY (STRATH 11)	76-101	113-331						1	

PCGENE	Pricetale	All Virgan (No Bacterian borns								
FILE KAME	PROTEIN	YIRUS	AREAL	1	AREA? AREA	AREA S	AREAS	ARCA?	AREA ! IA	AREA 9
PVD-0 VZVD	PROBABLE INTEGRAL MEMBRANE PROTEIN	VANCELLA ZOSTEA VIAUS (STRAIN DUMAS)	J	181.75	Г	Г	Т	Γ	Т	
PVIOL VACOC	(PROTEIN II	VACCINIA VIRUS (STRAIN COPENHAGEN)	89-110							
PVX01 VACCV	~	VACCINIA VIRUS (STRAIN WR)	19-110			-				
PVD1 VARV		VALIDLA VIRUS	911-61						-	ĺ
VKO VACC		(VACCINIA VIAUS (STRAIN COPENHAGEN)		ıì	316.339					
AND AND	PROTEIN K4 ;	VACCINIA VIRUS (STILAIN WR)		77.50	319-337					
200	MOTEUR IS	VACCINIA VINUS (STRAIN COPENIAGEN)	100	1		1	_			
100	THOUSEN ST.	WASHING SINCIPLES	100			ļ		!	-	:
	TACIEN LA	WALLING VINOS (STRAIN WR)	3	<u> </u>				:	•	:
	TROUGH L	U. ASSETT THE PARTY AND THE PA	T	٦						
	TROUBLE LA	WACLULA VIKUD (STRAIN CUPENHAGEN)	7	2 202-92	201.3115					
	TACI EUR LA	VACCURIA VIRUS (STIALIN W.K.)	٦	Т	292-315	-	_			
	THOUGHT	YACCAA VIAUS	2	2 (02.48)	291-314					
0 V V	TRUITAN LA	VACLIMIA VIALIS (STRAIN W.R.), AND (STRAIN COFENIAGEN)	673	İ			:			
	PROJECT CONTRACTOR	VARIATE PROPERTY NAME OF THE PARTY OF THE PA		-		-			 	
100	PROBABLE IN TROUBLE	COLICAINE MAINT (SHOTE) FAMILLOMAVINOS (STRAIN KANSAS)	110			-	4		1	
1000	PROPERTY OF THE OWNERS	INCOME CAPILLANDA VIA SELECTION OF THE TE	65.53	1		: -	1			1
POL BEAUG	MAICH COM PROTEIN LANGER 1	RECOVERING STANDS 1 / ROBERT IN THE ABOUT	Ţ	77. 17.	765 496	-	+		1	Ī
207.07	Manual In 1 a bacterial	INDICATE LANGE OF STRAIN COLUMNS	T	Т	2/1-76	+				1
1000	CONTRACTOR OF THE PROPERTY	MUNCAL SAME CALACTER SAME 1	2	1			1			
1000	Jetosa a 1 sector	TOTAL SALE CONTRACTOR OF THE PARTY OF THE PA								
1000	ALCONOCCE LE PROTEIN	HUMAN CALLLAMA VIALE 13								
2	INCOMABLE LA PROTEIN	HUBACA PAPILLOMAVIRUS TYPE 10	999	Ì						
A	PROBABLE LA PROTEIN	RUMAN PAPILLONIA VIRUS 1 VPE 11	33.59							
Y A C	PROBABLE LE PROTEIN	HUMAN PAPILLOMAVIRUS TYPE IA	213:228							
1	PROBABLE LA PROTEIN	HUMAN PATILLIANAVIRUS TYPE 2A]							
1	PROBABLE L2 PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 3!		443-462		7				
	PROBABLE LA PROTECT	HUMAN PAPILLONIAVIRUS TYPE 1)	٦	86-114 86-114						
100 PM	PROBABLE LA PROTEZIO	HUNGAN PAPILLOMA VIRUS TYPE 33	Ī				_			
	PROMABLE LA PROJECTA	THURSDAY PAPELLUMA VIALUE 41	I	9(4-9)		+				
	TACANA MANAGEMENT	MANAGEMENT AND LINE OF THE STAT	I	344.370		,				Ī
100	POOR AND RESPONDENCE	LITERAN BABILL MALA VIBIN COME CO	23.50		+				1	
100	PROBLET 1 PROTEIN	KINAAN PAMILIMAA UMIR TYPE GE	T	711.00	+					
W.3 15V4	PROBABLE 12 PROTEIN	KINAN PARLIONA VIRIS TYPE AN	Τ			1	-		1	
PWLS DAWE	PROBABLE LE PROTEZIN	EUROPEAN ELK PAPILLOMAVIRUS	20,00	T	-				+	I
WLI LIOVI	PROBABLE LI PROTEIN	INESUS PAPILIDADA VIRUS TYPE I	16.54			-	L		<u> </u>	
PVLJ JOVSE	PROBABLE L3 PROTEDA	HUMAN PANLLOMAVIRUS TYPE SB	J. 7						T	Γ
7. 1.00	MONOR CORE PROTEIN LANGIDA)	REOVERUS (TYPE 1/STRAIN DEARING	114.937						-	Γ
PVL REOVI	MONOR CORE PROTEIN LANGEDA 3	REOVERUS (TYPE 1/STRAIN DIVIONES)	114.737	213-1236	-					
W 1	MONOR COUR PROTEIN LANGEDA 3	REDVICES (TYPE I / STRAIN LANG)		T	T					
TATE OF THE PERSON	LWINGEL	IDULA MESSCENT VICES (TIV) (INSECT INDESCENT VIRUS TYPE I)	2	Т	646-711 845-861	_				
A PARTY	PACIETY MI	VACCIMIA VIRUS (STINAIN COPENITAGEN)	200	Ŧ	281-302		\downarrow			
AUVA 10VA	PROTEST LI	VARIA A VISIT	T		270-231	1			1	
PANTI BOVO	MINOR VIEWS STRUCTURAL PROTEIN MILLS	BEOVER 18 THEFT 17 STEAM DEADINGS	Ţ	Т	407-444	Т				
PWAI BEOW	MANOR VIRION STRUCTURAL PROTEIN MILLS	RECOMMISS TAVE I / STRAINS AMOS	T	T	Т		1			Ī
CACCE FORM	MAIOR VIRIOR STREET PROTEIN ARE LARGES	BEOVER CIVES 1/ STRANCO	T	Т	Т	Т				
VACE LEGVO	MAJOR VILLON STRUCT PROTEIN MU. IARU-IC	REDVINUS CTYPE 1 / STRADS DEARCHGS	10.14	†					1	
PVACE REDVI	INAJOR VILLON STRUC PROTEIN MU-INAU-IC	REDVINUS (TYPE 1/STRADY DY/ONES)	169	T		-	1		1	
PWG REOVE	INAJOR VIDION STRUC PROTEIN MU-IARU-IC	REOVINUS (TYPE I / STRAIN LANG)	16.192	l					1	T
PWO NEOVO	MAJOR NOWSTRUCTURAL PROTEIN MU-NS	REOVINUS (TYPE 37 STRAIN DEALING)	1	21.540	+				1	T
PACK BILBYA	MATRIX PROTEIN	BOVINE RESPIRATORY SYNCYTIAL VIRUS (STRATH AS1991)	T		-				Î	T
PVALAT COVO	KATRUX PROTEIN	CANTHE DISTEMPER VIRUS (STRAIN ONDERSTENOORT)	2	201-309					-	T
PVALAT HOLSVA	MATRIX PROTEON	S (STRAIN A2)	П	39.160						
7441 LYS	MATRIX PROTEIN	LA PEDAD-MICHOACAN-MEXICO VIRUS	311-336	1						
PVHA! PEASE	MAINA PROIEUR	MEASLES VINUS (STRAIM EUMUNSTUM)	283.309	1						

PCCUVE	PHICTLE	(All Virgers (Ne Becteriophages)	П	П	П		п	1 1	ГТ	
	PROTELN	Militra	J	AREA AR	AREA! AREA!	AREAS	AREA &	ARIAL AREAL	I AREA?	
PYMAT MEASH	KATRUX MOTEIN	MEASLES VIXUS (STRATM HALLE)	207:30		1		1		+	
POWER MAKE	MATRIX MOTERN	MEASUES VIRUS (STRAIN IP.3-CA)				7	1			
PWAY JAKU	MATALX PROTEIN	MEASUES VIRUS (STRAIN HUZ)	į		_					
PYALT LAUND!	KATHLY PROTEST	MODES VIXUS (STICATIV SBL-1)			336				4	
PWANT JABOS	MATRIX PROTEIN	MUNOS VIRUS (STILAIN SBL)			310-330				-	
PWAT NOVA	MATRIX PROFIEM	NEWCASTLE DISEASE, VIRUS (STICATA AUSTRALIA-VICTORIAVIZ)	135-151		57.0		1			
WAXT JOYS	HATTER MOTELY .	NEWCASTLE DISEASE VIRUS (STIAIN BEAUDETTE C/45)		190-208 309-329	129				اج	
1	KATEUX PROTEIN T	HUMAN PARADICUENZA I VIRUS (STRAIM C19)	193-217							
•	MATRIX MOTEIN	HEMAN PARABGELIENZA 2 VIRUS (STRAIN TOSIBBA) (PIV-1)	N1:14	189-205 308-328	338					
_	MATRIX PROTEIN	HUMARH PARADIGUENZA 4A VIRUS (STRAIN TOSISBA) (PIV-4A)	10:331							
7	MATTER PROTEIN	KERKAN PADADGELLENZA 48 VIRUS (STRAIN 64-33) (PIV-4B)	312.532	-					-	
-	MATTER PROTEIN	ADMORAPEST VIRUS (STRAIN KABETE O)	Γ	233-300	ğ					
	MANUEL PROPERTY	CENTRAL VIRES (STRAIN FLISHIAIN	Т	Т	-				-	
7	THE PERSON OF TH	THE COURT CASE AND IN POLICE					t		+	
7	MATRIX PROTEIN	SUNDAL VIAUS (STRAIM RAKALS)		1		:	_		_	
	MATRIX PROTEIN	SERDAI VIXUS (STXAIN Z)	٦		1	-	 		1	
PWAAT SEPVE	KATRIX PROTEIN	SUBACUTE SCLEROSING PANENCEPHALITIS VIRUS (STRAIN DIKEN)	٦	٦	-					
PVACAY_SV41	MATRUX PROTEIN	SIMONA VIRUS 41	133-154		304-324		-	-		
Г	MATHUX PROTED ⁴	SIMIAN VIRUS 5 (STRAIN W3)	1 11116	111-148 308-335	1 311			_		
Ļ	MATRIX MOTERA	SPRING VILENIA OF CARP VIRUS (RHABDOVIRUS CAUPIA)	141-167		-					
T	KANELY MOTEN	INTRACE MINISTRACIONES VIRUS	133:143						-	
Т	St. Cd VCNee Cherk	INCOME CONTRACT STRAIN MENTS	T	137.161	91:16			<u> </u>	<u> </u>	
Т	ALCONOMISE AND THE	LANGE AND PARTY AND	A CHANGE CONCRETE TABLE (3) INCIDE 6470)	T	77 201		1	1		+
	EL CE. YCUPHUTEUN	MUMAN COMMA VIAUS (STRAIN U.C.)	1	T		1	1			
PWG! CWAS	EI OLYCOPROTEIN	MURING CORCHAYIRUS MOTY (STRAIN ASY)					1			
	EI GLYCOPLOTEIN	MURUNE CORONAVIRUS MAY (STRAIN 1904)	وَ						1	
-	EI OLYCOMOTEIN MECURSOR	PORCING TRANSMISSIBLE GASTROENTERITIS CORONAVIRUS (STRAI	174.193	-	1					
_	EI CLYCOMOTEN MECURSOR	PORCINE TRANSMISSIBLE GASTROENTERITIS CORONAVIRUS (STRA)	169-193	134-193	1 1	I I				
T	ELOLYCOMOTEIN PRECIMIOR	PORCEME RESPIRATORY CORONAVIRUS (STRAIN RM4)	134-193							
_	EI OLYCOPROTEDI	TURKEY BATERIC CORDNA VIRUS	1 90-4	137-161 171-190	061					
•	E) OLYCOPROTEIN	A VIAN INFECTIOUS BRONCHITS VIALIS (STRAIN 6/22)	74.94	-					L	
PWAII 18V8	EI OLVCOMOTEIN	AVIAN IMPECTIOUS BRONCHITIS VIAUS (STRAIN BEAUDETTE)	10174							
	EI GLYCOPROTEIN	AVIAN INFECTIOUS BRONCHITS VIAUS (STRAIN BEAUDETTE NAT)	101-14				-			
PYAE! DVK	EI GLYCOMOTED	AVIAN INFECTIOUS BROMCHITIS VIRUS (STRAIN KB152))	24.98	\mid			r		L	
	PROBABLE MEMBERANE PROTECT	EMSTERN-BALLI VIRUS (STILAIN 1995-2)	11 181-161	138-203		F			L	
WAS CLAN	SKOVENEUT PROTEDI	CALLUS LOWER MOSAIC VIXUS (\$TILAIN CM-1941)	Γ		IQ2			-	L	
	MOVEMENT PROTEIN	CALLIFLOWER MOSAIC VIRUS (STRAIN DAI)	111174	147-164 113-201	100					
W-2-W	MOVEMENT PROTECT	CALLIFLOWER MOBALC VIRUS (STRAIN BBC)	110-174	147-164 113-201	ē					
WAS CLAW	LIOVELIENT PROTEDI	CALLIFLOWER MOSAIC VIRUS (STRAIN NYRIS)	X:==	147-164 113-701	ē			-		
•	MOVEMENT PROTEDY	CAUL DECOMES MOSALC VINUS (STRAIN STRASBOUNG)	711-11	147.164 113.201	Ī					
_	MOVEMENT PROTEIN	CALL DE LOWER MOSALC VIRUS (STRAIN W240)	Γ	Τ	Ī					
_	MOVEMENT PROTECT	CARACTION ETCHED RING VIRUS	T	Г			l		<u> </u>	
_	MOVEMENT PROTECT	PICWORT MOSALC VIRUS (STRAIN DXS)	115.131	180-191	_	L	-		-	
L	MOVEMENT PROTEIN	SOYDEAN CHECKOTIC MOTTLE VIXUS	122-147 3	273-299			-		-	
_	MAJOR SURFACE ANTICEN PRECURSOR	DUCK HEPATITIS B VIRUS (BROWN SHANGHAI DUCK ISOLATE SS)	K 822-10X	266-295				-	L	
-	MAJON SURFACE ANTIOEN PRECURSOR	DUCK HEPATITIS & VISUS (STRAIN CHINA)	194-221	268-294			\mid			
_	MAJOR SURFACE ANTIGEN PRECURSOR	DUCK HEPATITIS & VIRUS	157-184 2	231-257						
Ē	MAJOR SURFACE ANTICEN PRECUISOR	DUCK HEPATITIS & VIJUS (WHITE SHANGHAI DUCK ISOLATE S)!)	Г	260-295						
,=	MAJOR SURFACE ANTICEN PRECURSOR	GROUND SQUINKEL HEPATITIS VIRUS	304-236 2	271-295 310-395	500			-		
F	MAJOR BURFACE ANTIQUE PRECURSOR	HEADN HEPATITIS B VIAUS	236-262 2	24)-320					_	
=	MAJOR SURFACE AVTICEN	HEPATITIS B VIAUS	Γ	8.2	_		 -	-	L	
	MAJOR SURFACE ANTIQEN PRECURSOR	HEZATITIS B YOUTS (SUBTYPE ADWZ)	Γ	244-270					-	
PVACA JORVA	MAJOR SUMPACE ANTICEN PRECURSOR	HEPATITIS B YOUR (SUBTYPE ADMA)	185-202 24	244.270						
	IZZION BINITACE ANTIDEN PRECURSON	HEPATITIS B VIXUS (SUBTYPE ADW / STRAIN 991)	П					!		
_	MAJOR SURFACE ANTIGEN PRECUNSOR	MEPATITIS B WHUS (STRAIN ALPHAI)	134-191	133-139			H			
	KAJOK KUKTACE ANTIGEN	HEPATITIS B VIRUS (SUBTYPE AD)	П	70-96						
	MAJOR SURFACE ANTIGEN PRECURSOR	HEPATITIS B VIXUS (SUBTYPE ADW / STRAIN INDONESIA/PIDW (20)	ı							
PVNSA HPBVI II	MAJOR SURFACE ANTIGEN PRECURSOR	HEPATITIS & VIRUS (SUBTYPE ADW / STRAIN IAPANFIOW253)	114.191	253-256		H		_		

									i	
	7	All Virgon (No Betterlephages)								
THE CAPEL	ZKULKIN STREET	WKUS	1214	╗	AREA AR	ANEA A	ABEAS AR	ARTA & AREA ?	7 AREAS	ABYA 3
1000	т	MEZATITIS & VIRUS (STRAIN LSH7 CHIMPANZEE ISOLATE	14-191	233-139		+				
VANA VANA	4	MECALITIS BY VIAUS (SUBLIFFE AUR.) 318AIP MC-1)	27.	g Ż		1				
2000	_	PEZATITIS B VIRUS (SUBITYPE ADW / STRATH OR INAWA/POOWZIZ)	74.191	\$27.62		-				
AVACA TORONA	-	MENTILIS OF VINCE (SUB-1772 ADM / SIEAN PHILIPPINGPEDW194)	202.68	247-702		-		-		
1000	Ŧ	MCATILIS WIKUS (SUBITY: ADR)	202	244-270						
200	THE WAS DESCRIBED TO THE PARTY OF THE PARTY	MECKINIS WINDS (SUBTIFIE AR)	27	8			-		•	
WALES LIBERY	MAKAN BURN ALIS AND MORN PRECURSOR	MERALITIS B VIXOS (BOBITTE ADV)	174-191	233.259		-				
1200	MANUAL STREET,	METAINIS WINDS (SUC) THE ATM	16 181	\$57.62						
172	MANUA BURGALLA AMIJURIA PARLUASUR.	MEPATITIS & VIKUS (SUBTIFIE AD YW)	174-191	7						
10000	MAKER SUMPACE ANTINEM PRECUASOR	WOULD THE MENTING STRUGG I	207.234	П	178-393	•				
	MAKE SUBJECT AND MENTALLUXSUR	WUCCCHUCK HEPATITIS VIRUS 39	213-239		183.396					
Mary Mark	MAJOR SURVACE ANTIGEN PRECURSOR	WOODCHUCK HEPATITIS VIRUS 7	212-239	274-298	183-398		ŀ	-		
LANGY MINA	MAJOR SURFACE ANTIGEN PRECURSOR	WOODCHUCK HEPATITIS VIAUS &	\$12:23	Г	383.394	-	L	L		
PWEA WHYE	PROB MAJOR SUNFACE ANTIGEN PREC	WOODCHUCK HEPATITIS VIXIS & (INFECTIOUS CLONE)	213.239	274-294	M.(-(1)		<u>.</u> !	: . :	:	
PYMSA WHYW	6 MAJOR SUMPACE ANTIGEN PRECURSOR	WOODCHUCK HEPATITIS VIRUS WEA (ISOCATE PWS13)	123-149	Т		+				
WALL LAW	MATRUX (AC) PROTEIN	INFLUENCA A VIRUS (STRAIN AVAINA ALBORAGE)	77.		 	 				
PVATE LABAN	MATRIX (NO) PROTEIN	INFLIFICA A VIBILS STRAIN AMANCHORING			$\frac{1}{1}$	+	+	1		
WITH LATOR	INCATELY (ALS) PROPEDA	INSTITUTION A VISIT STRAIN AFORT WARRENINGS				1	†			
WATER LABOR	MATTER AND MOTION	THE ISSUE A COST OF A CHAIN AROUND BY ACTIVE CIRCLES ASSURED			+	-	1			
WHAT CHANGE	MAYOU SAME	MAINTENAL A MAIN AND AND A COLOUR VINCONDO COLOURS OF THE COLOURS	•		1	-	$\frac{1}{1}$			
	LA PERO AND LEGISLA	INCLUENCE A VIRUS (31 MAIN MYOWL TLACUE VIRUS/WETBALDOE)	27.48			-				
ı	THE PART OF THE PA	INFLUENCE A TIMUS (31 ICAIN ALEMINGUADO) 3457)	97.2							
Ŀ	MALITAC (M2) PROTEIN	DOLUEICA A VIRUS (STRAIN ALENMORAD/194/1757)	25-46						_	
	MATRIX (MZ) PROTEIN	INTLIENZA A VIRUS (STRAIN AMALLARIDMEW YORK#19078)	25-46			-		-		
	KATRIX (AC) PROTEIN	INFLUENZA A VIRUS (STRAIN APPLEATO ILICONIO)	25-46		-	-	L	-		
PWHT INSOR	MATRIX (NO) PROTEIN	INTELLENCE A VILLES (STRAIN ASINGADORE/1/31)	35-46			-		-		
PWATE JAUDO	MATRIX (AD) PROTEIN	DOTLUDIZA A VILUS (STILAIN AUDORINGOM2)	7			-		-		I
PWATE LAWE		DIVILUENZA A VIRUS (STRAIN AWILSON-SMITHUS))	79.55			}	l			I
PWATE LAWKY	_	MAYXOMA VIRUS (STRAIN LAUSAIGNE)	176.341		1	$\frac{1}{1}$		1		
PVNO4 MOTHS	HONSTRUCTURAL PROTEIN HS34	BOVINE ROTAVIAUS (OROUP C./ STRAIN SHINTOKU)	1114.151	-	1	ŀ	1			
PWS PWD	116 7 KD PROTEIN	POTATO VIRUS BISTRAIN PERUVIANI	31.34			\dagger		+		
PVAB INSBK	NS OLYCOPROTEIN	INTLUENZA B VIRUS (STRAIN ENSELINGVIAT)	11.30		$\frac{1}{1}$	+	1	1	1	
PASS DOMO	INS OL YCOPROTEIN	INFLIENCE I VIRUS (STRAIN RANGES KONCAL)		t	-	 	+		1	
PVNB BABLE	NB CLYCOPROTEIN	INTELENZA I VIRUS (STRAIN BA EKVO)	9.7	\dagger	+	+	+	$\frac{1}{1}$		
PUSSE SAVE	INB CLYCOPAOTEIN	DATE UENZA B VIRUS (STRADY BA ENDAGRADA) TOMAS	•	1		\dagger	+			
PVNB DVBVD	NB OLYCOPROTEIN	DOTUDOZA B VIETS (STRAM RAIARY) ANTONO		t	1		$\frac{1}{1}$			
PVNB INBNO	NB GLYCOPROTEIN				+	$\frac{1}{1}$	+			
PVNB DOBOR	NB CLYCOPEDITED				1	†	$\frac{1}{1}$			
PWCS ABVO	NOWCAPSID PROTEDY VS.1			21. 47.		+	+		1	
PWC AEDEV	NONCAPED PROTEIN NS.1	AEDES DENSONUCT EOSIS VIRUS (STRAIN GRV IN) 1655 (AEDES DENS		2	1	+				
PWCS PAYED	NONCAPSID PROTEIN NS.1				+	+	$\frac{1}{1}$			
١	INONCAPSID PROTEIN NS.1			1	+	1			1	
PVPSI AUSVA	INONSTITUCTURAL PROTEIN NSI	VIRUS (SEROTYPE 4/ STRAIN VACCINE)	16.53			+	1		1	
PWSI LLALLA	MONSTRUCTURAL PROTED/ NS!	Т	15	114.111	100	1	$\frac{1}{1}$	1		
PWK1 IANN	HONSTRUCTURAL PROTECN NS!	(Q)	T	Ť	67.103	+	1			
PWSI_LACAD	NONSTRUCTURAL PROTECTIONS		Γ	t	-	-	1		+	
Wisi Mad	MONSTALLICTURAL PROTEIN HSI		37:50	114.139 14	167.193	┞	-			
PWRS JACKO	NONSTRUCTURAL PROTEIN NSI	(84/N/)	8.13	167.192	-	ŀ	-			
PVMS] [ACKU	NONSTRUCTURAL PROTEIN NS)		17 27	64-189	-	ł		l		
PVMSI_LADAS	NONSTRUCTURAL PROTEIN NS		Γ	167.192	\mid	+		+	1	
PVNS1_LADE1	NONSTRUCTURAL PROTEIN INSI		28.43	14.13		+				Ţ
PVNSI LABUT	MONSTRUCTURAL PROTEIN MSI		Ī	164-189		\parallel	1			
PVNSI IAJOM	HOWSTRUCTURAL PROTEIN HS!	INTLUENZA A VIRUS (STRAIN AFORT MONDAOUTHVIAT)	31.58	T	167-192	\dagger	\dagger]
WOLAI INW	NONSTRUCTURAL PROTEIN INSI	K	8.5	T	167-192	ł				
PVNSI LAPR	MONSTRUCTURAL PROTEIN NS!		31.50	161-191		╀	+	-		
WS IVE	MONSTRUCTURAL PROTEIN NS	η.		114-137 16	167-192		L			
TWIST LALEN	MONSTRUCTURAL PROTEIN NSI				7-192		-			
PVNS IAMA	MONSTRUCTURAL PROTEIN MS!	INFLUENZA A VIRUS (STRATH AMALLARD/ALBERTATE/16)	31-50	261-191			L			

PWS LAKE											
PWS LAKE	I	MINERAL AND A CORP. A CARD A CARD A CARD A CARD CONTRACTOR OF CARD CON	S	30.5	70.50		1	1	, order		4
2	1	INTEGRAL A VIRGO (STANIA AMALIA MANATAR VORKASTATS)	2	167-192	+	†	\dagger	t	\dagger	t	
	Ť	INTEREST A VINIS (STEAT) ANYNAMIANEDA-THAMB)	197	164-189	+	†	T	\mid		\dagger	
1	Ť	THE THAT A VIRUS STRAIN APINTALIAL BERTAIN9791	167-193			t	T	┝		ŀ	
	MONSTRUCTURAL PROTEDING!	DIFLUENZA A VIRUS (STRAIN APINTALL'EERTA/121/79)	3:50	161-191	-	T		\vdash	\mid	 	.
WASI LANS	HONSTRUCTURAL PROTEZNINS!	DOLLIENZA A VIXUS (STRAIN APINTAL/ALBERTA/MIN'S)	8.E	167-192	-			Ц			
PWST AND	HONSTRUCTURAL PROTECTIVISI	DOTUDIZA A VIRUS (STRAIN APINTAL/ALBERTANSMY)		П	L		Н			4	
PWS1 LANCE	MONSTRUCTURAL PROTEDINS!	DOLLDENZA A VIRUS (STRAIN APUERTO INCORDA)		114-137	167.192			_			
PWRST_LATELS	HONSTRUCTURAL PROTEIN IS!	DOLUMA A VIRUS (STRAIN APPRICAY SETHER BESTACHLIT/1492-BA)11-30		167-192							
PWGI_LATKC	Г	INSTLEMEN A VIRUS (STRAIN A/TURKEY/CANADAM)		167-192							
PVISI LITER	Г	DIFLUENCA A VIRUS (STRAIN ATURKEYORECONIT)	31.50			7					
PWEI LINE	Г	INTLIEUZA A VICUS (STRAIN ATERNISOUTH AFRICANS)	128-47	164-189	H				I		
PVNSI WIRT	INONSTRUCTURAL PROTECT ASI	DELLENZA A VOLUS (STRÁIN A/TERMTURKMENIA/1972)	87.10	Г	L	-					
PWS! IALDO	f	(DOTLIENZA A VIRUS (STRAIN AGDONOVIOTITI)		114-137	167.192	-	r	-			
PANK! IAIRS	T	INFLIEDZA A VIKUS (STRAIN AUSSRAD77)	3-5	114-137	167.192	F					
WAT LAN	MOMENTAL PROPERTY.	DOTLEDGA A VIRUS (STRAIN ASWINGAOWALISTO)	8:	167-192	-	-:	l				
ANGEL PASS	Т	INSTLUENZA C VOLUS (STRAIN C/ANN ALBOR///SO)	222-249		-	-	T	┞	l	\mid	
	T	DOMESTIC VIRIA (STRAIN CCALIFORNIAN)	223-248		-	-		-	\mid	-	
PANCE BYVIS	Т	(RELEGIONGLE VIRUS (SEROTYPE 10/150LATE USA)	Т	201-123	-	†.				l	
PVNSS BTV19	۲	ALLETONOUS VALUS (SEROTYPE 17/1SOLATE USA)	192-161	201-223	-						
WANTE BOARS	MONSTRUCTURAL PROTEON NS3	BLUSTONGUS VIRUS (SEROTYPE I 71SOLATE SOUTH AFRICA)	Г		-	ŀ	T		-		
WASH BEVIE	T	SELUETOWOUT VIAUS (SELOTYPE 10)	192-161		-	1		-	\mid		
PWG1 BOV	L	EPIZOOTIC NEMORAHAGIC DISEASE VIRUS (SEADTYPE 1/ STRAIN AL			ļ			-	-	-	
PANCE LANGE	T	INSTURNZA A VIRUS (STRAIN APPURATO NUCOMOS)	15.51		-	-		-			
PANE LARV	T	DOLLENCA A VIXIUS (STRAIN AFRENSOUTH AFRICANS)	27.5		<u> </u>	-		-	-		
PWS1 PW	NONSTRUCTURAL PROTEIN 2	PARUMONIA VIRUS OF MOCE	53-64		-	-		-			
PWASI CANT	Т	PORCING TRANSMISSIBLE GASTROENTERITIS CORONAVIRUS (STIKA)	102-141111		L	1		L			l
PVNSS CVPFU	Т	PORCONS TRANSMISSIBLE GASTROCHTEATTS CORONAVIRUS (STRA	N 94-121			H				L	
PVASS CVPICE	Ē	PORCING RESPIRATORY CORDNAVIRUS (STRAIN RMs)	177-301								
PVNS3 LEV		NUCE STREME VIBUS	97.0			+					
DANKE CAND		HUMAN CORCHAVIRUS (STRAIN 229E)	8			-					
SANS CARE	MONSTRUCTURAL PROTEIN 4	MULTING CORONAVIAUS KOV (STRAIN S)			+	1	1	1	1	1	
TWE CARE	٦	PORCHINE THANKING SIGNED CASTROCHUM CONCRAVIALUS (STRAL	_		+	1	+	+	1	1	
	7	CACLME INAMESTED GAS INCENTED IN CURUMAY INC.	7		+	1	\dagger	1	\downarrow	1	
	A NONSTRUCTURAL PROTEIN	PORCENS RESPONDED CONORAVIOUS (STRAIN ROPS)			-	1	1	+	\dagger	\dagger	
2	NOWSTRUCTURED PROTEIN NO	MACAGE BITTO VICTOR	T	2	63,143	t	\dagger	+	\parallel	\dagger	
	T	JEEL MAINTENANC CHANALAVAINE (CTRAIN 74.1441)	T	Ť	+	t	t	\dagger	t	$\frac{1}{1}$	
VALUE OF STREET	Τ	FELDEL INTECTIOUS PERITONITIS VINUS (STRAIN 79-1146)	3				l		l	\dagger	
PANCE PINE	MONSTELLETURAL PROTEIN C	HÜMAN PALADYLLENZA I VIRUS (STRADY C13)	24.52		$\frac{1}{1}$	T		\mid		l	
PWSC NIK	NONSTRUCTURAL PROTEIN C	HEDGAN PAKATMELUENZA I VIKUS (STRAIN C19)	24-94		-			-			
PWSC HISD	NONSTRUCTURAL PROTEDY C	HEBITAN PARAPHELUENZA I VIRUS (STRAIN CI-S/7))	14-92	136-197	Н	H		-			
PWSC HING	П	HEBRAN PARAPHTLUENZA I VIRUS (STRAIN CI-1483)	76-92								
PVNST CVBQ	П	BOVINES CORONAVIRUS (STTIALIN QUIEBEC)	691-103								
PVNST BICCL		DULUDIZA C VIRUS (STRAIN CKIREAT LAKES/1167/9/)	222-248			Н					
TWST NCM	П	DIFLIDREA C VIRUS (STRAIN CACHANNESBURG) M46)	223-248								
PART POR	7	DOLUMEA C VINUS (STRAIN CAUSSISSIPPING)	200	1	-	1	1	1	+	+	
PVRST DICYA	MONSTRUCTURAL PROJECTS ASSESSED	MATCHESTA THE STATE OF STREET OF STREET OF STREET	200	1	1	†	1	\dagger	1	†	Ī
	INDICATE INTERAL PROTEIN NO.	SANDELY PRIVE SICELIAN VIRIS			1	T	T	+	+	\dagger	
	MONETH INTERNAL PROTECTIVES	LETEL SATE AND VOLUM	T	701-92	\parallel	t	1	ł	1	\dagger	
PACHITY BEGGY	1	PSEUDORABLES VIRUS (STRAIN KAM AN)	ļ	1801.081		1	1	l	\dagger	\dagger	
PUNC PLAN	:	DHON VOIUS (STRAIN INDIANISISMI)	123-139	297-324		T	T	\dagger		\dagger	T
PWACE EBOV		EBOLA VIRUS	159-176							H	
PVAUC LANA	١.	DIFLUENZA A VIRUS (STRAIN MANAS ACUTAPRIMORIE69576)	Γ	166-287		-		_		l	
PVNUC IXAN		(INTLUENZA A VIRUS (STRAIN A/ANN A/BONA/40)	173-197							H	
PWNC LABRA	NUCLEOPROTEIN	INTLUENZA A VIRUS (STRAIN ABRAZILVI IMI)	173-197		-						

PH P WANT		2000		Г	V STARY	AREA 5 IAN	FAC AREA?	l	
	PAOTER	TORKS.	7	4	I	T	0100	ANTA	3
PYNUC MAUD	MUCLEOPROFEIN	INTLUENZA A YIRUS (STRAÍN A/BUDGERIGAR/HOKKAIDO/1/17)	137-167	1	+		1		
WEC INC	MUCLEOPROTEIN	INTLUDIZA A VIRUS (STRAIN ACALIFORNIA/1071)	17-197	1	†			+	
PVNUC JACKO	MACLEOPROTEIN	INTLUENZA A VIRUS (STRAIN ACHICKENGERIANT/PAP)	141-141	1	+		+		
WALK LAGE	MUCLEURICIES	INTELLIGINAL A VIDING STRAIN ACTION CATEGORIST LANGUAGE	191761	\dagger	t	\dagger	1	T	
A LANGE	in in Schoolshi	INTLUENZA A VIRUS (STRAIN ADDICK/BELINGLINE)	191:181	f		l	-		
PWICE LABOR	MIC EOPTOTEIN	INFLUENZA A VIRUS (STRAIN ADDICK/CZECHOSLOVAKIA/S6)	173.169	\mid			_		
PWICE JABBI	MUCLEOMOTEIN	INPLUENZA A VILUS (STRAIN ADUCICENCILAND/1/56)	143-187	Ϊ					
	MUCI EDPLOTED	INFLUENZA A VRIUS (STRAIN ADUCKENGLANDHAZ)	191.197						
PVNOC IXENX	MUCLEOPROTRIN	INFLUENCE A VIRUS (STRAIN ADDOCKMONG KONGUIS)	197-197						
PYNUC IADAC	NUCLEOPROTEIN	INTLUENCA A VIRUS (STRAIN ADUCKAIEMMISM21/14)	173.197		7				
PUMIC LADACA	NUCLEOFROTEIN	INTLUENZA A VIBUS (STRAIN AIDUCKMANITOBAIIA))	133-197						
PVNUC IADNZ	NUCLEOPROTEIN	INFLUENCA A VIBUS (STRAIN ADDCK/NEW ZEALAND/) 1/76)	173-197		1		1	1	
PYNUC IADUI	MUCLEOPHOTEIN	INTLUDIZA A VIRUS (STRÁIN ADUCKURRAINE/2060)	172-197	1	1	1		-	
PVAIC INENS	NUCL ECPROTEIN	INTLUDICA A VILUS (STIAIN A/ENGLAND/1955)	73-107		1			1	
WALC IN ON	-	INTLUENCA A VIRUS (STRAIN AFORT MONMOUTH/1/47)	177-197	1	+			1	
VNC NOW	-	INCLUENCA A VICUS (STINAM APORT)	141.41	†	:	\downarrow	1	1	
PVAUC IATIO	-	TAPLOENIZA A VICUS (STICATA APOWE PLACUE VICUSIONOSON DOLO	141 184	1	+	1			
	MUCLEOFIGHER	INCLUENCA A VICUS (STINAIN APOWL PLACUE VICUS NOT COLUMN APOWL PLACUE VICUS NOT COLUMN APOWL PLACUE VICTOR		Ť	+				
PYRICE MORE	PUCLEUMOTEIN	THE CONTRACT A VIETO CONTRACT IN THE CONTRACT OF THE CONTRACT	101 561	\dagger	1	1			
WALC INCO	HUCCEURUIEN	INCLUSION A VINUS (STRAIN PROLLOMAN LLANGER)	101.00	+	1				
WALE LAGO	MOCLEOPHOTEIN	INTEREST A VINCESTATION AND LANGUA AND LANGU	141.00		†			 	
VNUC IAGI	- 1	LICELARIA A VICTO (STINATI MOLLIMATELARIA)	101.00	1	†	1			
	_	MALLENGA A VINCE AND AND LINES AND L	101.101	l	+	$\frac{1}{1}$			
THE PARTY	MACALOTROLEIN	Interest A Visit (che all Actal I Alakkachiisert Colob	10,76	T	†	\dagger	}		L
71	_	INTERPRETATION STRAIN ARTHUMOURSOTAWASTO	17.197		-				
VALUE AND	-	DITUDICA A VIRUS (STRAIN AMICKOX/40)	15.19	T	t				
VANC MU	NUCLEOPROTEIN	INVILIDADA A MRUS (STRAIN ARQUINGUILLINUM)	133-199			_			
PVNUC IANGO	MUCLEOPILOTED	DOLLONGA A VIRUS (STRAIN ARQUINE/LONDON/1416/13)	173-197			\mid			
PVNC INHE	NUCLEOPROTEIN	INTIUENCA A VIRUS (STRAIN ARQUINEAGAMUIA)	12:187						
PUNC JANOI		DVFLUENZÁ A VIRUS (STILADA AMONO KONCAINS)	11.11	-	-				
PWC MR	_	DATUENZA A VIRUS (STRADA AMONG KONGSAT)	17-197	1	1	1			
PWCC MARK	-	DOLUGICA A VICUS (STIADI ARGUDEPTIAGUE) (SA	141-141	1	1	1		1	
PARC MIT	-	INTLUENCA A VICUS (STITAIN APOUNDITENNESSEE/STIG)	261-62	1	1	$\frac{1}{1}$		1	
WALC IACE	MUCLEOFICIED	INCLUENCA A VINUS (STRAIN AVINUS VISAVI)	7614/1	1		$\frac{1}{1}$			
PWICE IALES	NACH EGYPTO BEN	INSTITUTE A VALUE (STEAM AND IT ARINA THE AND AND IT ARENA AND AND IT ARENA AND AND A STEAM AND A STEA	137.109		1	+	1		
300		INSTITUTE A VIETE (STEATH ARABITARDAGE YORKATSO78)	137.167	T	T	+		-	
PANEL LAKEN	-	[BOLUBRZA A VIRUS (STICAIN AMINICSWEDENIA)	137-197	T	T	ŀ	-		L
PVNUC LANTS	HUCLEOFROTEDI	DATLUENZA A VIRUS (STRAIN ANTRONS)	133-197			-			
PVNUC JADA	NUCLEOFICIED	DEFLUENZA A VIRUS (STRAIN ACHDOWN))	193-161		<u> </u>		L		
PYNUC DAM	MUCLEOFILOTEIN	[INFLUENZA A VIRUS (STILAIN APABLICITAL STERM)]	191-161		1				
FVNUC JAMUE	-	DATURAZA A VIRUS (STILAM APUBRTO NICORDA)	133-197						
WHICE LALLED	Ţ	INTIUTACA A VIRUS (STRAIN ARUDOY TURNSTONENEW JERSEYAM 175-197	7.10			-			
PVNUC IASED	-	INDILIDENZA A VIRUS (STRAIN ASEALMASSACHUSETTS/1/40)	173-197	1	1	+			
PVNC LASID	PRUCL EOPROTEIN	INFLUENZA A VILUS (STRAIN ASHEARWATER/AUSTRALIA/7)	137.107	1			1		
PVNUC IASIN	MUCLEOFICIEN	INTLUENCA YIRUS (STRAIN ASINGANULI)))		1				1	
PVNUC ATE	MUCI ZOPROTEIN	INTLUENCA A VIRUS (STRAIN ATEAUNCELAND/2010)	173-197	1	1	1	+	+	
PVNUC LATION	NUCLEOFROTEIN	INGLUENZA A VIRUS (STRAIN ATURK EYMINNESOTATION)	173-197	†	1	†	1	1	
PWC IATEO	PACE EOPROTEIN	INFLUENZA A VIRUS (STRAIN ATURKEYONTARIO77)246)	173-107	1	1	1	1	+	
PVACC IATES	MUCLEOFICIEN	INTLUDAÇA A VIAUS (STRAIM A) EXPOSULTI AFRICARIT	/AI-(/		1	+	1	+	
WACK LATE	NOCESOTRO EIN	INTEREST A VINCE STANDARD CONTRACTOR OF STAND	191.101	t	1			+	
STATE WITH	-	INTLUENCE A VIETA (STATIS AND AND AND AND AND AND AND AND AND AND	131-187	T	T	\parallel	-		
	_	DISTINUED A VIRUS (STRADA ACISSA ACIS)	173.167	T	†			 	
101	_	INTLINIA A VILLE (STALIN AVICTORIA/MI)	100	t	Ì	+	-		
TANK WILL	AUCENT TO LEAST	fraction and the second		1	1				

MCCENE			_	ABFA 1 AT	ARTA S LAREAS					
TILE NAME	MULIN		Ţ	П	_	Т	T	Т		L
WALL LAWIN	MUCLEOPROTED	DISTURNZA A VIRUS (STRAIN ANNIALENIAINE) JUNA)	A P	\dagger		+			L	
CHAY LAWE	INC. FORGOTEIN	EAWI976)	137-181	1		1		 -		
IMVI WIN	MAIN SOPROTEIN	1		1	1	1	$\frac{1}{1}$			ļ.
04 1 July	MICH COROLLON	INFLUENZA A VIRUS (STRAIN ASWINEZ997?)	73-197	1		\downarrow	+	+	-	
WAR 1474	Nice somersing.	INFLUENZA A VIRUS (STRAIN ASWINE/41/49)	173-197		1	+	-			
AND LANCE	MAY FORESTED	DATLUENZA A VIRUS (STRAIN ASWINE/CAMBRIDGE/1/13)	17)-197			+			-	
WART TATA	WICE SOMEOTEN .	DOTUBLIZA A VIRUS STRAIN ASWINE DANDONG 401)	4	1	1	+	+	 	+	
AND A PART	Manual School Park	INTELENZA A VIRUS (STRAIN A/SWINE/GERAIANY/A/1)	137-161			+	1			ļ
THE PARTY	Manage Colon	NOT LIENZA A VIRUS (STRAIN ASWINE/IONG KONGIA/16)	133-197	1		1		-		
10671	MINISTERNATION OF THE PRINCIPLE OF THE P	INFLUENZA A VIRUS (STRAIN ASWINISMING) KONGS 21472)	13.197			<u> </u>		1		1
AAA IN TANII	3134 SASON 1213	INFLUENZA A VIRUS (STRAIN ASWINEAUWA/1970)	173.197		$\frac{1}{1}$	+			1	
100	NUCLEAR PROPERTY	INSTUDINZA A VIAUS (STRAIN ASWINEADWA/1976/1))	133.167					-		:
7 P	TOUR PORT OF THE PROPERTY OF T		175.167			-	1			1
WALE AZE	HUCLEUPKO I ELM	INSTITEMENT A VIRUS (STRAIN ASWINEATAL YM) 419)	193-197	_		1	1			
WIE WAY	MUCEUMOTERA	INSTITUTE A VIRIUS (STRAIN ASWINE)/AMESINURGA?)	193-197			•		-	-	·
WALL LALL	MULEUTICI ELIN	INSTITEMENT A VIRUS (STEATH ASWUNGALAY)	193-197			-	-			-
ALC: MANA	FUCLEUM	INTELLEGISTA A CHAIR STRAIN ASSETTENT PIENLANDS 12051	193.193			:		-	-	-
PVAUC IAZME	MUCIFICANIOTEIN	MAN HOUSE A COMPANY AND MANUSCRIPTORY	133-110			H			-	
PVNUC IAZOH	MUCLEOPLOTED	THE COUNTY A CHAIR AND A THE A CHAIR CAN COUNTY STATE OF THE COUNTY STATE OF THE CANADA A CHAIR CAN	13.13			- -				
WELL INZWI	MUCHOPROTEIN	THE LOCAL A CARLIE ATTA AND A CONTRACTOR STATES	13).193			-				
PVNUC IAZWZ	MUCLEOPROTEIN	INCLUDAÇÃO A VINCIA (STRAIN AND AND AND AND AND AND AND AND AND AN	234.758	-		\vdash				
WALC BOLK	NUCLEOFEDITIN	INPLUENCE B VIACO (STRAIN GAMES AND COLORS C	214.258		-	-				
PVINC DAM	NUCLEO-RDTEIN	INCLURACY BY VICE (STRAIN BANK)	34.36			-	-	-		L
MACC DARK	NUCLEDITORIN	DOLUMAN WINUS (STRAIN BALESOW)	27.7			-		-		
PWALE DOS!	NUCLIONIONED	DOLUMEA B VIRUS (STRAIN BASINGATORE) 220 M)		171.141		-	-			L
RUC KASWA		MARBURO VIRUS (STRAIN MUSCARE)		1			-		-	L
PYRIC KABY	MUCIOHOTEN	MALBURG VIRUS (STRAIN PORT)	700, 000	T	136.111	+				L
DOI VACCE		VACCINIA VIKUS (3 I AAM CUTEATAUEA)	184.204	T	36.31	+	-			
WEST VALIV	PROTEBIOL	TANKET AND LANGE AND THE PARTY OF THE PARTY	846-865			-	+			
VOR! PON	ISS KD PROTEIN	LASSER LASTA VILLA	409-424	990-1010		-			-	4
YOU NOW	IN KD WOTEN	POTATO CIRCLE IN STRAIN BUSSIAM	97:104	1 4001-986	1251-1270 1103-1	1.1989				-
200	TO THE PARTY.	(POTATO VIBUS S (STRAIN PERUVIAN)	279-295	П	╗	\dashv	+			1
	ALL LA PROPERTY	POTATO VIRUS X	124-155	٦	1	ΞŤ			+	+
W	Let VA be Are in	POTATO VIAUS X (STILAIN CP)	126-155	٦	7	=+	0.01-0.0	1	-	\downarrow
	TATE OF THE OWNERS OF THE OWNE	(POTATO VIRUS X (STRAIN XJ)	128-153	1	306-322 1010	0101-010	+	1		-
	SECURITION OF THE PROPERTY.	OS STICKWOERRY MED YELLOW EDGE ASSOCIATED VIRUS	121-146	55-175		+	1		+	\downarrow
	TANK THE PROPERTY	WHOTE CLOVER MOSAIC VIRUS (STRAIN M)	121-146		-	+	+		-	1
	147 K3 PROTEON	WHOTE CLOVER MOSAUC VIRUS (STRAIN O)	131-146	Т		†	1	+	-	1
THE PERSON	PROBABILE MEMBRANE ANTIGEN 3	HERNESVEKUS SABARKI (STRACK II)	*		331-373	Ť			-	\downarrow
1100	POLICE DE LA COMPANION DE LA C	AUTOCRAPHA CALIFORNICA MUCLEAR POLYYEDROSIS VIRUS	ş.	42.59		+	1			1
200	Pio Pentada	CACYTA PSEUDOTSUGATA MULTICAPSID POLYHEDROSIS VIRUS	7		1	1	1			1
THE PERSON	PIBPLOTED	SPODOFTERA EXICUA MUCLEAR POLYREDAOSIS VIRUS (STRAIN US)	_	1	T	Т	100 100		+	1
VOTE STATE	PEOTEIN SIG	RICH BLACK STREAKED DWANS YIRUS	71-49	7	-CA1 -CO1	N7-64	7		+	1
All Viens	MONITOCHUMAL PROTEDY PASTO	WOUND TUNOR VIRUS (WTV)	1	Ť		1	+		+	1
VALUE OF STREET	3		24.713	200	311-32	+	+		+	+
7	PROB CAPSID ALLENDLY AND DNA MATUR PROTEI	ELEPSTEIN BALLA VIXUS (STRAIN BOS-E)	١	7		+	+		+	+
VOLUM SHOW	PACAR EXPERIENCELY AND DIVA MATUR PROTEI		77-101	122-149	912-00	+			-	1
12/12/1	PACHE CAPATED ASSESSMENT AND DNA MATUR PROTEI		592.92		+	\dagger	+		+	1
ONZA BIRM	CAPSID ASSEMBLY AND DHA MATUR PROTEIN	VAUCELLA ZOSTEN VIRUS (STRAIN DUMAS)	2		+	\dagger	+		+	1
IANI IMM	STRUCTURAL PROTEIN VPI PRECURSOR	SULFOLOBUS VINUS-LIKE PARTICLE SSVI			\mid	t	+	-		ļ
WATE ALCO	COAL MOTEON 721	ARTICHOUS MOTTLED CLUNKLE VIXUS		1		+	+	-		-
AG ITA	CORI PROTEIN PI	CUCUMBEN NECTOSIS VITUS	Î,		-	\dagger	-	ļ	-	ļ
MAS SAV	CONTINUED P21	CONTRACTOR PLINGSPORT VIACO	3			\dagger				L
PVP31 TBSVC	CORE PROTEIN POL	LABOARD BOOK STORY AND STRAIN AND SO	141-165	187.202	161-202					
AVED HONA	PROBABILE CAPSID PROTEIN VYZ.	LUCKERS SINGLEY VIRIUS (TVPS 1 / STRAIN 17)	197.220		-	\mid	-		_	
						1				

		All Virges (No Betertophages)	٦	٦	Ŧ	Т	Ì	1		1 1 1 1 1 1 1	į
TEL KAME	PROTEIN	Virits	J	1	3 3	AREA!		1	AREA?	4	1
CAZA (TAA	PROBABLE CAPSID PROTEIN VP23	VANCELLA-ZOSTER VIRUS (STRAIN DUMAS)	<u> </u>			-					
WPM NOVAC	P26 PROTEIN	7	T	T		T	T				
PVPI AUGV4	OUTER CAPSID PROTEDI VP2	MAIN VACCINE)	1	T			1			ŀ	
WP1 BTV10	GUTER CAPSID PROTEIN VP2.	BLUETONGUE VIRUS (SEROTYPE 10/150LATE USA)	1	7	1	6		1		Ī	
WAY BEVILL	OUTER CAPID PROTEIN VP2	BILLETONGUE VIAUS (SEROTYPE 11 / ISOLATE USA)	٦	٦	Τ	200			İ		1
PVP3 BTV13	OUTER CAPAD PROTEIN VP3	BILLETONCUE VIRUS (SEXOTYPE I) / ISOLATE USA)	\Box	420-431	017-632	637-676					
PV72 BTV17	OUTER CANED PROTEIN V72	BILISTONOUS YIRUSKSEROTYPE 17/1SOLATE USA)	٦								
WHI INTA	OUTER CAPSO PROTEIN VP2	BILLETONGUE VIRUS (SEROTYPE 1/15OLATE AUSTRALIA)		٦	╗						
FUEL BRUIS	TOUTER CAPSED PROTEDY VP2	BLUBTONGUE VIRUS (SEROTYPE I / ISOLATE SOUTH AFRICA)			420-438	654-681					
PVPS BADVI	CATTER CAPSED PROFILM VP2	EPIZOOTIC NEMORUMAGIC DISEASE VIRUS (SEROTYPE I)	_			,					
	BLIA BOARDA BOARDA USA	BOVDER ROTAVIRUS (STRADALIS)	115.100	334.360	\$22.543	613-618	15. Je				
1	AUG-GROUP TRUSTED VICE	SANCTION OF A VIET RECEDENCY	T	T	ı	765-790				L	L
TATE LOTTED	INA-EMODING PROTECT VEZ	TO THE PARTY WAS ASSESSED.	T	Т	ı	414.700	114.700				
PVP1 ROTHW	ANA-EDIDONG PROTEIN VP2	HUMAN KUTAVIRUS (SEKOI TPE I / SINAIN WA)		Т	1			Ī			l
PVP1 LOTING	ANA-ENDONG MOTEON VP3	PORCONG ROTAVIRUS (GROUP C / STRAIN COWDEN)	1	1	ŧ		I		1		
Mar Long	BUA-ED-CORPO PROTEIN VP3	SEMINAL II ROTAVIRUS (STRABA SALI)	34.57	219-240	302-316	335.76	**:52	BV-74	703-790		
PAPE LIABAN	LINKON MUCI LOPEOTEIN VP30	INAMBURO VIRUS (STRAIN MUSOKE)	50-75			-					
SUPPLY ARENT	PALINCEAL/NORCOTTON P12	AFRICAN SWINE FEVER VIRUS (STRAIN BASIV)	441-741								
	LANCE ACTUAL ACTUAL TO SECURE THE VEHICLE OF SECURITIES AND ACTUAL ACTUAL OF SECURITIES AND ACTU	FECTA VALUE	233-234			ľ					
	1	MANIETHA VIETR (416 AN MANE)	Γ	2014		•					
AVEN BARAN	Т	ALA MENT DE COMPANY DE COMPANY	Ī	1017							
Mary Cont	POLYMERATE CURCULA PROJECTA V7.3	INTERCOLO MANAGEMENT CONTRACTOR	Į,								L
7433 VACO	GOACHOOOD CAN'T ENVILOPE PROTEIN PIS	VACCING VIEW (31) AND VIEW CONTINUENT	101	Ī							
VACCV	DOCUMBOOMINANT INVELLORS PROTEIN 733	INTELLIGIA VICTOR STANDARD	100.00		I				ļ		
PVEUS VARV		VAUCA VIEW	200			-					ļ
DEVISION BLAVE	_	MANER'S DISEASE PERPESVINUS (STRAIN GA)	27-607		Ī	ŀ					
NOW BY BY AND		MANER'S DISEASE HEIDESVIRUS (STRAIN MOTORIZAL)	22-62								
PVPS NOVAC	~	AUTOCALMIA CALIFORMICA MUCLEAR FOLYNCIONOSIS VIRUS	1								
DAM HAM	NALIOR CAMED PROTEIN	OROTTA PEDIDOTSUGATA INILITICATSID POLYHEDROSIS VIRUS	Ţ	214-240	243-316	-					1
PVPJ_AJUSV4	VP3 COAS PROTEIN	APRICAN MORSE SICKNESS VIRUS (SEROTYPE ASTRAIN VACCINE)	1		217-617	74.					1
WE BIVIE	VP) COLL PROTEIN	BLUETONGUE VIALIS (SENOTYPE 10/150CATE USA)	7	113-227							
TWE BIVIT	VP) COME PROTEIN	SELUCTONGUE VINUS (SENOTYPE 17/15OLATE USA)	Ī	î		+					
PVPJ BTVIA	VPJ COLIE PROTEIN	(BLURTONGUE VIRUS (SEKOTYPE I / ISOLATE AUSTRALIA)	ł	/22-22		4					\downarrow
IVOU CAVI	VP3 CORE PROTEIN	EPIZOOTIC HEMORINAGIC DISEASE VIRUS (SEROTYPE I)									
PVP1 LIMOVA	VP3 CORE PLOTEDI	EMZOOTIC MEMORANAGIC DISEASE VIRUS (SEROTYPE 2/STRAIN AUS	201:121	2	Т	, ,	***		200		ļ
VAL EW	MAJOR 114 KD STRUCTURAL PROTEIN	ACT DWALF VIOLS (ADV)	1	36.5	267-393		742.750	746-788	20.91		
WHI KOTIC	DANKA COME PROTEIN VPS	PORCENE ROTAVENUS (GROUP C./ STRAIN COWDEN)	Т		Т	22.0					1
PVPJ KOTSI	INNEA CONT PROFEIN VY	SDELAW II ROTAVIRUS (STRAIN SAII)	I		200	779-M/					1
VED 64VY	CAPSID PLOTEIN P46	EPSTEDGLEADA VIRUS (STRAIN 895-6)	Ī								1
HARR WAVE	CANSID MICHEN NO	HOLDSHIP SOLD X VIXUS (TYPE I / STRAIN 17)									
DASH OWA	CAND ROTHIN NO	EQUIDE HELPESVICE TYPE I (STRAIN ABAP)	1	į	*						1
PAPED HISVEA	CANSID PROTEIN PAG	HEXPERVILLS SABJUR (STRAIN 11)	747.76								1
PUND ETVE	CAME MOTERING	INGECTIOUS LANYMOOTIACHEITIS VIRUS (STRAIN THORNE VIII)	Z S								
TANKED LALANA	С	MARBERS VRUS (STIADY MUSCKE)	95:10								\downarrow
PAPE JALASVI	Т	MARINGE VINUS (STRAIN POPP)	1								1
MINTER DAME	STRUCTURAL OLYCOPROTESY P40	BONGNY MONI POCLEAR POLYHEDROSIS VIRUS	_	F							\downarrow
CAZA ONAA	CANSID MOTEUN VP34	VALCELLA-ZOSTER VIRUS (STRAIN DUNAS)	٦								1
PVIMI NIPVAC	STRUCTURAL OLYCOPROTEIN CPAI	AUTOCRAPHA CALIFORNICA MUCLEAR POLYHEDROSIS VIRUS	1	202-278							\downarrow
PVPMI_ROTAL	OUTER CAPSED PROTEIN VPM	SDAZAN 11 BOTAVIRUS (STIAIN SAII)	Ī								
PVP43 LOTS!	OUTER CAPSID PROTEIN VP4	SDIGAN II ROTAVIRUS (STRAIN SAII)	_	S.							\downarrow
PVP41 NVAC	VIEW, TRANSCRIPTION REGULATOR PAP	AUTOGRAPHA CALIFORNICA NUCLEAR POLYNGERUSIS VIXUS	•								
PVP48 MOVOP	Na Morsion	ORGINA PSEUDOTSUGATA MULTICAPSID POLYHEDROSIS VIRUS	5	Ī]	1
PUPAA VARV	MAJOR CORE PROTEDI PAR PRECURSOR	VAUGLA VAUS	1177								1
PUPUL VACOC	П	VACCINIA VIXUS (STRAIN COPENHAGEN)									
WIND VACEV	П	VACCING (STAAM WR)									1
PVP40 VARV	MAJOR CORR PROTEIN PAR PRECURSOR	VAUUCA VUUS	Ţ	911.346	146.461						\downarrow
NA BIVIO	VP4 COME PROTEDN	BLUZIONCOE VINOS (SEROTIVE TO TSOLATE COA)	Τ	971.11	115.313						L
PVP4 BTV11	VP4 CORE PROTED ⁶	BLCETONOCE TROS (SENOT TRE III (SOCK) IS USA)	T	11.740						L	
PVP4 BTV13	VP4 CORE PROTEIN	REUETONGUE VIRUS (SEROITEE 117 ISOLATE USA)	I	437.644	337.00						

CCEME	PICTURE			Y TEL	AREAS	77.74	- XXXX	3	2		
LEMAME	PROTEIN	VIRIS	10172	27.5	Т	Τ	Γ	Г			L
WH BIVE	VPA COAE PROTEDA	BEUETOWOCE VIRUS (SEROITYPE 27 ISOLATE USA)	107								
VAN KOV	OUTER CAPID PROTEIN VP	PERRASKA CALF DIAUCHEA VIRUS (STRAIN MOVICINCOLN)	107 101		777.7	Ī					
Vot LbV	NOWSTRINCTURAL PROTEIN PHSA	NICE DWARF VIRUS	701			}	1			ŀ	
WAY BOTTLE	BUTESI CAMILIO PROTEIN VIA	BOVINE ROTAVIRUS (SEROTYPE & / STRAIN B641)								Ī	
Wet acting	OUTER CAPSID PROTEIN VP4	BOVINE ROTAVIRUS (STRAIM CAM)	20.10				T	I			1
	CATIFE CAPAD PROTEIN VP4	BOVING ROTAVIRUS (STRAIN UK)	ξ (): χ					I			
I	CHARLE CARGO MODEN VP4	EQUINE ACTAVIRUS (STRAIN H.2)	326-250	8				I			
Ŧ	CATHER PARKET BENEFIT UPA	HURAN ROTAVIRUS (SEROTYPE I / STRAIN 10%)	101-207	114-249	417.30						
1040	CAPPER PARENT PROTEIN VM	HUBLAN ROTAVIAUS (SEROTYPE 27 STRAIN RV-5)	(181-30)	114.249	412.501						
	ACTION PARTY BEATTER VOA	HUMAN KOTAVIRUS (SEROTYPE I / STRAIN 69kl)	483-306								1
	Carried Colors and Children	HUSLAN BOTAVIRUS (SEROTYPE 27 STRAIN DS!)	102-181	336.349	482.501	•					
TATE ROLLED	CUITA CATALINA TANAN LAL	MINISTANTOTA WRUS (STRADN KB)	487-506	524-348							
	COLEX CATALON PROFESS VIV	LAPLAND AND MANAGEMENT MANAGEMENT	16-91	101-201	234-249	413-507					
PAN LOTHER	OUTER CAPID PROFESS VY	1000000 100000000000000000000000000000	121.207	234.360	442.507						
N POTHE	OUTER CAPSID PROTEIN VP4	MUNICIPAL AVIAGO (CIRCINO CANT	181.307	314.340	482.507					L	L
WH ROTHON	OUTER CAPSID PROTEIN VP4	MUMCAN ROTAVIRUS (SEAU) TPE I F SIRALA MA /		100	100	-					L
VAN ROTTON	CUTES CAPSED PROTEIN VP4	HUMAN ROTAVIRUS (SEROTYPE 3 / STRAIN MCN13)	3								ļ
Vine 6 hrite	CLITTE CAPATO PROTECTI VP4	HUDALAN BOTAVIRUS (SEROTYPE 1/STRAIN ?)	(QZ-)	234-749	20.20						1
	AN HARM PARKED BROTTED VOL	Hablan Botaviaus (Seagtype 4/Strain St. Thomas))	181-207	234-149	425-301	1					1
	A THE PARTY OF THE	HABICAN BOTAVIBUS (SEROTYPE 4 / STRAIN VAN)	181-207	482-507		1					
A 101	COLEA CASE PROJECT VICE	MANAGER AND STREET WELL STRAIN WAS	101-203	482-307		••					4
VIN ROTHW	DUTE CAND PROTEIN VIA	TOTAL PARTY OF THE PERTY OF THE AND CALLS	235.356	483-506						_	
VP LOTH	OUTER CAPSED PROTEIN VP	CACCAM AND A VINCE CACCAM AND CONTRACTOR AND CONTRA	417.512								L
PVP ROTPC	OUTER CAPSED PROTEIN VP	FORCING ROLL A VINCE (CROSS C) 4 (NO. 1)	600.700	483,507							L
N LOTTO	OUTER CAPSID PROTEIN VP4	PORCINE ROTAVIRUS (STRAIN COLTIVIED)	1	200		F					
VM LOTPY	OUTER CAPID PROTEIN VP4	PORCINE ROTAVIRUS (STIAIN YM)			1	1					ļ
WH LOTTEN	OUTER CAPED PROTEIN VP	ANGESTS ROTAWRUS	2	\downarrow	$\left \right $	1					ļ
WAS EASTED	CONTRACT CAPAGE PROTICIO VPA		42 - X			ł					\downarrow
200.00	CATTOR CAPAIN PROTEIN VIA	SDIZIAN IT ROTAVIRUS (STRAIN SATI-SEM)	395	S.		1					\downarrow
201	In technical	SOUTHERN BEAN MOSAIC WALUS	8 14 14								1
	MONETAL PROTECH PASS	WOUND TUMOR VIRUS	193-215	Ş	406.5	25.39					\downarrow
AND BENIEF	ALTER LANCE MOTHER VPS	BLUETOWOLE VIRUS (SEROTYPE 10 / ISOLAT'S USA)	295-317	24.0							\downarrow
1011	APPEAR CAPAIN PROFEIN VPS	BLUETOWOUR VIRUS (SENOTYPE 11 / ISOLATE USA)	795-317		2	1					1
West Bredit	CATTER CAPSID PROTEIN VPS	BLUETONGUE VIRUS (SEROTYPE 137 ISOLATE USA)	205-310	Š.							
A Profit	CALTER EAMED PROTECT VPS	BELIEFONGUE VIRUS (SENOTYPE I / ISOLATE AUSTRALIA)	87-103								1
1000	A HEE PAREIT DECITEDA VPS	BLUETOWOUR VIRUS (SEASTYPE 1715OLATE SOUTH AFRICA)	295-317								1
	ATTER CARE SECTION VP	BLUETONOUE VIXUS (SEADTYPE 2/ISOLATE USA)	195-317								1
	A HELD CALLY INCREMENT IN	INICE DWALL VIEUS	188-384	622-639	690-715						
A 20	COLER COAL PROTECTION	IN STATISHING WALLS (SEROTVIE 16/15OLATE USA)	6.23	203-249	261-276						
VIVE BIVIO	AND COLUMN	ATHEORY AND CALLFORNICA NUCLEAR POLYHEDROSIS VIRUS	121-337	438-462							
WAL MAKE	In the recition	ACTION AND IN VIBILITY OF BOTTON 107 ISOLATE USA)	177	257.272							
VIEW BTV10	VIN PROTEIN	MANAGEMENT PROVIDES	130-146								
VIE VOO	PROB MONSTRUCTURAL JE & ALL PROTEIN	DECOMA DESTRUCTE INTERACTOR OF A PRINCIPLE OF A PRI	20.23	235-253	286-313						ļ.,
2000	MAJOR ENV GLYCOPAGIEM PAEL	ATTENDED A MALE A PART OF	14:103	238-255	-					L	L
WET POAC	MAJOR ENV GLYCUPACIEUR PAEC	ACTIVITIES LIGHT DATE I A MAINT FAR POLYNODEOSIS VIRUS	155-172								
MAN MAN	MAUR ENVELOPE OF TOUR OF EACH	Tai Herradum Vietra (SPROTVPR 11 / 1501 ATE (15A)	2.5	22.245	257-272						
	VI PROJECT	INTERPORTER VIRUS (SEROTYPE 13 / ISOLATE USA)	5.23	228:243	257.272						
VICE BIVIS	VP6 PROTELIN	INTERNACIA VILLIS (SECOTIVE 197 ISOLATE USA)	7:50	231.245	257.272						
AN BEAL	VID TACIETY	IN THE PARCETS VIRIUS (SEROTYPE 1/150LATE SOUTH AFRICA)	4.27	333.249	261-276						
AN BIAIS	VICE TROUBLY	INTERPORTE VIRILE (SEROT VPR 3 / ISON ATE USA)	204.22	233-248							
VA BTVZA	VP6 PROTIETA	WOLDS TAKE VALIS	374-397								
AIM MA	STRUCTURAL PROTEST IN	WOLDEN TI MOR VIXUS (STRAIN ND	374-397								
ALAN MALAN	BIRUCIOSOL PROJECTIVE	ALTHORIAMA CALIFORNICA MUCLEAR POLYHEDRÓSIS VIRUS	354.235	L							
APPLE NO. VAL.	BEAGING BLACKED AND ANTICEN 25	HERPESVRUS SALVING (STRAIN 11)	127-147	L							
VVIII MANA	THE LANGE STATE OF THE PARTY OF	AUTOGRAPHA CALIFORNICA MIXILEAR POLYHEDRÓSIS VIRUS	174-301	405-470	678.704						
WEST STATES	Ver Coak Pentand	BLURTONGUR VIXUS (SEROTYPE 137/1SOLATE USA)	197-222								4
TOWN BOND	CONT. PROTEIN	ENZOOTIC NEMORAHAGIC DISEASE VIRUS (SEROTYPE I)	105-222	301.333							4
	MONSTRUCTURAL PROTEDY PAST	MICE DWALF VIRUS	\$	_	_						_
											ļ

NO. COLUMN	916 54-56-56							
FILENAME	PROTEIN	Vinesa (No Becterophages)	,	Т	Т	1		П
PVPED MPVAC	CANTO PROTESTING	ALTOGRAPHA CAI JEORNICA MIRI KAR BOI VARDROKIE VIRIN	J	V V V V V V V V V V V V V V V V V V V	A DELAC	ANIA CARA	LAND AREA!	A ABA
PART ROVO	CANAD PROTEIN PIT	OROYA PSEUDOTSUGATA MAIL TITAPEM POLYMEDANCIS VARIET	Ţ		†			1
PVM BTV10	HONSTRUCTURAL PROTEDY PS	BLUETONGUE VIRUS (SEROTYPE 10/150) ATR 115A)	20.00		+			+
PVM BTVII	NONSTRUCTURAL PROTEIN PA	RELIENCE VIEW CONTRACTOR IN THE PROPERTY OF TH	3 5 5		+			1
	NOWSTRUCTURAL PROTEIN PS	BLUETONGUE VIRUS (SEROTYPE 1) / ISOLATE USA)	104-170				1	
	NONSTRUCTURAL PROTEIN PS	BLUETONGUE VIRUS (SEROTYPE 17/150LATE USA)	104,120	 				1
L	NONSTRUCTURAL PROTEIN PE	BLUETOWGUE VIRUS/SERDTYPE 1/150LAYE AUSTRALIA)	8178		-			1
ΙI	NONSTRUCTURAL PROTEIN PA	BLUETONOUE VIRUS (SEROTYPE I / ISOLATE SOUTH AFRICA)	91.40		+		+	
3	MONSTRUCTURAL PROTEIN PE	BUJETONGUE VIAUS (SEROTYPE 1/150LATE USA)	104-120		-		+	1
	OUTER CAPSED PROTEIN PR (INCE DWARF YOUS	374-400					+
AM KGDA	OUTER CAPSID PROTEIN PA	NICE CALL DWARP VIRUS	177.202 216.242	262 399-42				-
AACC	STRUCTURAL PROTEIN VPB PRECURSOR	VACCINIA VIRUS (STRAIN COMENNIAGEN)	225-242					
A AVOLA	STRUCTURAL PROTEIN VP8 PRECURSOR	VACCINIA VIRUS (STRAIN WR)	115-141					
	STRUCTURAL PROTEIN VPB PRECURSOR	VARIOLA VIRUS	115-243	-	Г			
	OUTER CAPSID PROTEIN PI	WOUND TUNOR VIRUS	111-129 214-241	143-153 152	379-405		-	
ALA 100	MONSTRUCTURAL PROTEIN PASS	ALCE DWALF VIRUS	31-72		-			
VOD KOOV	MONSTRUCTURAL PROTEIN S9	AICE GALL DWARF VIRUS			-			
VYC NOVAC	29 KD POLYMEDIKAL ENVELOPE PROTEIN	AUTOGRAPHA CALIFORNICA MUCLEAR POLYHEDROSIS VIRUS	145-166 225	225-245				
LANGE BOACH		DROYLA PERUDOTSUGATA MULTICARSID POLYHEDROSIS VIRUS	122.144				-	
PVTKI ADEIL		HUMAN ADENOVIRUS TYPE 12	161-181		-			
PVPRT NO CTV3		MOUSE MANAKARY TUNIOR VIRUS (STRAIN BAS)	43-63		-		-	
WART LONG		SINGAN MASON PFIZER VIRUS	80.08				-	
PVPRT SACKVH	PROTEASE	SQUIRABL MONKEY RETROVIRUS	256-271		ŀ		-	
PVPRT SAVI	PROTEASE	SIMIAN RETROVINUS SAV. I	8-93		ŀ		-	-
MAC HVISI	VPU PROTEIN	HUMAN MORTHODEFICIENCY VINUS TYPE I (BITTO ISOLATE HXII)	1.2			-		
YVPU HVIBB	WPU PROTEIN	HUMAN INDAMINODEFICIENCY VIRUS TYPE I (BIII ISOLATE)	1					
PVPU KVIBN	VPU PROFILIN	HUMAN HAMIDNODEFICIENCY VIRUS TYPE I (BRAIN ISOLATE)	2	<u> </u> 	-			+
PVPU KVIBB	VPU PROTRIN	MANAN MANUMODEFICIENCY VIRUS TYPE I (BRI) ISO(ATE)	1	-	-		! 	
WAS HVIET	VPU PROTEIN	FILMAN INGRODEFICIENCY VIRUS TYPE I (ELT ISOLATE)	3.26				-	<u> </u> -
MAN MAN	IVPU PROTEIN	HUMIAM INDAUNODEFICIENCY VIRUS TYPE: I (HXH2 ISOLATE)	4:37				!	
MAN PANTE	VPU PROTEDU	HUMAN WORLMODEFICIENCY VIRUS TYPE I (IRCSF ISOLATE)	1:20		7			
	VPU PRUIEW		13-27		,			
TATE AND	MUMAN DOGUNDDEFICIENCY VIRUS TYPE I (NIN ISOLATE)	R.						
COLUMN COLOR	WO TAUTUM	HUMAN DOPUNOCEFICIENCY VIRUS TYPE I (NDK ISOLATE)	2					
PORT DOTAL	VIOLUTE OF THE COLUMN TWO IS NOT THE COLUMN	MUMAN BOMONOCEP KLIENCY VIRUS TYPE I (PVZ ISOLATE)	12.					
TOTAL DOLLAR	VIO PROTEIN	MUNICAM BONDHOUSE KIENCY VIRUS TYPE I (SFILZ ISOLATE)	3.38					
WHI IN(1)	Chel ban Terra	INTERNAL MANAGEMENT VINUS 1 TTE 1 (SC 150LATE)	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1		$\frac{1}{4}$			
200	Veribalitative	RUMBER BUILDING AND AND AND THE TABLE AS A CONTROL OF THE TABLE	77.78		$\frac{1}{1}$			
PVPX HV384	VAX PROTEIN	MALE POLICIONAL ADENOMATIONS VIAUS (PANOSIES IN SELF RES	25.50					
PWX HVECA	VYX PROTEIN	HOMAN BOADNOOFFICIENCY VIRILE TYPE 1 (1904 ATE CANS)	100		1			
MX XMB	VPX PROTEDA	MANAN DARANDOEFICIENCY VIRUS TYPE 2 (150) ATE DISA			-		+	
PWX INTER	VPX PROTEIN	HUMAN BANDHOGE PICIENCY VIRUS TYPE 3 (150LATE 5265.1)					+	+
PVPX KVXGI	VPX PROTEIN	HUMAN BOAUNODEFICIENCY VIRUS TYPE 2 (150LATE GHANA.1)	100					
PVPX HVZNZ	VPX PROTEIN	HUMAN BOACHODE HCIENCY VIRUS TYPE 2 (ISOLATE NIH-Z)	<u> </u>	-				+
WX HV20	VPX PROTEDY	HUMAN BANDNODEFICIENCY VIRUS TYPE 2 (ISOLATE ROD)	10.33		-		-	
PVPX HV2S	VPX PROTEIN	HUMAN INOKUNOCEFICIENCY VIRUS TYPE 2 (ISOLATE SBLISY)	10-33				-	
PVPX HV2ST	VPX PROTEIN	HUMAN BOAUNOCEFICIENCY VIRUS TYPE 2 (ISOLATE ST)	10-32				-	
A CANA	VPA PROTEIN	LACTATE DEHYDADGENASE-ELEVATING VIRUS	593-521					
74.7	WA MOIEM	SUBLIAN DIGHTANDER NICHT VIRUS (ISOLATE AGM / CLONE GRU-1) (S						-
PVAX SIVE	VAN PROTEIN	SOUTH DONNOCE FCIENCY VIRUS (AD1142-13 ISOLATE) (SIV-NIAC)	10-33					
100 VAV.	CAN PROTEST	SUMAN MONITORER REPORT VIRUS (KeW ISOLATE) (SIV.MAC)	10.33					L
TANK TANK	NATIONAL AND	CHOAN BACKBOOK ICIEMO VIRUS (R.78 ISOLATE) (SIV-MAC)						
TAN TANA	VPX PLOTED	SOUTH MANAGEMENT FINDS (FLIBSHOFF ISOLATE) (SOUTH M. SOUT						
PVECA BONV	ALPHA-A PROTEIN	BALLEY STUDE MOSAIC VIETS (900)	26.00	95				
WG KOTEK	NOWSTRUCTURAL PROTEIN NOVY	BOVING BOTAVILLE OF LANGE	Ţ					
		SOTING AVIATING LITERAIN AVI	160-137 661-487				_	
						į		

CLAR	Pitchill	com (No Becterioghage)	AREA! ARE	1 AREAJ	AREAN	AREAS	ARTAL	ABEA! AB	ARTA!	ABLAS
T WALK	PROTEIN	CARLO CONTRACTOR STATE OF CARLOS CONTRACTOR	140-137 428-450	Ι-	Г				_	
PVSc5 ROTIG	MONSTRUCTURAL PROTEST AC VY2	N COWINEN)	BR-113	_				-:	-	
os korre	MONSTRUCTURAL PROTEIN YSSS	1	Jen-dil	:						١
PVS65 ROTSI	MONSTRUCTURAL PROTEIN PCVP2		202-125				1		1	
SOL ROTTER	VM PROTED	TRAIN SHINTOKU)	64-85				1	$\frac{1}{1}$	†	١
	VA TROILES	BOVING ROTAVIRUS (STRAIN UK)	201-115				Ť	-	Ť	1
VSO KOTEL	VIEW MATERIAL	EQUING BOTAVIRUS (STRAIN FLIA)	201-215	1			-	-	-	
THE PERSON	VALUE OF STATE OF STA	EQUINE ROTAVIAUS (STRAIN II.2)	202-225	+	1			\dagger	T	
Web Portor	VPs PEOTEDS	ROTAVIAUS (CROUP B / STRAIN ADRY) (ADULT DIABUHEA ROTAVIRUZZ-40	22-40							
WEST SONGE	VN MOTEN		100,000				Ī	-		
VEST TOTAL	VAL PROTEIN	HUMAN KOTAVIAUS (SEXOTYPE I / STRAIN 1978)	101707	-	-		Ī			ľ
WEST BOTHE	VN PROTEIN		300 506				Ī			
VSoc LOTHS	VPN PROTEIN		310.00							
VSOS ROTHW	VIN PLOTEIN	MUMAN ROTAVIRUS (SEKOTYPE 1/81KAIN WA)	114.340	9	-					
VSOL KOTPC	VP6 PROTED ⁴	MORCHOE MUTAVIANS (CANOCY CY 81 ANN CONTROL	Ļ	-	-					
VSOI ROTTO	VPs MOTITION	TORCING TO LANGE AND LANGE OF STREET	131-155		:					١
VSor ROTEU	CLYCOPEDITION VP1	BOVOC ROTAVIROS (STRAIM RAMA)	17:136	-	-					
VSOL ROTPC	CLYCOPIOTEDI VP7 PRECURSOR	PERCENT IN PAYAGE RECORDS (AT A)	274-295							١
VSOL ROTS	MONSTRUCTURAL PROTEIN MCVP4	BOOMER BOTA CORPORATE & STRAIN 61 A)	131-155		i				1	1
PVSOR ROTTE	GLYCOPROTED VP7	BACONG BOTA VIELS (STEAD) A44)	131-155					1	Ì	١
VSO LOTA	GLYCOPROTEIN VP?	EGGGG BOTAVIRIE (FEBOTYPE 10 / STRAIN B12)	131-155							١
VSOF BOTTES	GLYCOPIOTEDN VP7	BOUNE BOTAVIRIE (STRAIN KK))	131-153						1	١
West Long	CL YCOPILOTELIN VP	SOCKER BOTA VIBILIS (SPROTVPR 1 / STRAIN 1449)	131-159		-			1	1	١
VSO BOTH	CL YCOVROTELIN VY	CHICAGE ROTAVBUS A (SEXOTYPE 77 STRATH CH2)	134-158						1	1
	GLYCOTA NEW VICE	EDUDAS ROTAVOLUS (STRAIN L.) 19)	131-135						T	l
	CATOMAGNETIC OF PRICEIN TOR	ROTAVIRUS (CROUP B./ STRAIN IDIR)	1		1				T	İ
	CI VICENTEIN VP7	MUMAN ROTAVIRUS (SEROTYPE 4/ STRAIN RV-4)	1	137-213	ŀ			+	Ī	١
VIOLENIA VI	CL VCOPLOTEDA VP7 (HUMAN ROTAVIRUS (SEROTYPE 2/ STRAIN HUS)	197-212						Ī	
CHUCA SOLVE		HUNGAN KOTAVIRUS (SEROTYPE 27 STRAIN UST)	107.213		-				П	l
PVSOF ROTHER	-	MUMAN ROLAVICA SERVITE AT STANK SERVICES	L	197.213						ì
PVSOL ROTHE.		THE PART HOLD VINCE (STREET AND THE PART IN STREET MIN)		167.312						ĺ
/ toe konou		CANADA MONTO (SEE OF COMPANY NO AND STRAIN DO	Ī	215						ı
VED ROTHO	_	MUMAN KOLA VASIS (SEA) STRAIN P	131-133							١
ALLOW HOLD		CHALL EXPLOITE (CERCITYEE 1/STRAIN RRV)	131-155							1
rvsoj kotra	7	WINAM BOTAVIRUS (SEROTYPE 27 STRAIN 52)	197-313						1	ļ
VED ROTHS	OLYOPROJEM VY	HUMAN BOTAVIRUS (SEKOTYPE 4/STRAIN VA70)	П						1	1
VSG EGTIV	т	HUMAN ROTAVIAUS (SEROTYPE I / STRAIN WA)	П	167:212					Ī	l
NASO ROLL	Т	PORCING ROTAVIAUS (SERGITYPE S/STRAIN OSU)	131-155 197-212							l
	т	POACONE ROTAVILUS (SEROTYPE 5/STRAIN TFR-41)	3:132		$\frac{1}{1}$				Ī	l
	Т	PORCINE ROTAVIRUS (SEROTYPE 4/STRAIN BEN-144)	107-212							
MADE POLICE	Т	PORCINE ROTAVIRUS (SEROTYPE 4/ STRAIN BAIL-I)			+					
WEST ROTH	Т	INESUS ROTAVIRUS	20-101							
VYSOF LOTS!	Г	SDEGAN 11 ROTAVIUS (STRAIN SATT)	134-153							П
PVSII JIDTOA	П	HOLY VIRUS (CROOK OF STACKE AND TRACES OF STACKED AND THE STAC	7	-						ı
PVSH JALBVA	П	INCHASE STREET AND SALLE AND MUNDS VIRUS (STRAIN SBL)	\$3.7							İ
PVSH MUMO!	٦	No nation will a full transcaution 1.4.6)	2.5	_						1
VEN MOOR		NAME OF THE AND STRAND STRAND STRANDS	1.29							1
No Por	SHALL HTMOTHORY, TACHEST	MUMOS VINUS ISTILATIV MATSUTANIA)	10-29							ļ
Y TOWN	┪	MUNDS VIXUS (SPILATN BELLFAST)	1.29							١
		MUNCH'S YOU'S (STRAIN ENDERS)	1.29		1					
	T	MEMOS VIRUS (STRAIN JEAY). LYNN)	**		+	1			I	l
A STATE OF THE PARTY OF THE PAR	-	MONOYS VIRUS (STRAIN KILHAM)		 					Ī	
MEN LABOR	SALL INDROPHOBIC PROTEIN	MUNGS VIRUS (STRAIN BRISTOL I)	2							
	TELLA LEVISIONAL PROTEIN	MUNOS VIRUS (STRAIN MIYAHARA VACCINE)	19.67							l

POSEMI	1915CH 518	All Manus (the Entertainment)	-	ŀ						
PILE NAME	PROTECT	VARIS	4864	* **** * ****	1				Т	
PVIN MUNOR	SMALL HYDROPHOBIC PROTEIN	MEMORY VIRUS (STRAIN RW)	ī	Т	i	1	0240	7000	200	707
PVSH MUMP	SMALL HYDROPHOBIC PROTEIN	MUNUS VIRUS (STRAIN TAKAJIASIII)	8.0	<u> </u> 	† †					Ī
PVSH MUNOU	SHALL HYDROPHOSIC PROTEIN	MUDDE VINUS (STRAIN URABE VACCINE ALM)	62,01						İ	1
PVSII REOVI	SICHA I PROTEDI PRECURSOR	REDVINUS (TYPE I / STRAIN LANG)	110-136	+	1		1		1	Ī
CVOLA LIZOVO	SKOMA) PROTEIN	RECVIRUS (TYPE 3 / STRAIN DEARING)	152.170						Ť	
PVSD REDVI	SIGNA S PROTEDI	REDVIRUS (TYPE 2 / STRAIN DAXONES)	132.170		-					1
PVSD REGVI	SIGNA'S PROTEIN .	RECVIRUS (TYPE I / STRAIN LANG)	152.170			-			Ť	
PVSII REDVI.	SIGNA I S PROTEIN	LEOVIAUS (TYPE 1 / STRAIN LANG)	101.4%		-				1	
PVST2 HBIVBU	STRUCTURAL MOTERN 2 PRECURSOR	HEPATITIS E VIRUS (STRAIN BURMA)	111.00		ŀ				1	
WITH HEWA		APPATITIS E VIRUS (STRAIN LIFE YOUR)							1	
PVST3 MEWAY	ISTRUCTURAL PROFESS 3 PRECUSOR	HEPATITIS E VIRUS (STRAIN MYANMAR)	110,000		†				1	
PVSTS NBVPA	•	KEPATITIS F VIBILS (STRAIN PARISTAN)	111 000		1					
PVST2 HEVEH	_	APPARTITE CHIEF JICALATE BIFERING	-		+					
PVT2 CTV9	THINDS MACHINES FACTOR LOS DECENTOS DE P	ANYMANA UMINI ATTO ANAL ATTO ANAMA				1				
A COUNTY		PLANMEN VINCE (STANIN LAUGHARY)	701-707		1					
PARTY VILLA	SECOND COMMENT OF THE PROPERTY	STATE FURGING VIEWS (STRAIN KASCA)	270-289							
	PACIFIC ISA	CAMINAX VIKUS (STRAIN 149-1)	16-13		-					
Y X X	TATKOTEIN	SHOPE FIGHOMA VIRUS (STRAIN KASZA)	123-148	Г						Ī
WIEL EBY	PROBABLE DNA PACKAGING PROTEIN	EPSTEIN-BANK VIRUS (STRAIN 1995-1)	13.13	166-192		!	! :		; ;	1
PYTER HOMYA	PROBABLE DNA PACKAGING PROTEIN	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	T	T					1	
PATER HSVII	PROBABLE DNA PACKADDAG PROFEIN	HORBORIS SINON DE VIREIR CHYPE I / STRAN 151	Τ	****	†				1	
PVTER HEVGU	PROBABLE DAIA PACELACING PROTEIN	APRESE ENJOY SX VIDING CHARGE A VETT A FILL LICENSE A 11011	Т		1					
PVTER HISVER	PROBABILE DATA PAPER ACTIVADO PROFEIN	COUNTY LEBESCOTE IN TOTAL I AND A DAME		1						
PVTFE LIEVIL	Personalis maia barreactico	MACHINE MACHINE IN THE CONTRACT OF THE CONTRAC	1		***			_	_	
AVYER USINEA	DESCRIPTION DATE AND DESCRIPTION OF STREET	Control institute of the control of	1	-						:
A 100 A 100	TANAMAS INTO TANAMAINO PROJEIN	PEATER VINUS SALMIN (3 TIAIN 1.)	216-241		-					
CATA NEW		VAUCELLA-ZOSTER VIRUS (STRAIN DUMAS)	372-319		-					
TX NOTICE		ORDONO SQUIREL HEPATITIS VIRUS	\$1.19	_					l	Ī
IAHA X		WOODCHUCK HEPATITIS VIRUS I	57-73	_						ĺ
WHA!	PROTEIN X	WOODCHUCK HEPATITIS VIRUS 59	3		-				\dagger	
PX WHV7	PROTEIN X	WOODCHUCK HEPATITIS VIRUS ?							İ	Ī
PX WHW	MOTERNIX	WOODCHUCK HEPATITIS VIAUS I	57.53			-				Ī
PX WHYE	PROTEIN X	MODICINICAL HEMATTHS VIAUS I (INFECTIOUS CLONE)	50.50						1	
PX WHYWE	PROTEIN'X	WOODCHUCK REPATITIS YILUS WAS (ISOLATE PWS2))	2		†				1	
PYION ADEBY	ROTEIN	HUMAN ADENOVIRUS TYPE 7	153	l	-	ļ			t	
PYICE SSVE		ULPOLOBUS VIRUS-LIKE PARTICLE SSVI	98-99		-				1	
PYIOK MSVS		ANDE STREAK YRUS ISOUTH-AFRICAN ISOLATE)	24-47		-				1	1
PY118_\$3VI	HYPOTHETICAL 11 8 KB PROTECK	SULPOLOBUS VALUE PARTICLE SSVI	13.50		-				1	Ī
PYIIK PASV		PANDOLIM STREAK VIRUS	50.00						1	
PY12K BNYVO	OTEN	BEBT NECROTIC YELLOW YELN MOSAIC VIXUS (ISOLATE GI)	1						1	Ī
PY LIK CAPAL	2	THOUDING MOSAIC VINUS (STRAIN SINGAPORE)	91	-	+				1	
		HURAN ADENOVICUS TYPE 2	2.5		-				1	1
PYLIK CLVK	Ī	CASSAVA LATENT VIRUS (STRAIN WEST KENYAN 944)	16.56							
	HYPOTHETICAL 13 1 KD PROTEIN	CASSAVA LATENT VIXUS (STRAIN NIGERIAN)	1			-			1	7
	HYPOTHETICAL ISSED PROTEIN	TOWATO YELLOW LEAF CUT, VIRUS (STILAIN MADUANDE)	10.27		+				1	Ī
`		TOMATO YELLOW LEAF CURL YINUS	34-33		\mid	ſ				Ī
- 4		HUMAN ADENOVIAUS TYPE 1	108-133					T	\dagger	T
PYICK CENT		HEORIS STRIATE MOSAIC VIRUS	34.80						1	1
PYIIK SSVI	HYPOTHECTICAL 18 0 KD PROTED!	SULFOCOBUS VIRUS-LIKE PARTICLE SSVI	_	141.162	-			T	1	1
PY204 ADE07		HUMAN ADENOVINUS TYPE ?	T		\mid			1	1	T
PY15K BNYVF	OTED	DEET NECEDITIC YELLOW VEIN MOSAIC VIRUS (ISOLATE F2)	163-184				Ì		†	Ī
PY29K NOVAC	OTEIN	AUTOGRAPHA CALIFORNICA NUCLEAR POLYHEDROSIS VIRUS	8:8						1	I
PY2 SOCIAV		SOYDEAN CALCACTIC MOTTLE VINUS	04-59			I		Ť	†	T
PY32K KSVI	2	SULFOLOBUS VIRUS-LIKE PARTICLE 15VI	122.143		-					T
PYGKO SSVI		IULFOLOBUS VIRUS-LIKE PARTICLE SSVI	1			1		1	1	1
PYTK4 VACCV	2	VACCINIA VIXUS (STRAIN WIL)	71.70						1	1
PYTK KELASH	Z.	MEASURS VIXUS (STRAIN HALLE)	- F		\ 			T	1	Ī
PYT BOOM		SOYBEAN CHLOROTIC MOTTLE VIRUS	e		-	I		İ	T	T
PYOSK SSVI	HYPOTHETICAL 03 7 KD PROTEIN	SULPOLOBUS VIRUS-LIKE PARTICLE SSVI	I	155-173 543-565	657-475	744.714		İ	\dagger	
			1	1					1	7

PCCLME	PISCHILLE	wes (Ne Bacterlophages)	14497	2 2 2 4 4 2	MY TYARY	APPAR AREAS	A S AREA 6	A G AREA?	AREA	Y
TO STANK	PROTEIN A PROPERTY	SOVERAN CHI OROTIC MOTTLE VIRUS	Г	Т	1	Г	Г	Γ		
The second	INTERIOR TO THE PARTY OF THE BARE VERTICAL		2.11		-	-	-			Ţ
1000	TANAMETER A STATE PROTEIN	IKE PARTICLE SSVI	Ī	62.73						
П	DOSOTINETE'AL BALBI PROTEIN		203-220	l						
R	HYPOTHETICAL BANGGORF! PROTEIN	UNICHI	154-374							
VECT ROLL	HYPOTHERTICAL BANGO COULT PROTEIN		104-121				+			
PYBOL FOWTH	HYPOTHETICAL BANGE GATS PROTEIN		19.69		1	+	$\frac{1}{1}$		1	
THAO:	HYPOTHERICAL MANDEL CAP 10 PROTEIN		1		+	+	\dagger	+	+	
PYRIL FOWPH	HYPOTHETICAL BANGE-ORF 12 PROTEIN	FOWLPOX VIAUS (ISOLATE HP-43IQMUNICH))	1	2			1	1		\downarrow
PYREE BYNE	NA. 3 PROTECT		17.12	1	+	+	+		1	\downarrow
VIELT JOANN	BELS MOTEIN		27-78		1	1	\dagger	1	1	ļ
PYDHI INVSC	HAYP 24 7 KD PROTECN IN DIGHT STREETIN		077-077	+		+	\dagger		-	
PYDED HEVIC	HAYP 9 5 KD PROTEDN IN DIGTR TRECEION	(88)	2	\dagger	1	-	1		 	\downarrow
PYECA LIBV	HYPOTHETICAL ECRES PROTEDS	EPSTEIN-BAAR VIXUS (STRAIN 1993-4)	177.002	1		+	+	1	1	1
PYCAL HISTORY	INVESTHERICAL 13 6 KD PROTEIN		017-170	1		+	+	1	+	\downarrow
PYCA! MSVNOA	INVESTIGATION IS 6 KD PROTEIN	MALLET DESCRIBE HELPENYSUS (STRAIN MDS)		1		1	\dagger		-	1
WEL HOW			10171	†	+	-	+			-
WOU WACK	HITP HOST RANGE IT 4 KD PROTEIN		77171	T		+	+			L
S CO	HAT PLOTED IN NUCLEUCATED ON	WILELES CALL CALL CALL	77	T		-	+	ļ		ļ
	MYP PROTECT IN NUCLEUCATSID ON	TO BE ROLL TO BE COME TO STATE		1	-		+			ļ
PYOR CAMES	HAT PROTEIN IN POLICE CASE OF		67.90	T		+		-		
VAL. 20	INTRODUCE BANG TANGER	MINAM ADDINOVIAUS TYPE 41	5:33			-		_		
	TOTAL PROPERTY		8 4	128-155 2	215-241 336	330-350	-			L
THE PERSON	INVESTIGATION 15 B KD PROTEIN	T INDESCENT VINUS TYPE 22)	Γ			-				
DATE LANGE	-	Τ.	39.66			-	-			Ц
Average Annual Property	_		\$6-03			1				
PYOAT TIVE	_	THEDWORKOTEUS TENAX VIRUS I (STRAIN KIALI)	13.40						-	1
PYONE COVIN	HYPOTHETICAL 13 KD PROTEIN		\$ 7.5			-	+			-
PYORE MAY	HYPOTHETICAL 25 6 KD PROTEIN	EQUIDAE ARTERITIS VIAUS	165-191		$\frac{1}{1}$	+	+	+	+	1
YOUR LELY	HYPOTHETICAL 28 4 KD PROTEIN	LELYSTAD YOUNS	7,7	1			\dagger		+	\downarrow
MOUS TAX	HYPOTHETICAL 11 8 KD PROTEDI	LLT YUKUS X	2.00	T		1	+		+	\downarrow
PYOU DON	HYPOTHERTICAL 14 ED PROTEIN	EXAMPLES OF THE PARTY OF THE PA		1		+	+			ļ
YOU MX	HYPOTHERICAL IS NO PROTEIN	MONTH OF THE MANAGES				-	\mid	-	L	
		S (STIALIN NO	\$7				\mid			Ľ
WORLD WOMEN	MYPOTIGETICAL 13 KD PLOTEIN		16.31							Ц
PYORS ABEDI	HYPOTHETICAL 31 3 KD PROTEIN	S) (FOWL ADEMOVIRUS 1)	98-69			-	1		-	1
PYORT JAN	HYPOTHETICAL 28 7 KD PROTEDN	EQUINE ARTEXITIS YOUR	139-158			\dagger	\dagger		+	4
PYOKE NOW	HYPOTHETICAL 10 KD PROTEIN	NARCISSUS MOSARC VIRUS	2		+	$\frac{1}{1}$	$\frac{1}{1}$	+		\downarrow
PYON TIVE	HYPOTHETICAL 16 6 KD PROTEIN	STREET STREET STREET STREET STREET				1	\dagger		+	\downarrow
PYORL TIVE	HYPOTHETICAL 10 3 KD PROTEIN		L	213.256		1	+		-	ļ
TOWN TO	CONTROLLED TO BE SECURIAL	STRAIN KRAII	Ţ		-	-	-	-		L
A L	NYPOTHERICAL PAPEOTEDA		23	104-136			-			L
PYP24 KTHVP	HYPOTHETICAL PA PROTEDY		32.33	104-126			H			
PYPAT NEVAC	HYPOTHETICAL 43 5 KD PROTEDM	_	211-234							
PYPE JOYOU	HYPOTHERICAL 13 % KD PROTEIN		23.18 18		1		+		1	1
PYPE JOVOP	HYPOTHETICAL 46 6 KD PROTEIN	YNEDKOSES VOKUS (OF	X-12	213-230	1	1	\dagger		\downarrow	1
PYPTS THYO	HYPOTHETICAL PTS PROTEIN	TOBACCO RECRUSIS VILUS (STRAIN D) (TRV)			1	1	1		$\frac{1}{1}$	1
PYPOL MAND	HYPOTHETICAL 6 S KD PROTEIN	LYNANTUA DISPAR MULTICAYSID MUCLEAR POLTHEDROSIS VINUS	19.33	1	\dagger	\dagger	\dagger	+	+	1
PYLY JUSTIN	HYPOTHERICAL PROTEIN NO.		16.5%				+		-	
CALL PROPERTY	INVESTIGATION PROTECTION (IV)				-	ŀ	ŀ		-	L
PYEN BW	REPETITIVE PROTEDY ON!	ESCENT VIRUS TYPE 6)				ŀ	H			Ц
WAN BW	MEPRITHINE PROTECN ORF4		69-11							
į	S PACTORING TO APERI APER		121-131	179-204	260-285					_

POC PUT	610-1-019	Att Manual (No Beat and about)	l	-	-					ſ
FILE RAME	PROTEIN	YARUS	AREAI	AREA 2 AREA 3	S AREA I	ARFAS	A N. P. A.	ABTAS	ABEAT	ARCAG
PYRI EBV	HYPOTHETICAL BILD! PROTEIN	EPSTEIN-BANK VIRUS (STRAIN DPS-6)			Г		Т	Γ	Т	Ī
Very Lavy	HYPOTHETICAL BILLY PROTEIN	EPSTEIN-BARK VIRUS (STRAIN BOS.S)	164-162	-	L				-	1
PYSR! EBV	HYPOTHETICAL BSIVI PROTEIN	EPSTEIN-BALIK VIRUS (STRAIN DOS-1)	43:113							Ī
VET ESV	HYPOTHETICAL BITUI PROTEIN	EPSTEIN-BARK VIRUS (STRAIN B95-6)	383-461						-	
AC82 KPVO	HYPOTHETICAL 34 0 KD PROTEIN	ORGYLA PSEUDOTSUGATA MULTICAPSID POL MIEDROSIS VIRUS (OP	=							
	HYPOTHETICAL IN 2 KD PROTEIN	VACCINIA VIXUS (STRAIN COPENHAGEN)		140-136						
200	NITOTRE HALL TO BE PROTECT	VACCINIA VIKUS (STITALIN COPENHACEN) VACCINIA VIRUS (STRAIN AND VACCINIA MBITS (STRAIN COPE	9	3	+				┪	
TYVAT VACES		VACCINIA VIRUS (STRAIN WR) AND VACCINIA VIRUS (STRAIN COPE	7	<u> </u>	-				1	
TYBE VACCV	HYPOTHETICAL 16 STD PROTEIN	VACCINIA VIRUS (STRAIN WR), AND VACCINIA VIRUS (STRAIN COPE	9-28		-	$oxed{oxed}$			Ì	T
PYYNG VACCC		VACCINIA VIRUS (STRAIN COPENHAGEN)	2.55							I
PWCA VACCE	-	VACCINIA VIAUS (STRAIN COPENHAGEN)			-				t	T
PYVDE VACCY		VACCINIA VIRUS (STRAIN WR), AND VACCINIA VIRUS (STRAIN COPE	T	36.55	-	ļ				
PYYDA VACCE	HYPOTHETICAL 9 3 KD PACITEDA	VACCINIA VIRUS (STRAD) COPERINACIEM		192					t	T
PYYDA VACCV		VACCONTA VIRUS (STRAIN WR)	Ī	22.33	1				t	T
PYWA VACCE	HYPOTHETICAL 7 I RD PROTEDI	ENHAGEN		Γ	-				t	Ī
PYVEY VACCE	HAYOTHE TICAL I I KD PROTEIN		1	-	 -				T	
PYYON VACOC		VACCINIA VIRTIS ISTRAIN COPENDIAGEN	104.127	-					l	Ī
PANCE VAPOR	HYPOTHERICAL 4 6 KD PROTEIN	VACCINIA VILLE (STEATH COSTALAGE)	5		1					T
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	INTERNATIONAL / 4 M. PROJECT	VACCURA VECUS (STROIT WA)	96-12							Ī
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PYALLEDV	HYPOTHETICAL BALFI PROTEIN	EPSTEEN-BARK VORUS (STICATA BES-IN)	٩							T
PYBO! FOUTH	HYPOTHETICAL BANDE CAUT PROTEIN		134.7%		-					T
PYROT FORFIL	HYPOTHERTICAL BANDELORFY PROTEIN	ISOLATE NP-/ SE(pADMCH))	12170						T	
PYBO FOUR	HYPOTHETICAL BASON CR.P. PROTEIN		49-61		_	L			-	
PYSIO DOVIN	HYPOTHETICAL BANGGORVIO PROTEIN)	П							Γ
PYSII FORTH	HYPOTHETICAL BANGGORVIZ PROTEIN			34.18						
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_2 &	PROTEIN HYPOTHEREAL IN EXPROPERN HYPOTHERECAL	VIRUS AVIRA DEMOVIRUS CALI (STRAIN PIELES) (FOWL ADENOVIRUS 1) COMMELINA YELLOW MOTTLE VIRUS THERMOPHOTEIS TENAX VIRUS I STRAIN KKAI)	\prod	ABEA1	ABEA 2 ABEA	T VIEW	A. ARKAL	4 ARIA 2	QRIA!	OH CAT
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	DVSOTNETICAL 11 5 KD PROTEIN	S) (FOWL ADENOVIRUS 1)	98-69		H				1	
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П	CAMPAGE AT 15 KM DECITEDA	NABESTREINS MOSANE WIRDS	10-28	-	┞	Ļ		-		
1	DANGER PROTECTION	THERMOPEOTEUS TENAX VIRUS I (STRAIN KRAI)	13.32	-	L	-	_			
Г	CONTRACTOR IN CITE PROTECT	PAGE MAGNICULES TENAX VIRUS I (STRAIN KIA)	5,4		_	<u> </u>	_			
	DESCRIPTION OF THE PROPERTY	THE BLANDSOTEINS TENAX VIRIES I (STRAIN KRAI)	L	233-254	-	-		-		
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1	STATE OF THE PARTY	BECK TIDECED BACK LIFORM WRITE	Γ	101:124	-	-				
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	INVENTORISM BEING PROTEIN	EPSTEIN-BARR VIRUS (STRAIN 305-4)	164-163		<u> </u>			_		L
T	GARGING WE'AL BOOK INCOME.	EPSTED-LAARE VIRUS (STRAIN BPS-8)	92-113		-	\mid				
Ī	LANDAR STATE BEST DECITEDA		383-401	\mid	L			L		_
	HAPOTHERICAL MOKEN PROTEIN	POLYNEDAOSIS WAUS (OP	133-153			H		Ц		
Τ	AVECTOR TICAL 18 2 KD PROTEDY	VACCINIA VIIUS (STIAIN COMENUACEM)	82-99	961-091	\mid	L				
7-	HAPOTHETICAL 64 KD PROTEIN	VACCENIA VIAUS (STRAIN COPENHAGEN)	17-40	11-61	L	Н				
т	HYPOTHSTICKL 9 9 KD PROTEIN	VACCORIA VIRUS (STILADI WAL AND VACCINIA VIRUS (STILAIN COPE	21-43							
~	KYPOTHETICAL 1 FKD PROTEDI		39-46							
-	PAPOTICAL 10 3 KD MOTEDI	CINIA VIRUS (STRAIN COPE								
	PROTESTICAL TILY SED PROTEIN	VACCENIA VIXUS (STILABI COPERINGEN)			-					
•	HYPOTHETICAL TO IND PROTEIN		16-35			+				
	HYPOTHETICAL 14 KB PROTEIN	CINTA VIRUS (STRAIN COPE	Ž	25.25	$\frac{1}{1}$	+				
	HYPOTHETICAL 9 1 KD PROTEIN	VACCERIA VIRUS (STILAIN COPENHAGEN)		1	+	+	1	+	4	
1-	HYPOTHETICAL # 1 KD PROTEIN	VACCORIA VOLUS (STRADI WR)		77.38	2			-		4
Г	PROTESTICAL TIED PROTEDI	IVACCEMIA VIRUS (STRAIN COPENHAGEN)	48-67	-	-	1				
Γ.	HYPOTHETICAL 4 3 KD PROTEIN	VACCERIA VIRUS (STILAIN COPENPLACEN)	13-43		$\frac{1}{1}$	$\frac{1}{1}$				
	HYPOTHETICAL 14 3 KD PROTEIN	VACCOMA VIRUS (STRAIN COPENHAGEN)	105-127		1	+	+			
×	HPPOTHETICAL 90 KD PROTEIN	VACCINIA VIRUS (STLAIN COPENHAGEN)	24-70	1	+	1				
Т	HYPOTHETICAL BZLF1 PROTEIN	EPSTEIN-BAUD VIXUS (STRAIN BOS-6)	150-166			-		_		

TABLE XIV

SEARCH RESULTS SUMMARY

FOR P23TLZIPC MOTIF

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PPOLG SPAVA	GENOME FOLYPROTEIN		351-5151	2044-2089					
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	TO	HINDAM BITINOVIRUS 2 (HRV.2)	146-1475	8	1976-1012				
2	CENOME POLYFROIDIN	THE A STANDARD OF THE VAPOR	1460-1492	1833-1876	1920-1026		-		
اء چ	CENTRAL AND	STATE OF STATE STATE STATE	101.1145					Ì	
LANG HILL	CHINDALE FOLLYPROTTEIN	IN STRAINCH	133.360						
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HONSTRUCTURAL POLYPROTEIN	TRUCTURAL POLYPROTEIN	IAUS (STRAIN GULU) (DNN)	2	404-1439					Ī
HON-STRUCTURAL POLYPROTEIN	STRUCTURAL POLYPROTEIN		-	163-1384					
NOWSTRUCTURAL POLYPROTEIN	TRUCTURAL POLYPROTEIN		1146-1175	406-1441					
PAR N. CINTAS MANASTRINGTURAL PAR VERSITIN	TRINCTURAL FOR YEROTEIN	FLOOVSTRAIN (DSNYN RPS)	34-1496				j		
VINDA PARMANTAL THE ALEGATION	MIN TEMAL I'VE VINCELLIN	IIA	45			$\Big]$]

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VIII	STRIP THEAT POLYPROTEIN	PUSS BIN BY IRIN (STRAIN 148) (RRV)	1216 1250				- <u>;</u> 		i
200	Committee for visit in	SLANCK! I ORI ST VIRUS	1315-124						
12	Table treat per vernish	SINDDIS VIRUS (SUDIATE OCKELBO) SIRAIN EDSNYN 12:5)	1147-1233						
		CINDRIC CIPITS CONTRACTOR AND URLPS	1193.1233						
	SINGLIGHT TO THE SECTION OF THE SECT		1169.1334				İ		
PPG S WEEV	STRUCTURAL POLYFROTEIN		11111111				İ		
PPG 200	POL POLYPROTEIN								
100	MINISTER AND STREET	INDVINE INIMINADISEPICIENCY VIRUS (ISOLATE 127) (PIV)	142.771						
	1	INCVINE LEINERITA VIRUS (AUSTRALIAM (SOLATE) (BLV)	143.174						
2	- 1	TO SECURE OF THE PROPERTY OF T	204,340	132.55					ĺ
701 757		LAFRING AN INCIDENTIAL VINCTURE OF THE PROPERTY OF THE PROPERT			201	9		ĺ	
Fig. Syk		COMMELINA VELLOW MOTHE VIRIES (COYNIV)					İ		-
2 12		EQUINE IN ECTIONS ANEMIA VIRUS (CLONE 1949) (EIAV)	26 - 22	2		j			
i		EQUINE DE ECTIONS ANEMIA VIRUS (CLONE CLAS) (ELAV)	161-991	506-539					
		POSITIVE THE PUBLIC ANSAULA CIRILICACO ATE WYOMINGS (1747)	16.191	505-538					
- XX									
FPCII. FOAMV		HUNIAN SPUMAKE HUVIRUS (FORMET VIRUS)					İ		İ
> 100 Mag		GIBBON APE LEUKLMIA VIRUS	148-178						!
		RAIN A TRY (HILV-II	637-663						
	Ì	11.7.11	919-619						
Prof. HTLC				111					i
PPO EVIA	ı	HENTAN INCHUNODE PICIENCY VIRUS TYPE I (ARVINITED ISOLATED (FILLY-I)					j		
10121	١.	INDIAN MINUNODERCIENCY VIRUS TYPE I (DITIO ISOLATE) IIII !	14)-176	312-344					!
		CHAIRM MANN MONTENTING VIRUS TYPE I JUNE 150LATE CHIV- II	341-176	\$12.540			!		
	1	CONTRACTOR OF THE PROPERTY OF	141.134						
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PPOR. FIVIER		ICHINCT VINUS LITE I IEEE ISOCATE ITHIS						Ī	
POT HVIX	POL POLYPROTEIN	j		9				Ī	İ
100	POLYPROTEIN		135.168	504-341					
ALAINI POR	ı	HILINIAN INMINODEFICIENCY VIRUS TYPE I (MAL ISOLATE) (IIIV-I)	330-363						
	1		334.367	503-540					
	- 1	L'ATTICLE A PRODUCTION OF A PARTY	311.164	11.00					
2	1	THE PERSON NAMED IN COLUMN TO A PART OF THE PE	131.01	12			_		
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7	THE THE YEAR IN	HILIAIAN MANIMBARI KII NCY VINIIS IYMI I (PVZI ISIM,ATC) (HV-I)	10).176	312.54			ĺ		
12	i	HILINIAN ININIUNOUEFICIENCY VIRUS TYPE I (REGIAT ISOLATE) (HIV-1)	110-163	166.536					
	н	HISTORIAN DESCRIPTION OF VIRIA TYPE I CERRIN DEANDAR FIND ATE	310 363	197.536					
	i	THE PARTY OF THE WAY VIRIATIVE TO STATE OF THE PARTY OF T	110.363	\$1.50					
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12		CITIEST STATES AND STATES OF STATES	IFF. 270						
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AND MILES	NI II		10:19	102-130	101.216	161.191			
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7 E E E	THE YEAR OF THE PERSON OF THE		ı			:	:		:
I'ME EINVE		NEW YORK					1		
Don't Civil	POR POR YPROTEIN	SINIIAH BOAMY VIRUS (TYPE) / STRAIN LK I) (SFV-1)	337.345					Ī	İ
	AND THE CONTRACTOR	CHIMPANYTE MAINMANTTOPMEN VIRITATIVITY (TIVITY)	164.188	\$34.4v					:
		ANYDEAN CHEUROTIC NOTICE VINUS	17.35	=======================================			-		
A WING	П		130.61						
20.	- 1	7 15(1)	111.03	301.315	937:11				
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PPOL VIEW		VISAA LENIIVIAUS (SIRAIN ISIA CEUM EVITRAI)			VII.		l		
10 VI VI	1			67:107	2			Ī	
PPP4 HSV6C	Г		1						
74.04	T	AUTOGRAPHA CALIFORNICA MUCLEAR POLYHEDROSIS VIRUS	53.83						
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İ	AND PROTEIN		2.3	Ī		Ì	T		Ī
•	REVPROTEIN		2.2		İ		İ	Ì	
łl	REV PROTEIN		24.104						
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VIII ASPIN	DUCTASE LANGE	AWI LIL 10/1) (ASFV)	Ť					j	
PRINT IN MAN	ALECANOL LOSGO DIPROSPIATE RESILEMENTE CARGE CHI	FIGNIAN CYTOMEGALOVINUS (STRAIN ADISM)	_	2	140.477		j		
THE CAPPE	MINORACE COSIDE CITATORIA DE REDUCTADE LA FUE CITATORIA DE PROPERT	LOUNE HERES VIRUS 1 YES 1 (STRAIN ANATYCEMY)	T	163:00		1	1	Ì	
A LANGE	BACARTE INSIDE MINIOSTRATE REPORTATE LABOR TO SECOND	VALCINIA VINOS (SI PAIN CONTINUADO NA	111.07			•		1	
PRINT VANV	BISCHALL SOUNS DISHOGNATE REQUESTAGE LABOR CHI	VALUE A VINCE	101-101	Ī	†		1		
PRINI VZVO	AUBONUCLE DSIDE: DIPHOSPHATE REDUCTASE LANCE CH	VARICELLA JOSTER VIRUS ASTRABADIDA ASLUCEVA	Т	236.344	715-117	+	1	\dagger	
	AMIL SERING HABONING PROTEON KINASE TLANSFORM	AVIAN BOKIS, ASSOCIATED VIRING TYPE	Ţ,	T		t	1		Ī
	SAME SEAMONTHE ON THE PROTEIN KINASS TRANSFORM	AVAN ESPONENCE IN THE PROPERTY OF THE PROPERTY			1	+			Ī
PRIM VACCV	NNA. POL YMERASE ASSOCIATED TRANSCRIPTION SPECIF	WAL AND VACCINIA VIRUS (STRAIN COPENIAGE		Ī	1	l		1	ļ
ŧ	MA-POLYMERASE ASSOCIATED TRANSCRIPTION SPECIF	-	390.023		\dagger	T			
PRPOI VACEV	DNA-DIRECTED RNA POLYMERASE 147 KD POLYPEPTIDE	VACCINIA VIRUS (STRATH WR)	1601-1001	Ì	Ť		\dagger	Ì	Ī
_	DNA-DIRECTED BNA POLYNERASE 113 KD POLYPEPTIDE	CAPRIPOXVIXUS (STRAIN KS-1)	Ť	969.79			l	Ì	Ī
	DWA DIRECTED RIVA POLYNGRASE 133 KD POLYPEPTIDE	COMPOX VIRUS (CPV)	Γ	12.57	T	-		T	Ī
٦,	DNA-DIRECTED RNA POLYMERASE 111 KD FOLYPEYTIDE	VACCINIA VIAUS ISTRAIN WRI, AND VACCINIA VIRUS (STRAIN COFEMIAGI	102.234	143.518					Ī
7	DNA DIRECTED RNA POLYMERASE 133 KD POLYPEPTIDE	VARIOLA VIRUS		143.578					
MACCY VACCY	:	S (STRAIN WR), AND VACCINIA VIRUS (STRAIN COFENIACI	3						
PROJ VARV	PKD POLYPEPTIDE		# 1					-	
TATOR FORM	IN KO POCYPELTIDE	AIN FP.!)							
J	RNA-DIRECTED MA POLYMERASE		=	Ť	1426-3493				
Т	RAM-DIRECTED AND POLYMERASE			1041.3073					
**************************************	The state of		1	\$ 174					
Т		INTERFER A VIRIS (STRAIN AVICTORIA)	021-30						
FRRP. LANDY	BNA DIRECTED ANA POLYNGRASE SUBLACT PT	ABBORISMON	A.			1			
T		Velian	Т		1		İ		
Т	BUNIT PI	1051001010	110	1	1	1	1	+	
Г	NAA-DIRECTED RAA POLYMERASE SUBUNIT PI		414.518	T		1	1	1	Ī
PRIPT INITO			100	İ	\dagger		\dagger	Ť	Ī
		INTLIFICA A VIRUS (STRAIN AEQUINE/TENNESS) E/5/46]	115-70	İ			+ 	\dagger	Ī
PARP3 JAKOK	DUNIT PI		115-311		\mid		\dagger	t	
┪	SECTION 1		484-518						Ì
		INTUENZA A VIRUS (STRAIN AL ENINGRADAI 34/17/53)	486.518						
Т	ĺ		414.51						
Т	Ī	AAT DEBTAZZEGOS		1	1		1	1	
Γ		Т	414.516	Ì		ł	†	1	Ī
۵	ANA-DIRECTED RNA POLYNIERASE SUBUNIT PI	VENEW JERSEY/41/83)	414.516	T		\mid	\dagger	+	T
П		П	48-518						Ī
_	3000	ESOTAN13/80)	116-540				r	-	Γ
٦	Jacobs P2		484-518						
ī	Jamest P.		484-518					-	
	RMA-IMAECTED RMA FOLYMERASE SUBORITY		414-518						
Т	ALKIN K	IMILITARIA A VIRUS (STRAIN ASWINEARONG KONG/156/12)	614.518						
7			200						
Ť		A VIRUS (STRAIM AND INCIDENTESSECTATI)	7					-	
Т	MA-DMECTED BNA POLYMERASE SURINITES	1 4 N A A VIDIG STRAIN AGOME IN ACTE VILLANDS OF THE			+				
T	RAA-USECTION RAY VALVALIEASE STORE PI	THE NAME A VISING A COUNTY AND PROPERTY OF THE PARTY OF T		Ť	1				
Τ	RNA DIRECTED RNA POLYMERASE SUBURIT PI	Ī		1	1		1	1	
PARPS TABUA	RNA DIRECTED RNA POLYMERASE SIMITALI PI		115.413	İ			1	†	İ
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PCCENE	PRICTIZIE	All Virupes (no Bacteriophiges)	П		П	11	П	П	
LILEMANE	PROTEIN	VINUS	4	TOTAL	7	1			
TANK TANK	_	INSTITEMENT A VIRUS (STRAIN ANALLANDAGE WORKA) 50719				T		T	
PART AND		INSTITUTENZA A VIAUS (STRAIN AAUDDY TURNSTONENEW JERSEY/4783)	115-613						
FRAFI TASES	~	INTLIGHTA A VIRUS (STRAIN ASEALAIASSACHUSETTS/131/41)	383413					j	
PRRPI INTEM		INTLIERZA A VIRUS (STRAIN ATURKEYAINNESOTAVIJA)						1	
TREE IN		INFLUENZA A VIRUS (STRAIN ASWINDIOWALENO)				1		İ	
PREF WATE	AMA-DIRECTED BINA POLITICIANS SUBURILLY	INTEREST A VIRUS STRAIN MANN ARTHOUGH COLD ADAPTED IN	97.7			T		Ť	
PREST INSAL		INST. LENZA B VIRUS (STRAIN BVANN ARBORVING WILD TYPE)	135.749					T	
PREP. INCOL		INSTUENZA C VIRUS (STRAIN CREAT INVINS)	19.60						
FREE INCL	ANA-DIRECTED ANA POLYNERASE SUBUNIT PI	INFLUENZA C VIRUS (STRAIN C/11/30)	17.60						
PRINT TROOP	KNA-DIRECTED KNA POLYNGILASE SUBUNIT PI	THOGOTO VIRUS (THO)	99.145	174.556					
MAPA CVIII	RNA-BIRECTED KNA POLYMERASE	HUMAN COROMAVIRUS (STRAIN 229E)	410.443	13.745	1262-1295		2074-2112	2474-2501	23.79
PRRPA CVMIH	ANA-DIRECTED RNA POLYMERASE	INTIME CORONAVIRUS LOIV (STRAIN NEW)	708-740	334-337	133.113	1937:3861			
		DERVE VIRUS (9EV)		2137.2169			1	İ	
		MILTINE CORONAVIRUS LOIV (STRAIN A 19)	2		1084-1772	_		1	
	RNA-DIRECTED ANA POLYMERASE	(KIURINE CORONAVIRUS MITY (STRAIN TIDM)		21.71		F. 17	ZBW8-Z1/28		
		CHICINE IRANSMISSIBLE CASTRUENT PRINT CONCORDINGS	T	W(-17)			1		
THE CYPE	_	PORCINE RESPINATORY CORONAVIRUS	414 630			1	+	1	Ī
PREPORTE		A VIAN (APECITIONS BRONCHTHIS VIANS (STRAIN GENOLET IC.) (187)	101.11	100K.1 39		T		1	
LEET BOWN	MAN FOLT PREMATE	MANY AAN MANY STRAIN 14. HELIKORPANI GELORBINAGIC FEVER VIRUSI	1030-101			T			Ī
PREST VECTA		GRAMAN RESPUENTORY SYNCYTIAL VIRUS (STRAIN A2)	103.003	1181-1313			-	Ì	
TANKY I	BAA DIRECTED BAA POLYMERASE	MARBURG VIRUS (STRAIN MUSOKE)	Ī	666.736	1013-1074	1631-1671		Ť	
FREE LIABVE			144-176	646-736		11111111	ľ		
Т	BNA POLYNERASE BETA SUBUNIT	ASTON		647-613	+-	8611-0911	1896-1914	İ	
PRRP. MONOW	RNA POLYMERASE BETA SUBUMT		2						
	RMA POLYMERASE BETA SUBUNIT		П	8	П	_			
	ANA POLYMERASE BETA SUBURIT	HUMAN PARAINFLUENZA Z VIRUS (STRAIN TOSHIBA) (FIV-2)	٦	٦	Ī	┪	181-1912 30	1011.1011	
	ANA POLYMINASK HETA SURUMIT	VIRUS (STRAIN MIT 4781)		٦	7	110.2139			
_	ANA POLYMIRASE HETA SUBUNIT		T		⇁	201	1	1	
TARP. MAVS	ANA POLYKERASE RETA JUBUNIT	RABIES VIRUS (STRAIN SAD BIV)	P - 100			201.014	+	1	
704	RAN-CHECTED HAN FOLTPIERASE	BUT LAST BY SEVEN CHERCARD AND MAKED MICHAELS	1011.104	1009.3044	Ť			\dagger	Ī
Т	MANAGEMENT OF THE PROPERTY OF	STADAT VIETE STATE FULLANTS	1	231.364	11.14	11.11	1140.213	İ	Ī
2 Z Z		NI MIN VINEN (NI MIN MIN MIN MIN MIN MIN MIN MIN MIN M	•		T	13		•	
	RNA MALMASE HELA SUBURIT	SENIM VIRUS (STRAIN Z)	18:35	131.769	Ť	Ë	1140-1177	İ	
PART SEGUA	RINA DIR ECTED RINA POLYMERASE	SEOUL VIAUS (STRAIM NO.39)	194.4)[П	2011-2119				
FABRE SVSWR	THA POLYMERASE BETA SUDUNIT	SIMIAN VIRUS 5 (STRAIN 21004-WR) (SV3)	7	≅Ī	_	T			
FREPL SYNV	HAY POLYNERASE BETA SUBUMIT	SONCHOS TELLOW NET VIRUS ISTRAY)	Ţ	ī	Т	7	_		
LANGE TOWN	HWA TITLE THE WAY TO THE WAYE	TOWN TO STOLL BY WILL VINCE THE STOLEN THE S	1011		20.77-4077	700.740.7		C1017-1860	
PRESENT VEVIII	BINA POLYMERASE BETA SUBLINIT	VESICULAR STOMATITIS VIRUS	+	313.349	Ť	Ť	934. 1919	T	
FREFE VSVIO	RIVA POLYNIERASE BETA SUBUNIT	VESICULAR STONATITIS VIRUS	E	1954-1989	+	1		l	
PRIPL VSVSI	AMA POLYMERASE BETA SUBUNIT		111.11	306-346	113.340	1961.99	1011.101	2111.90	1001-110
	PUTATIVE RNA-DIRECTED RNA POLYMERASE		146-174						
FARIN BYDYL	MITALIVERNA THE CITE BEATE YEAR OF STATE	<u> </u>	£						
TREC BYUVE	FUTATIVE RNA-DIRECTED RNA POLYMERASE		£ .					Ì	
PREPO BYDYR	PUTATIVE INA DIRECTED INA POLYMERASE	MARLET TELLOW DWARF VIRUS (ISCALLE PARY) (NYDV)			Ì	İ	<u> </u>	İ	Ì
PREPOCATIVE	PROBABLE ANA DIABELIED MA POLIMENASE	100 100 1 0 1 1 1 1 1 1 1 1 1 1 1 1 1 1		777	****	2021 2771		Ť	Ī
	PUTATIVE ENA DIRECTED INVA PAR THERASSE	Τ	Т	6	7	× 13%	 	1	
	PROGRAM E BUA MARCHES BUA POL VICEBACE		Τ	363.106	100.00	1		T	Ī
- 1	PLITATIVE BNA.DRECTED BNA POLYMENASE	SISEASE VIRUS (STRAIN 52/10) (IRDV)	_	Τ		Ì	T	t	
Ì.	MITATIVE RIVA-DIRECTED RIVA POLYNGRASE		П		599-627			T	
1 1	PUTATIVE INA-DIRECTED NAA POLYMEIJASE		П	346.336					
	PUTATIVE RNA-DIRECTED RNA POLYMERAKE	INTECTIONS FANCREATIC NECROSIS VIRUS (SERUTANI: SPLINNY)	745.140	140.71					

LILERANI		And the same of th			7	٦		٦	
	CROICIN	CONTRACTOR STREET, STR	435	3	4	3	ABEA	AREAS	APTA!
PRINCE VOVE		AND THE COMMENT STATES OF THE	3						Ī
PRINT MONT	_	AIAIZE CHLOROTIC AWITLE VIRUS (AKAIV)	16-48	33.11					
PRENC PLRVI	PUTATIVE RNA. DIRECTED RNA POL	MOTATO (EAFRIM L'VINIS (AFRAIM I) ITI RV	176-60)						
TATE OF TAXA	PUTATIVE BIANDIETTITE BIAN POLYMERANG	Principal Carterial Vinos (States and States)	17.46	302.710	119.101	1064.1104	101.144		
FRIEND RCHAIN	PUTATIVE RNA DIRECTED RNA MY.	ALD CLOVE'S MICROTIC ABISAIC VIRUS (BENIN)	378.314	38.33					
THEOVE	ANA-DIRECTED ANA POLYMERASE	ALCUVIRUS (TVPE 17 STRAIN DIJIONESI	284.315						
PRINTO ROTER	ANA-DIRECTED ANA POLYLIERASE SL	NOVINE ROTAVIALIS (STRAIN RF)	23-60	100.21	247.276				
PRRPO ROISU	RMA-DIRECTED RNA POLYMERASE \$	BOVING ROTAVIALIS (STRAIN LIK)	200	30. 23		·			
2101010111	-	KINALD IT BOY AVIETY PORTED CALL	3		347,334			Ï	1
PRES TACV	BNA PRI VALERACE	FACARIDE VIRUS	12	100	2078.2112		Ī	Ī	
PREMO 185VC	PROBABLE RNA-DIRECTED RNA POLYNERASE	TONIATO BUSHY STUNT VIRUS ISTRAIN CHERRYLCTISVI	20.00				T		
PRING TCV	PROGRABLE RIVA-DIRECTED RIVA POLY	TURNIP CRIMILE VINUS ITCV)	110-318				Ī		
FRAIN THICKIV	PUTATIVE ENA-DIRECTED ENA POLYNERASE	I OBACCO MILLD GREEN MOSAIC VIRUS (TMV STRAIN UT)		131-139	209-264	316-406	650-41)	155:11)	1337.1559
PRRPO TMV	PUTATIVE KNA-DIRECTED RNA POLY	TOBACCO NIUSAIC VIRUS (VULGARE) (TAIV)		376-406	100-738	1313-1565			
PARPO THVKR	PUTATIVE ANA-DIRECTED RNA POLY	108ACCO MOSAIC VIRUS (STRAIM KOREAM) (TNIV)		176-406	П	1333-1563			
PRRPO THYTO		HOBACCO MOSAIC VIRUS (STRAIN TONIATOR) (Thiv)	П	176-406	100.128	197.689	1833-1861		
V 2	RMA-DIRECTED ANA POLYMERASE	IOBACCO NECROSIS VIRUS (STRAIN A) (TNV)	=				Ì		
OAL OTHER	ANA-DIRECTED MAY FOL TAIL MASE	CAUNCE METERACES VINOS (SIRAIM D) (INV.)	211	27.50				1	ĺ
100	THE PAY VALUE ARE AS DITA COMPANY						Ì		
10721 00 00	BUA BOT WATER AT ALL ALL ALL ALL ALL ALL ALL ALL ALL	NEAC FOR CHARLES IN THE CHARLES IN T				Ī			
-	INTERNATIONAL SERVICE AL PRINT SINGLE PARTY	AGE ASLES VIRUS (STRAIN YANIAGATA-1)				T	Ť		
	RNA POLYNIERASE ALPHA SUBIDITA		311.348						
	KNA POLYNEKASE ALPHA SUBLINIT	Ġ	313.349				İ	Ī	
PRRPP MUNCH	RMA POLYNIERASE ALPINA SUBUNIT		112.249						
ı	KNA POLYNIERASE ALMIA SUBUNIT	(AGN) ()	330-355						
PRRFF NOVE	ANA POLYNERASE ALPHA SUBLINIT	AUDETTE C45) (NUV)	ŝ						
	MAN PULTHERASE ALPHA SUBURII						Ì	1	
PRESENTATION OF STREET	BIAN PALTAGE ALTHA BURGALL	HANDEN PARAMETER AND A VINITA COMMENTAL PROCESS		113.164				T	
PARP PAR	TIMA POLYSCEASE ALPHA SUBURIT		Ţ	77.11		Ī		Ī	Ī
FRREP PIRYV	NAM POLYMENASE ALPHA SUBUMIT		ī				Ì	Ī	Ī
PRRPP RABVA	ANA POLYMERASE ALPHA SUBUNIT		316.324						
PRAPP RABVC	ANA POLYNERASE ALPIN SUBUNIT		216.344						
PARP RABVE	П	RABIES VIRUS (STRAIN ERA), AND RADIES VIRUS (STRAIN PA)							
	т	Ì	٦	116-344					
1	т	KABILS VIKUS (STRAIN SAU DIV)				1			İ
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THE PERSON	THE NATIVE TANK AF PILA SI MUNITIFIED	NIDAL VIALIS (STANIS)	300			:	:	:	:
PRINT SENDH	MAA POLYAGETASE ALPITA SURUNIT		510.504			Ī	İ	Ī	Ī
PRRIPE SENDS	RNA POLYKERASK ALPHA SLRUMIT	SENDAL VIRUS (STRAIN ?)	10.34						
PARP SVS	ANA POLYMERASE ALPIIA SUBLIMIT								
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_	LABOR TECHNENI PROTEIN	HURPES SMIPLEX VIRUS (19PE A 1STANIN GS)	13.139		_	1436-1469	1037-2072		
Т	ABCE PECANGET SECTION	(CIIV.1)	Γ	159.584	1077-1106	1361-1361	_		
Т	AND		105.497	15:131	133.641	634.960	1437-1534 2421	1421.7445	_
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7	MA ICAMINAL PROJECT	IF BIREDEABORNIA CIBING ASAV	10.767	Ī	T	Ī	<u> </u>	<u> </u> 	Ī
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:	CIRKIN PRINTIN BRIDE	CAN III.RM.SVIRUS 4)	38:186		-	Ì	<u> </u>	1	:
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	PAGIEN ULI	HERYES SIMPLEX VIRUS (TYPE I / STRAIN 11)	1.3						
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PIRET HISVER C	GEME 40 PROTEIN	7) (8)1V-1)	194-121						Ī
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10			163-103						
-	PACHAMI P MAJOR ENVELOPE CLYCOPROTEIN BFLF	HERDESVIRUS 4)	167-405			1			
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ATT HEAVY	PROBABLE MAJOR ENVELOPE OLYCOPROTEIN 40		136-301					1	
T	PROBABLE MAJOR ENVELOPE CLYCOPROTEIN 16	(VZV)	<u> </u>		1	1		1	
7	GENE LY PROTEIN	III AFESVIAUS SAIMINI (STAAIN 11)	0		1	1		1	1
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PLL 16 HCMVA	HYPOTHETICAL PROTEIN ULSA	INDIAN CYTOREGALOVIRUS (STRAM ADIM)	189-521		T	П	Т	Т
M 1.33 EBV		EPSTEIN-BARR VIRUS (STRAIN B95-B) (HURIAN HERPESVIRUS 4)	18:133			-		
13 13 VEB	GENE 2) MOTEIN	FQUINE HERPESVIRIS TYPE I (STRAIN ARRY)(EIIV.I)	32.51	978-812		+	<u> </u>	
×	- 1	HERPESVIRUS SAIMIRI (STRAIN 11)	\$64-602				_	 -
200	GENE 21 PROTEIN	VARICECLA-ZOSTER VIRUS (STRAIN DUNIAS) (VZV)	592.629	106-736	176-506			
1	HATCHER AL PROIDE NOTE	HUNIAN CYTONI GALOVINUS (STRAIN ADIGA)	2					
	MARINE AND THE PROPERTY OF THE PARTY OF THE	VARIA ELLA COSTER VIAUS (SERAIM DUNIAS) (VZV)	274.10			İ		
	STATE OF THE PERSON OF THE PER	MENTED SIMPLEA VIRIS (1175 17 SIRAIN 17)	2			1		
VALUE OF BUILDING		MARICELLA CONTER VIRUS (STRAIN PRINTS) (VCV)		27.70		1		
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200	SECONDARIA PARA PERSONAL SECRETARION OF THE PARAMETERS AND THE PARAMET	BOVINI: HIGHESVINO'S LITTE I (STRAIM FE.2)	33.166			1		
1000	THE SERVICE STATES AND	LEAST CONTRACT VINCS (STRAIN MASSE) (HIGHIAN HISRITS VINCS 4)	282.017			+		_
	THE RESIDENCE TO SELECT STATES OF THE SELECT STATES	THE REPORT OF THE STATE		5	<u> </u>	-		
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	ن د	HILLIES SAINING (STRAIN III)	229.787	376.41				
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121	HIVE THE FIRST PROTEIN OF AS		1			-		
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VIII) CHIL		EFSTEIN BARR VIRUS ISTRAIN 1991-13 (FIUNIAN INTRE) SVIRUS 41	9.14	1		1		
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rta.95 Linv		HERFESVINUS 4)	111.143	İ		$\frac{1}{1}$		
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HULL HEMA			19.			<u> </u> 	<u>i</u>	: :
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HING VACCC	=	CINIA VIAUS (STRAIN CONTINIACIAN)		Ì	1	+		
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TUNG VARV	URACIL-INFA GLYCUSYLASE	:	1111	İ		<u> </u>	<u> </u>	
PUSOZ INCARVA	HYPOTHETICAL PROTEIN HOLF?		1:3		-	-		
PUSO INCHIVA	INTOTICE TICAL PROFEIN HALFS		933-186			┞		
PUSO ICHVA	HYPOTICETICAL PROTEIN HXLF)	HITMAN CYTONEGALOVIRUS (STRAIN AD169)	119:11			_	_	
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FILENAME	PROTEIN	5000	П	ANGA	VIEW	AREA!	AREAL	ABEAS	ARCAL
VISS ANYLE	135 KD PROTEBA	ALIALFA MOSAIC VIRUS ISTRAM 421 150LATE LEIDEM	26)-143					1	1
PVIJK TRVPL	16 KD PROTEIN	TOBACCO MATTLE VIRUS ISTRATIN PLIN	74-62					1	Ī
PVIAI NPVAC	HILKASE	AUTOGRAPHIA CALIBORNICA NUCLEAR POL YHEOROSIS VIRUS	201.21					1	
PV 17K BSMV	IT KD PROTEIN	DARLEY STRIFE NIOSAK VIRUS (#SVIV.)	6.3				1	1	ĺ
PY IA CHIVEN	I A PROTEIN	CLCURINER MOSAIC VIRUS (STRAIM PAVICAIN)						†	Ì
Pt 210 ASF81	Lad PROTEIN	APRICAN SWIZE PLYER CRUS (KTRALY RAZIVI) (ASK)				1	-	İ	
PY:24 BINAV	24 PROTEIN	RECAD REAM MOTILE VIPUS	Ť	167 917	141 100	İ		†	Ì
PV34 CCNV	N PROTTIN	LOWING THOROTHE AND LESS TO THE STATE OF THE	T	91				t	
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VIA BONV	JA PROTEIN	BROAD BEAN MULLE VIAUS				†	$\frac{1}{1}$	İ	
PVIA BAIV	IA PROTEIN	BROME MOSAIC VIRUS (BMV)	A		1	1		1	Ī
PVIA CCMV	1A PRINTEIN	COWPLACIA COLONIC MOTTLE VINUS (CCATV)	ġ		1				
PVIA BIVE	1A PROTEIN	AVIAN INFECTIOUS BROXCIIIIS VIRUS (STRAIN BEATIDE ITEL (IIIV)						1	
PVJA (BVM)	IA PROTEIN	AVIAN INTECTIONS BRONCHISTS VIRUS INTERIOR INTERIOR					1	Ì	1
FVIA STVP3	IA PECULIZ	AVIAN INI LC 110US (IRUMA, 11111) VIRUS			1			Ì	Ī
	IA PROTEIN	AVIAN BY ECTIOUS BRONCHITIS VIRLING UKUTION (IIIV)				1		1	
	SO KO PROTEIN	AFFICIONOTIC LEAF SPOT VIRUS (ALLSV)	3	Ì	1	1		†	Ī
PVSIK DWYVF	1 KO ROTEIN	(RET WESTERN VILLOWS VISOLATE FL. I) (BWV)			1	1		İ	
	SI KD PROTEIN	BLET WESTERN YELLOWS SIRCH GRIJ (DWYV)	8		j			İ	İ
PVSK PLIVI	SEED PROTEIN	POTATO LEAFACH, L. VIRUS (STRAIN 1) (FI.R.V.)	20.00					İ	1
PVS6K PLRVW	SE KD PROTEIN	POTATO LEAFROLL VIRUS (STRAIN WACENINGEN) I'LI RVI	260.792	j				j	
PVSK BSNV	SO KO PROTEIN	DARLEY STRIPE MOSAIC VIAUS (BSMIV)	20.00	Ī	Ì			1	Ī
PV TOK TO RVI	AND PROTEIN	POTATO LEAFROLL VIRUS (STRAIN I) (PLRV)	230-257						1
PVICE PLEVE	W TKO PROTEIN	POTATO LEAFROLL VIRUS (STRAIM WAGENINGEN) (PLRV)	120-021				-		
t.	PO KO PROTEIN		103.131						
1	PEDIEIN A4		213.231						
PVAM VACCV	PAOIEIN A4	VACCINIA VIRUS (STRAIN W.R.)	217.151						
1	PROTEIN A4	VARIOLA VIRUS	207.241						
PVATI VACCE	FROTEINAL	VACCINIA VIRUS (STRAIN COPENITAGI.M)	~ ~						
	PROTEIN ATI	VARIOLA VIRIIS	16.13						
	SO KO ABONTIVE LATE PROTEIN	VACCINIA VIRUS (STRAIN COPEMIAGEN)	127 Oa						
PVAIL VACCV	16 KD ABOATIVE LATE PROTEIN	VACCINIA VIRUS (STRAIN WR)	28		j			1	Ī
	SEKD ABORTIVE LATE PROTEIN	VARIOLA VIRIJS	_		1]		i	İ
FVATS VACCE	PROTUN A21	VACTINIA VIRITS (STRAIN CIPINIAGEN)	Ī	E S	1				
- 1	FROIEIN A2)	VARIOLA VIRUS	1	2	1			1	
1	PROTEINAL	VACCINIA VIRUS (STRAIN COPENIJACEN)	2		1	1		1	
اد	PROTEIN A11		2		1	1		1	
- 1	PROTEIN AU	VARIOLA VIROS			1	1		†	Ī
LVA13 VACCV			-		<u> </u>	•			
PUNE VALET	Partition And	VACCINIA VIRUS (STRAIN COPENIAGEN)		Ī		İ		Ť	Ī
PVA(1 VACCC	PROTEIN ACT	VACCINIA VIRUS (STRAIM COPERITAGEN)	94-129					t	
PVA(1) VACCV	PROTEIN A43		64.13						ĺ
١	PROTEIN A41	VARIOLA VIRUS	95.130						
	PROTEIN AVI	VACIONIA VIRIIS (STRAIM COPLINITAGII NI	161.141			,		-	
VAN VACT	PROTEINA	VACUINA VISITA (STRAIN WE)		Ì		1	_ - 	1	İ
rváli BČEV	ALI PROTEIN	BEET CUMLY TOP VIRUS (BCTV)			1			+	Ī
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	AL PRINCIP	•		i		 	<u> </u>	<u> </u>	-
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ı	AT 1 SPOTEIN	IN CAST RENVANDAS	71.113					┞	Ī
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PVAT CALIVE	APHID TRANSMISSION PROTEIN	CALL IFLOWER MOSAIC VIRUS (STRAPH CM-1941) (CAMV)	S e	911:10		-		-	İ
PVAT CALVO	APHID TRANSMISSION PROTEIN	CAIR FLOWER MOSAIC VIRUS (STRAIN DAIL) (CAMV	20-53	103-130	Ī		<u> </u>		
PVAT CALIVE	APHID TRANSMISSION PROTEIN	CAILIFLOWER MOSAIC VIRUS (STRAIN BBC) (CAMY)	30-53	911:19					
PVAT CALINA	APILID TRANSMISSION PROTEIN	CALE IFLOWER MOSAIC VIRUS (STRAIN MYRIST) (CAMY)	300	911:18			_	-	
PVAT CALIVIP	APIND IRANSMISSION PROTEIN	CALL IFLOWER MOSAIC VIRUS (STRAIN PVIA) (CAMV)	П	91116					
PVAT CANIVS	APHID TRANSMISSION PROTEIN	CAULIFLOWER MOSAIC VIRUS (STRAIN STRASHOURG) (CANIV)		11:11					1
PUBON VACCC	PROTEIN B4			400-525					
_	PROTEIN BY	S (STRAIN WR)	120.156	489.525	-				
_	ı		\$25-489	_					
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т-	INTERLECKIN'I BINDING PROTEIN PRECURSOR		39-136			_			
т	SURFACE ANTIGEM S PRECURSOR	VACCIMIA VIRUS (STRAIN COPENIACIEN)	113-344	-		_	_	L	
PVBIS VACCD	SURFACE ANTIGEN SPRECIMSOR		111-343						
7	LUEFACE ANTIGEN S PRECURSOR		2					-	Γ
_	CIRPACE ANIMEN S PRECURSOR		111:243	ĺ		-			
Ī	ARI PROTEIN	NOSAIC VIRUS	166 109		-				
۰	C.PROTEIN COUPLITO RECEPTOR HOMOLOGICS	(\$i v)	94.130						<u> </u>
PVEBA VACCE	PROTEIN CO		26:50	187.316				L	
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PYCOS VACCE IS	PROTEIN CO	N CONTROL	171410			-			
+-	PROTEINCO		911.610					<u> </u>	
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	Ī	GENE 2 PROFEIN		T	86,336				+	
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	ı	PROBABLE MAJOR GLYCOPROTEIN	NEL CATFISH VIRUS) (CCV)	6					+	
PROBABLE TRANSCRIPTOR ACTIVITY ACTOR DEAD! INCREMENTATION ACTIVITY ACTOR DEAD! INCREMENT ACTOR D	PVC44 IBVSA			139-337					1	Ì
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HYPOTHERICAL GENE 54 PROTEIN CTALUND RETRESTING CHANNEL CATEGORY 144-376 144	PVG31 IBVI	SIYPOTILETICAL GENE SS PROTEIN		٦				-	1	
	PVG16 HSVII	HYPOTHETICAL GENE 16 PROTEIN /	CHANNEL CATFISH VIRUS) (CCV)	٦	3	1091-1126			+	
GENG SP PROTEIN ILEM-SYNING SANAMI (STAIN II) 11-40 19-131 11-40 1	PVGSE HSVII	HYPOTHETICAL GENE SI PROFEIN	NNEL CATFISH VIRUS) (CCV)	٦	2				1	
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INTEGRICAL GENE 65 PROTEIN CTALUND REALESVIRUS CHANNEL CAFFISH VIRUS CCY BIG-118 1590-1318 INTEGRICAL GENE 67 PROTEIN CTALUND REALESVIRUS CHANNEL CAFFISH VIRUS CCY 1150-118 GENE 6 PROTEIN CTALUND REALESVIRUS SAININI (STRAIN 1) CCY CCY CONTROL CAFFISH VIRUS CCY C	FVGA IISVII	HYPOTHETICAL CENE IN MOTERN	CHANNEL CATFISH VIRUS) (CCV)		41-461.	**************************************		-	_	
HYPOTHETICAL GENE 67 PROTEIN ICTALINAD HENESVIRUS I (CHANNEL CATFISH VIRUS) (CCY) 1150-1165	PVCAS 115VII	HYPOTHETICAL GENE 65 PROTEIN	(CHANNEL CATPISH VIRUS) (CCV)	П	M. 1174	1290-1326			\dashv	
CÉPICE PROTEIN STRICT SANDIS SEVI-RAZA B (604) INFOSITIOTICAL CHARLES PROTEIN (12 FINANCIAL SANDING STRICT SAN	PVGC) HSV	HYPOTHETICAL GENE 47 PROTEIN	CCV	1150-1115						
INFERIORITATION (MARCH CHART) PROTEIN (CTALUND MEANERS SAMINI (STRAIN I) (STRAIN MALE) (CCV) (MACH (MACH CHART) (MACH CHA	PVG SPVD	GENE 6 PROTEIN		9					1	
INVESTIBILITY GUNE 12 PROTEIN (ICTALUMD HEAVENUS I (CHANNEL CATFISH VIBLE) (CV) (44-475 (126-75) (1154-116)	PVG71 1ISVSA	IIVPOTIBILICAL CIENT PLYOTEIN								
	PVG72 IISVII	HYPOTHETICAL CLENE 12 PROTEIN			10-13	11.44	1252-1205			
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PY COS HIS VII	HYPOTHETICAL GENE TO PROTEIN				Ì		-	
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FCG1 IBVR	FIPEOTEIN		7	137.183				
Y CIG HON'Y	CLYCOPROTEIN 1301 PACLORNOR		1350.1294					\downarrow
			19-59			1		1
	CAL VOTEDIEIN PRECUESOR	DOVINE CORONAVIRUS (STRAIN LY-138)	24.		1		 	
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			20.66		ĺ	1		
1200	FY GLYCOMOLEIN PRECURSOR			Ī	1	1	 	<u> </u>
	CONTRACTOR PRECUESOR		937-1038		1			
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1160	P) G: YCOPROTEIN PRECURSOR				****			-
	ES CLYCOPROTEIN PRECURSOR							+
VCL) CVRI	ES GLYCOPROTEIN PRECURSOR	NA NEW			3		<u> </u>	+
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1	ES GLYCOPHOTERN PRECURSOR	(IN DEAUDETTE) (III.)		111111111111111111111111111111111111111	1	 	<u> </u> 	1
15	CL YCOPROTEIN B PRECUASOR						-	+
PVCO B HCNVT	ICL VCOPROTEIN B PRECURSOR						l	1
UNVELLE HEVAL		PE 67 STRAIN UGANDA-1102)		1			 	+
PAGE B 115VAI		BOVINE HERMSVIRUS TYPE		Ī	Ì			
FYCH MISKIN		OVINE PIONISHED IN STREET	116.196	1	Ī			-
PVCLB HISVDC	CLYCOPROTEIN I PRECURSOR		3					
PVGLB II.1V6	CA VCOPROTEIN B PRICURSOR	CALL HARD LAND THE PROPERTY OF	652.482	Ì				
Treat I Take	CELYCOPECIFICE PRI CLIRSOR	311111	200-25	Ī				
ונום ונוגו	CLYCOPROTEIN B PRICURSON		191-563	111.776				
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באבוים ביים	GLYCOPHOTEIN C PRICORSON		83.1					
PVGLC HSVIK	CATLOTES OF STAT		13.465					
TAKET LISAS	CHANGE CONTRACTOR CONT		19740					1
JUNE LIZA	GLYCOPROTEIN GILL PRECURSOR	=	9					1
העבור עבעם	CH. VCOPROTE IN CIP.	VARICELLA.ZUSTI & VIRUS (STRAIN DUNIAS) (VZV)	331-186			1		+
PVCI.C VZVS	GLYCOPACIEIN (PV		201.00				<u> </u>	1
PVCI D IISVEA	CLYCUPROTEIN IN PACCURSOR	THE PROPERTY OF THE PROPERTY O		10-420		!		<u>:</u>
1 V C C C C C C C			41:10	20750				
PVGLD 115VEK	SCTOTAGE OF THE CONSON		95-125					4
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TVE TOWN	CA.V. OFRUILING FRICIESON		5::	11.12	!	; ·	<u> </u>	_
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PVCLF BRSVR	_	Т	W. 1. W.				<u> </u>	<u> </u>
event coyo	1 1	CANINE DISTRICTER VIXOS (STRAIN CODERSTEROGRAPIACO)	44.513		Ī		-	L
VGL F IXEV	_	l	484.513					
PVCL F HESVA		SIRAIN LONG)	444.513					
PVCE FIRST	┰	LUS (STRAIM RSS-2)	618-913				$\frac{1}{1}$	$\frac{1}{4}$
PVCU F LIEASE	Т	INEASLES VIRUS (STICATA EDAKONSTON)	22-23	₹ ₹	1		1	
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ULCEASE	PROTEIN	MICAGE CIRUS (STRAIN D.) CA		(37-15)		1	1		1
┰	POSIGN OF TOO ROLL OF THE CONTROL	JATA-1)	*	200		1	+	1	
T	FINEST PLACES OF THE PARCUASOR		-	10797		1	1	t	
72	FINISH OF YCOPROTTIN PRECUASOR	ATIAKA VACCINE)			1	Ť	\dagger	1	۱
	FUSION GLYCOFFOILIN PRECURSOR		Т	11.777	T	T		T	
1	FUSION CLYCOPROTEIN PRECURSOR		1			1		T	
	FUSION GLYCOPACIEIN PRECURSOR	NEWCASTLE DISEASE VINOS (STRAIN HALLES STREET)	29.55						
	FUSION CLYCOPROTEIN PRECURSOR		35.15				-		
^	FUSION CLYCOPROTEIN PRECURSOR	PROCENE DISTRICT VANCS	1						
J	FUSION CLYCOPROTEIN PRECURSOR		17.5				ŀ		
Ϊ	FUSION CLYCOPROTEIN PRECURSOR	STATE AND ADDRESS	187157						
PVCL! PINH	FUSION GLYCOPACTEIN PRECURSOR		Т	441.480					
PVOLF RINDK	FUSION GLYCOPROTERN PRECURSOR (T	447-480				T	
Ī.	FUSION GLYCOPROTEIN PRECURSOR		T					T	
SCM35	FUSION GLYCOPROTEIN PRÉCUTSOR	MULANIST	100					T	
Г	FUSION GLYCOPROTEIN PRECURSOR							İ	
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, Carrie	FUSION CLYCOPROTEIN PRECURSOR		40.46			İ	1	1	Ì
Т	FUSION CLYCOPROTEIN PRECURSOR		44	Ī		1			١
Ţ	TITLION OF VEOPEOTEIN PRECURSOR	(TRIV)	42.4			1			
10	CL VCOPROTEIN G PRECURSOR	(AB4P) (EIIV-1)	27.16			1		1	١
	CONTROL OF VOODED TEIN PRECUTSOR	┪	374.533			1		1	
Division of the	This is yearen from Precursion	(SERGI YPE INDIANA / STRAIN GLASGOW)	450-488					1	
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	TOTAL DI VIOLENTIN PRECIPIEDE		450-488					Ì	
2000	CHICA OF COMPANY PRINCIPLY SOR	JAN)	450-410		ĺ				1
	CI VEDALOTEIN II PRECURSOR		69:-3:0				†		
_	CLASSING REPRECIESOR		٦			1		1	
Т	S CONTRACT IN INCIDENCE SOME		٦	2003		1			
	CI VIOREDIES II PROCUESOR		25.55				1		
Т		EQUINE HERPESVIRUS TYPE I	107.043			1			
T	MONEY MAN TO VALLE VIEW OF THE PROPERTY OF THE	US (STRAIN ADIGN)	ī						
NAME OF BRIDE			٦	3-46	682-1020	1069-1084		Ì	İ
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_	AND AND AND THE PROPERTY OF THE PARTY OF THE	ININA AVIETS SALVESTAL HART:	22.22	¥.1			j		
_	!	IIIUNYANWERA VIRIIS	П	47473	623.054				
				417-11	11. JI	915.004	193.14	1	
		٦	٦	2 2			1		
1 1 1 1 1 1 1 1 1 1	M PON VPROTEIN PRECURSOR	HANTAAN VIRUS (STRAIN HOLO)	٦	242	200		j	1	
_	NI POLYMONEIN PRECINSOR	HANTAAN VIRIIS (STRAIN LITT)		1		1		Ì	!
_	MINNE VIRGINISM PRI CURSOIR		7	10.510	121-120		1		ŀ
•	NI POL YPROTEIN PRECUESOR	VIRUS (INSV)	200.302				1		ŀ
PYCLIA PILV	NI POR YPROTORIN PRINCIPACIA	PROSPICT III.I. VIRUS (FILV)					†	Ī	
PVGLM PTPV	M POLYFAUTER PRICORSON	PUNTA TORO PHILEBOVIRUS							
PVOCE PUDANT	M POLYPROTEIN PRÉCURSOR						İ		
PVGIAI PUUNIS	ALPON YPROTEIN PRINCIPISOR	A.F. 9)	100.070					T	
PVGLE RVIV	LI POLYPROTEIN PRICURSOR	AIFT VALLEY FEVER VINUS (RVFV)	0.00-0.0	177.05	77.1				l
ZA TAN ITIDAL	AFPOLYPROTEIN PRECURSOR	RIFT VALLEY FEVER VIAUS (STRAIM ZIII-NAB ALIZ) (RVPV)	200			I	†	Ī	
PVCLN SEEUS	IN POLYPROTEIN PRECURSOR	SCOUL VIEWS (STRAIN #0.74)	M 010	41.00			ŀ	Ī	
PVGLM SEOUR	M POLYPROTEIN PRECURSOR	SEOUL VIAUS (STARIN RZZ)						T	l
PVCINI SEQUE	_	CLOUP, VIRITA (STAAN ARTIO) CANTON AND VINCING		1					
15.1	M POR VPROJETN PRECIMSOR	THE KINNE MINISTER COLINA		Ê			1	Ī	
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MININ A TON	GLYCOPROTEIN POLYPROTEIN PREC	ILIVIN ARENAVIRUS					Ī	Ī	
PVOLY LASSG	CLYCOPROTEIN POLYPROTEIN PRECURSOR	LASSA VIRUS (STRAIN GA)41)		İ					
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	LYCOPADIEIN POLYPROTEIN PRECURSOR		8.52					1	
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_	ENOME FOL YPROTEIN M	(STRAIN DO)		419-515			1	†	
	GENOMIE POLYPROTEIN M		166-799					1	
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IAJOR SUB ATE ANTIGEN PRECUISOR WOODCHUCK HEPATITIS VIRUS 1 IAJOR SUB ATE ANTIGEN PRECUISOR WOODCHUCK HEPATITIS VIRUS 1 IAJOR SUB ATE ANTIGEN PRECUISOR WOODCHUCK HEPATITIS VIRUS 1 IAJOR SUB ATE ANTIGEN PRECUISOR WOODCHUCK HEPATITIS VIRUS 1 IAJOR SUB ATE ANTIGEN PRECUISOR WOODCHUCK HEPATITIS VIRUS 1 IAJOR SUB ATE ANTIGEN PRECUISOR WOODCHUCK HEPATITIS VIRUS 1 IAJOR SUB ATE ANTIGEN PRECUISOR WOODCHUCK HEPATITIS VIRUS 1 IAJOR SUB ATE ANTIGEN PRECUISOR WOODCHUCK HEPATITIS VIRUS 1 IAJOR SUB ATE ANTIGEN PRECUISOR WOODCHUCK HEPATITIS VIRUS 1 IAJOR SUB ATE ANTIGEN PRECUISOR WOODCHUCK HEPATITIS VIRUS 1 IAJOR SUB ATE ANTIGEN PRECUISOR WOODCHUCK HEPATITIS VIRUS 1 IAJOR SUB ATE ANTIGEN PRECUISOR WOODCHUCK HEPATITIS VIRUS 1 IAJOR SUB ATE ANTIGEN PRECUISOR WOODCHUCK HEPATITIS VIRUS 1 IAJOR SUB ATE ANTIGEN PRECUISOR WOODCHUCK HEPATITIS VIRUS 1 IAJOR SUB ATE ANTIGEN PRECUISOR WOODCHUCK HEPATITIS VIRUS 1 IAJOR SUB ATE ANTIGEN PRECUISOR WOODCHUCK HEPATITIS VIRUS 1 IAJOR SUB ATE ANTIGEN PRECUISOR WOODCHUCK HEPATITIS VIRUS 1 IAJOR SUB ATE ANTIGEN PRECUISOR WOODCHUCK HEPATITIS VIRUS 1 IAJOR SUB ATE ANTIGEN PRECUISOR WOODCHUCK HEPATITIS VIRUS 1 IAJOR SUB ATE ANTIGEN PRECUISOR WOODCHUCK HEPATITIS VIRUS WAS HER PATITIS PATITIS WOODCHUCK HEPATITIS WOODC	7	i PRECIDISON	1889ATITIS B VIAUS ISUDITYPE ADYWI	133-261						
MAJOR SINT ALE ANTICEN PRECURSOR WOODCRUCK HEPATHIS VIRUS 39 MAJOR SINT ALE ARTICEN PRECURSOR WOODCRUCK HEPATHIS VIRUS 39 MAJOR SINT ALE ARTICEN PRECURSOR WOODCRUCK HEPATHIS VIRUS 31 MAJOR SINT ALONG MAJOR ALTHERN PRECURSOR WOODCRUCK HEPATHIS VIRUS 31 MAJOR SINT ALONG MATCH PRECURSOR WOODCRUCK HEPATHIS VIRUS 31 MAJOR SINT ALONG MATCH PRECURSOR WOODCRUCK HEPATHIS VIRUS 31 MAJOR SINT ALONG MATCH PRECURSOR WOODCRUCK HEPATHIS VIRUS 31 MAJOR SINT ALONG MATCH PRECURSOR WOODCRUCK HEPATHIS VIRUS 31 MAJOR SINT ALONG MATCH PRECURSOR WOODCRUCK HEPATHIS VIRUS 31 MAJOR SINT ALONG MATCH PRECURSOR WOODCRUCK HEPATHIS VIRUS 31 MAJOR SINT ALONG MAJOR MATCH PRECURSOR MAJOR		PAFFURSOR	WOODCITICK HEPATITIS VIRUS I	201.24	264.305					
SALON SUBFACE AFFICEN PRECURSOR WOODCHICK REPAIRIS VIRUS 1 LANDR SUBFACE AFFICEN PRECURSOR WOODCHICK REPAIRIS VIRUS 1 FACERALIC SALOR SUBFACE AFFICEN PRECURSOR WOODCHICK REPAIRIS VIRUS 1 FALOR SUBFACE AFFICEN PRECURSOR WOODCHICK REPAIRIS VIRUS WAS 100 ACCOUNT. THE PAIRIS WAS 100	_	J PE FCLESOR	WOODCHUCK HEPATHINS VIAUS 19	113.246	274.318					
ALACOR SUPLICES PRECURSOR WOODCHUCK REPATITIS VILUS IN PECTICUS CLONE) FACES ALLE ALACIS RUN ACE ANTIGEN PECULSOR WOODCHUCK HEATTITIS VILUS IN PECTICUS CLONE) HANDE SUPLICE PACE ANTIGEN PRECURSOR WOODCHUCK HEATTITIS VILUS IN PROSECUE CLONE) HANDE SUPLICES ANTIGEN PRECURSOR WOODCHUCK HEATTITIS VILUS WAS INDUCTED ANTIGEN PRECURSOR IN-11 HANDE SUPLICES ANTIGEN PRECURSOR WOODCHUCK HEATTITIS VILUS WAS INCOMEDIATED. IN-11 HANDE SUPLICES ANTIGEN PRECURSOR WOODCHUCK HEATTITIS VILUS IN PROSECUE CONTROLLED ANTIGEN PRECURSOR IN-11 HANDE SUPLICES ANTIGEN PRECURSOR WOODCHUCK HEATTITIS VILUS IN PROSECUE CONTROLLED ANTIGEN PRECURSOR IN-11 HANDE SUPLICES ANTIGEN PRECURSOR WOODCHUCK HEATTING ANTIGEN PROSECUE CONTROLLED ANTIGEN PROSECUE CONT	_	1 PAECINSON	WOODCHUCK HEPATITIS VIRUS 7	313.344	274.310					
HIGH THE MAJOR SURFACE ANTIGEN PRECURSOR WOODCINCK REPAINTS VIRUS (INTECTIOUS CLONE) MAJOR SURFACE ANTIGEN PRECURSOR WOODCINCK REPAINTS VIRUS WESTSCATE PWEED) MATRIX MATRIX MATRICINS INTERING MATRIX MATRIX MATRIX PROPERTY OF THE PAINT MATRIX	_	4 PRECURSOR .	WOODCHUCK REPATITIS VIRUS I	313-346	174.110					
MANOR SURFACE ANTICENPRECIASOR 1 WOODCHACK REPAIRS VINUS WAS (SOLATEPWISS) MATRIX MISHING STATEMENT STATEM	_	CE ANTIGEN PRECURSOR	WOODCHUCK HEPATITIS VIXUS 8 (INFECTIOUS CLONE)	112-346	274-505					
NATRIX MATERIX MATERIAL BY THE STREET OF THE STREET WAS WASHINGTON AND THE STREET WASHINGTON AND	PULISA WHYWE MAJOR SURFACE ANTIGEN	V PRECURSOR I	WOODCIFECK HEPATITIS VIRUS WER (ISOLATR PWS2)	135-161	j				j	
	NICELLY 14711 MATRIX (M2) PROTEIN		INITITIENCY A VIRITY (STRAIN ASSEINSMINEMENTALIVAL)	10.43						

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PCGENE	PUCTULIP		454	417	4	1	_	T	
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PWITS MYXV	INIT'S PROTEIN		3			Ī			
PVNO VACCO	PROTEIN W.		•			1			
2000	CHOILE NO.	VARIOLA VIRUS	77						
PUNIA BOTH	NONSTRUCTURAL PROTEIN NSM	FORCINE HOTAVIRUS (GROUP C. / STRAIN COMMEN)	9	165.401					
PUNCA AAVI	DNA REPLICATION PROFEIN	ADENO-ASSOCIATION VIRUS Z (AAV2)	62.9	146.177	19.63				
PVNCS PAVILO	-	MOVIN: PARVOVING (IPV)	351.340						
PVNSI AIISV4		AFRICAN MONEY SICKNESS SINCE S	14-101						
PVNS TAALA	₽	INTEREST A VICE STRAIN AND ABBORAGE	14.144						
PVNS I PANY	NONSTRUCTURAL PROTEIN NS!	INFLERZA A VIRUS (SI KAIM ACAIM SI AM	19.14						
FVNSI IACHI	HONSTRUCTURAL PROTEIN HS!	INFLUENZA A VIRUS (STRAIM ACTILICATION)	07:144						
DAYEL IACKG	NOWSTRUCTURAL PROTEIN NSI	INTLUENZA A VIRUS (STRAIN ACHTER ENAMERINA)	104.12						
FUNCT IACK!	NONSTRUCTURAL PROJETH WST	INTELEGIZA A VIRUS (STRAIM ACHICKEMBATANZO)	101						
Water Labas	NOWSTRUCTURAL PROTEIN NSI	INTUENZA A VIRUS (STRAIN ADUCINALIBER I ABOUT)	1						
WAST TABEL	MONSTRUCTURAL PROTEIN MS!	INTUENZA A VIRUS (STRAIN ANDER REPORTATION)	10.10						
WALE IN NOT	MONETHINGTHAL PROTEIN MS!	INTEREST A VITUS (STRAIN ADUC KONNEND)							
170.17	MONSTRIKE LINAL PROTEIN MS!	INFLUENCE A VIRUS (STRAIN APORT MUNICIPATIVE)							
AND THE PERSON NAMED IN	WALCHER PROFESSIONS!	INTLUENZA A VIRUS (SPRAIM AFORT WARREWING)							
10 10 10 10 10 10 10 10 10 10 10 10 10 1	MONEY BIRTHIAL PROJECT NS	INTERESTATIONS ISTRAIN AFORT PLACUE VIRUSHOSTOCKITAL	1						
1000	MOLECULAR PROTEIN NS	INTELLENZA A VIRUS (SPRAIN AA ENINGRAFY 1945)							
TANKS I WITE I	TONG THE THE AL PROPERTY AS	INTLIENZA A VIAUS (STRAIN ALENINGRADISCI)						Ì	
ANSI ALEM	NAME OF TAXABLE PROPERTY.	INTLUENZA A VIRUS (STRAIN ANIALLARDVALBERTACTORS)	10/-10						
	NONSTRUCTION OF THE PROPERTY OF	INTE UENZA A VIRIJS (STRAIN ANIAL LARIANEW YORKAS)9078)							Ī
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PVNSI IAPIO	NONSTRUCTURAL PROTEIN PS	INTLUENZA A VIRUS (STRAÍN APINTAIUALBERTAVIZIM)	- E						
200	MONSTHUK LUNCH THOUSEN AND	INFLUENZA A VIRUS (STRAIN APINTAIL/ALBERTAZOS/78)	101.14						
TANSI IVA	CONTRACTOR AND PROPERTY IN MS	INSTUENZA A VIAUS (STRAIN APINTALLALDERTA)SUTY)	103:14						
111111111111111111111111111111111111111	COLLEGE AT THE AL PROJECT NAS	INSELLENZA A VIAUS (STRAIN APUERTO RICOMIA)							
TANSI PAROS	NOWSTRUCTURAL PROTEIN NS	INSTURNZA A VIAUS (STRAIN AMURKEY-BETHLEHEM-GLILITITYS-87-2)							
1000	NOWSTELL TURKL PROTEIN NS!	INTLUENZA A VIXUS (STRAIN ATLIKET CAMADAN)	17.70						
2 1 1 1 2 1 2 1 2 1 2 1 2 1 2 1 2 1 2 1	Т	INFLUENZA A VIRUS (STRAIN A/TERMSOUTII AFRICANI)							
TALE IN THE	┰	INFLUENZA A VIALIS (STRAIN ATERNTURKRENIA)							
OKUIV INA	~	INTUENZA A VIRUS (STRAIM ANDXORMA)							
FVKS1 IAUSS	-	INTLUENZA A VIRUS (STRAIN AUGSBOWN)	10%.144						
PVNS1 [AZII	MONSTRUCTURAL PROTEIN WSI	NA CANADIO	106.79						
PVMS INDPA	NOWSTRUCTURAL PROTEIN WS! "	INCLUENZA B VINOS (STRAIN BOTALS)	311.316						
PVNSI INCAA	NONSTRUCTURAL PROTEIN NSI	INSTITUTE OF CHAINS (STANING CONTAINED BOOK AND CON	52.53						
PVNSI INCCA	HONSTRUCTURAL PROTEIN MSI	TAYLOCALA CANDA CANDA CANDA CANDA CANDA CANDA DA STRAIN 19553	9						
PVNS2 (IRSV)	MONSTRUCTURAL PROTEIN 2	CALACA DESCRIPATORY SYNCYTIAL VIRUS (STRAIN A2)	6702						
PVMS2 JEESVA	NONSTRUCTURAL PROJECT 2	INTERNAL BVIRUS (STRAIN BA EDA)	41.37						
PVNS1 PABLE	NONSTRUCTURAL PROTEIN WAS	INTLUENZA B VIRUS (STRAIN BYAMAGATAIM)	46.73						
AND THE A	NOTE THE PROPERTY OF THE PROPE	LIURINE CORONA VIRUS MWY (STRAIN S)							
PVISA CYMS	TOTAL TANK TO THE	PORCINE TRANSMISSIBLE GASTROENTERITIS CORONAVIRUS (STRAIN FST)							
PVNS	MONSTANCE DEAD PROTEIN 4	PORCINE TRANSMISSIBLE GASTROENTERITIS COROMAVIRUS (STRAIN PUR					-		Ī
NAS CALL	Т	PORCINE AESPIRATORY CORONAVIAUS					 -		Ī
100 1000	Ť	MURINE CORONAVIRUS MITY (STRAIN AS9)	3						
1	NO KD NOWSTRUCTURAL PROTEIN	MULLINE CORONAVIRUS MOIV (STRAIN DOS)							
	NONSTRUCTURAL PROTEINS HSI-N	INTLUENZA C VIRUS (STRAIN COREAT LAKES/116/794)	31.35						
2 12 12 12 12 12 12 12 12 12 12 12 12 12	HONSTRUCTURAL PROTEINS HS1-	(NILUENZA C VIRUS (STRAIN CJONANNESSURATIVE)	137.44						
NOX POX	NOWSTRUCTURAL PROTEINS HS1-N	INFLUENZA C VIRUS (STRAIN CANISMISTING)							
WAST DCYA	1	INFLUENZA C VIRUS (STRAIN OT ARABACA)	74.75			L			
PUNITA PRIVA	=	FACILITY AND STATES AND	E	P. 15					
FVMIK' IMIVII	NET LERITIEM								

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CILCRAME	PROTEIN	((8/1/	П	П	П	П	П		
WALE LACK			154-313					1	
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PVOOL VACCC	PROTEINO	SINAIM LOPEMIAGEN	818:118						
PVODI VARV	=+	MANAGERIA LINEATO VIETA PANA	87.12	16-14					
VOR! NAIV	→	POTATO MENE ELICIDADE ELICENISTO VALID	667.1703						
PVOR! PVICE	_	IATED VIRUS (SMYEAV)	131-153						
VOR! SHYEA	LESS NO THOUSAND AND AND AND AND AND AND AND AND AND		443-403				1		
ANNO HISTORY		LEAR POLYNEBROSIS VIRUS (ACADRV)	t-38				1		
AND MENO	PIGPLOTEIN	2	\$C-\$				1		
VOTE LINEDV		RICE BLACK STREAKED DWARF VIRUS (ROSDV)	26.29				T		١
PUPIP HISVES	CAPSID ASSEMBLY AND DNA MATURATION PROTEIN		200	281-182			T	T	١
PVP33 HCMVA	PROBABLE CAPSID PROTEIN VP23	HIGHAN CYTOMEGALOVINUS (STRADA AD 169)	141-172	304.318				T	
PVP11 HSV6U	PROBABLE CAPSID PROTEIN VP33	174					ľ		
PVP15 HSVEB	PROBABLE CAPSID PROTEIN VP13	EQUINE MEMESVIRUS TITE I IS INAIN ABART (BARTI)	224.253				T		
PVF33 V2V0	PROBABLE CAPSID PROTEIN VIII	KAIN VACCINE)	100-101						
PVP3 AMSV4	MINER CANNOT AND THE TANK THE		649-643						
2012	MISSES A PERIOD BAD TERM UP 3		556.586	649-683				Į	İ
	CATABOLIS PROTEIN VP.		391-424	564-593					
ALUES BYOLK	CHITCH CAPTION PROTEIN VP2		634-688						
VP3 ATVIS	COTER CAPSID PROTEIN VP2		52.621						
PVP2 EIIDVI	OUTER CAPSID PROTEIN VP3	ISE VIRUS (SEROTYPE I) (ENDV-I)		****			1	T	
PVP2 ROYBR	MAA-BINDING PROTEIN VP2						\dagger		
PVP1 ADTBU	RNA-BINDING PROTEIN VP2	BOVINE ROTAVIRUS (STRAIM UK)	Ι					I	
PVP2 NOTIN	ANA-BINING PROTEIN 172	177	L	200.613	3		İ		
PVP1 ROINC	PAA-ELYCHOLEN 172		Τ	523.550			T		
PVP2 ROTS	RNA-BIXDING FROIEIN VT		37.31						
WAS VACCO	.,.		278-311						
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PUPIN NEVOF	MAKOR CAPSED PROTEIN	POLYHEDROSIS VINUS (UPKINI'V)	107.141						
VP3 ENDVI	(P) COAE PROTEIN	(SEROTYPE I) (ENDV.1)	21713	7,4.78					
PVPJ EIDVA	(P) CORT. PROTEIN	IC DISEASE VIRUS	311-412	24.72					
PVPI BIN	NIAMEN IN KID STRIKT TIMAL PROTEIN P		2000				T		
VP3 ROTS!	INNER CORE PROTEIN VP)	SINIAM THE LANGE CONTRACTOR SALLY	130-453				Ī		
PVP60 ENV	CAPSIO PROTEIN PEO		19.152	ļ					
VALUE III VAN	SAN SERVICE SE	THORNE VIEZ (ILTV)	64.119		١				
DAZA GRAN	CAPELD PROTEIN P40		415-514						
VP47 NPVAC	-	X YHEDROSIS VIRUS (ACAINPV)	219-270				1		1
WAY VACCE	_		23.58						
PYPAA VACCV	-	VACCINIA VIRUS (STRAIN WR)	10.10				Ì		
VP4A VARV	_			467.140			-		
7V74 ROTG	OUTER CAPSID PROTEIN VP		378-108	95775			1		
VIV.	MONSTRUCTURAL PROTECTION		1	381.186			-		
200	CHEST TARGET PROTEIN VPS	TYPE I / ISOLATE AUSTRALIA)	195-324						
IN IS NOT	LATIER CAPSID PROTEIN VPS	III III EIIMAN VIRIIS (SI RIJIYM: I / IKN ATI: SOUTII AFRICA)	193-124						
rvrs nivi	CALLER CAPSID PROTEIN VPS	III IN TOPELA SMIN (SIRUIYNE I/ISOLATE USA)	395-324						
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111 5 5 5 5 5	75.7C.14	VIRUS		10-245				1	
01/10			13-61	122-257					
Very termy		MAIZE ROUGH DWAXF VIRUS (FIXOR)	\$15-582						
	TALKE FARET DES PLYCOPROTEIN PRECURSOR		281-316						
	THE WAS READER OF YOUR BUILDING PRECURSOR		161.211						
	LA INSTITUTE OF CLYCOPROTEIN		144.101						
			146.101						
	VIT COLUMN	A PRICAL							
BIVIS	Vy6 PROTEIN	BLUEFONGUE VIAUS (SEROTYPE 1/ ISOLATE USA)							
PVP6_BTV2A	VP4 PROTEIN		5				ŀ		l
ALM MAA	SIRUCTURAL PROTEIN 79		100 200						
INA WINE	STRUCTURAL PROTEIN P6	ILYHEDROSIS VIRUS (ACMMPV)	405-447						١
TVP 14 MPVAC	PAKO PROTEIN	_	454-490						
7,477	LANGE THE PROTEIN PAST		37.112						
	7.15(i) ph/76(N P0)	Section of the sectio	164.130						
OAN MAG	CATALOGUE AT DE AFRINGE								
We Brylo	MONSTRUCTURAL PROTEIN TO	THE TOWARDS VINUS (SERO) YPE 11/150LATE USA)	5						
PVPE BTVII	NONSTRIECTURAL PROTEIN PE	STATE CONTINUE PERSON VPE 31/ ISOLATE USA)	04-139						
Ver Sivil	NUNSTRIKCTURAL PROTEIN PO	- 15 COLONIOS VIENE SER DE COMO A 15 CIGAL	9(1.10)						
	WALES BITTINEAL PROTEIN PO	DI UETOWGUE VIKUS (SEKUL) TECHNOLOGICA	04.130						
	NA NIE TO TO THE PROPERTY OF	BILLETONGUE VIRUS (SCROTYPE I / ISOCATE AUSTRACA)	130						
¥ 1 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	ACAS INC. LONG.	BLUETONGUE VIAUS (SEROTYPE 1/ ISOLATE SOUTH ANDLA)							
BIVIS	NOWSTRUCTURAL PROTEIN PR	BITH TONGITE VIRUS ISEROTYPE 37 ISOLATE USA)	8:13A						
PVFI BTVIA	NONSTRUCTURAL PROTEIN PE	With the big to the second sec	114-412						
ryre RIV	CALLER CAPSON PROTEIN PR		164-165	119-411					
212		WOUND TOHOR VINOS (** 1. C) THE BOY CHEDBOOK VIBILS ACKING VI	143-173						
	TATE THE VIETNA AT ENVELOPE PROTEIN	AUTOGRAPHIA CALIFORNICA NUCLEAR POCT RECROSSIS SISSIS AND AUTOGRAPHIA	133.141			L			
	THE PARTY CHEST AT TAXABLE OPE PROTEIN	OKCYIA PSEUDOTSUCATA MULTICAPSID POLITICADSIS VINCA (C.	77.				L		
		HUMAN INMUNODERICIENCY VIRUS TYPE I (ARVEST 190LA 1971)							
PVPR IIVIA?	IVA PROIEIR	THE BLAN (ABLINERS ICH NOV VIETS TYPE 3 (ISSUADE DEN) HILLY			_			:	:
11/21/6	VIETE PROBLEM	IN BARMAN MANING MANING AND STREET (ISSUED) (ISSUED) (ISSUED)	16:31			ļ			
PVFH HVX'A	VIN PROTITION	. HASTER HANDEN FICHENCY VIRUS TYPE 3 (ISOLATE DIM) (IBV-1)	41.13						
PVPR 11V2D3	VPR PROTEIN	11 11 11 11 11 11 11 11 11 11 11 11 11	41.11						
PVPE HV2D1	VPR PROTEIN	TOTAL THE STREET	41.13						
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HEZAH MAAA		HENDELS BENEFICIENT RUINCY VIRUS 1976 2 (1878, ATE STOCKY)							
TVPR IIVS	VTW FRUITING	CHINIPANZEE DANIUNODEFICIENCY VIRUS (SIVICPZ)) (CIV)	Ž.					\downarrow	
PVPE SIVEZ	VPR PROTEIN	CINITAL INVESTMENT PIECE VIEUS (NOVI 43-8) (SOCATE) (SIVAIAC)	17.69						
INVE SIVA	VPR PROTEIN	THE REPORT OF THE PARTY OF THE	13.60						
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TANK PLA		SINITAN ISTRICTMENTERICIENCY VIRUS (PUINCEL) ISOLATE) (SOOTY MANGADIE	33.48						
VFR SIVSP	VPR PROTEIN	THIRIAN INARTHODEFICIENCY VIRUS TYPE I (BHIG ISOLATE HXD) ISOLATE							
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ASIAII IIA	WINGER STATE OF THE STATE OF TH	SHEEF PULMONARY ALIENDALA TOSIS VIRUS					-		ļ
PVPU ISRV	VPUTROITER	LACTATE DEHYDROGENASE-ELEVATING VIRUS (LDV)	2				<u> </u>		1
MAX CDV	VPN PROTEIN	BECKINE INVINODEFICIENCY VIRUS (ISOLATE 13) (BIV)	33-71						1
VPY BIVE		BARTEY STRIPE MOSAIC VIRUS (DSMV)	190-319	676-705					
ANS PAN	_	CHAST COTAVIETS (STEAD) (GV.20.1)	194.230						1
PVSOS BOTH	Г	TOWNS TO THE POPULATION OF STRAIN COMPENS	611.11	138-392					1
A101 10	Ē	TOTALINE NOT THE SET AND CALLS	1115-347						
15201 1020	Т	SMILAW II ROLATING STATES	33.83	L	L				
VENT POTER	T	BOVINE ROLAVIROS (STRAIN IN 1916) IN CHILAPOPIN	13	313-340	_				
	T	BOVINE ROTAVIRUS (CROOP C. STRANGE STREET CO.)							-
	ALCOUNT OF THE PARTY OF THE PAR		÷.	_	.				

FULL MANE PVSOS ROTER PVSOS ROTER PVSOS ROTER	PROTEIN								
VSOS ROTEH			28.35			Г	Г		
PVSOS ROTEH		TOTAVIRUS (STRAIM FILIT)	35.63						
PVSO6 ROTH!			5						
	VM PROTEIN		T	13.140			-		
PUCOS BOTHE	VP4 PROTEIN	HUMAN ROTAVIRUS (CROUP C/STRAIN BRISTOL)	T				-	T	
PV66 BOTTS	VPA PROFEIN		T	111.14					
PUED BOTHU	VIA PROTEIN		Ī					Ī	
20104	VN PROTEIN	OWDER	T	111.346			İ	T	
FUEN BOTTO	VPLPEOTEIN							Ī	
100 000	254 APO 1574		Ţ					Ī	
TV SUR BOTT	MONETHING ALL PROTEIN NOVPA		234-302		1		Ì	T	
1000	TOTAL STATE OF THE PARTY OF THE	(Y)	8		1		+	T	
200 EOLE	CLICOTAC CO.	STRAIN BEN-144)	2				+	T	
TV3CF	LINESTEIN AT ALL VERNETH NEVPS		2.2					Ī	
PVS10 RUIDA	POPS FOR CALCULATION OF CALCULATION	BOVINE ROTAVIAUS (STRAIN UK)	53.89					1	١
PVS10 ROTBU	NONSTRUCTIONAL CENTORING INC. 17		52-03						
PVS10 ROTHZ	NONSTRUCTURAL CETCORNICES PARTY DE CONTRACTOR	/CLONE 2)	51-19				1	Ī	
PVS10 ROTH?	NOWSTRUCTURAL GLTCUPAUTEIN MUVES		49-86					1	
PVS10 ROTHS	MONSTRUCTURAL GLTCUPRUIGIN MAYS	(AA)	41.15						
PVS10 ROTHW	NONSTRUCTURAL GLYCOPROTEIN PLV73		53.69						
PVS16 ROTS1	Ĭ	RAIN WA)	99.130						
PVSII ROTHW	MINOR DUTER CAPSID PROTEIN	TOVIETE CTARE STATE AND DESCRIPTION OF STATE OF	146-314						
PVSII REDVI	SIGMA I PROTEIN PARCURSON		110:147						
PVSII REDVI.	SIGNA I PROTEIN PALLURSON	CONTRACTOR VINITA (TRAIN KASZA) (SFV)	281-193						
PVTI SIVKA	PROTEIN TI PRECURSOR		261.290						
PVT2 MYXVI.		ALLONE EMBERGA VIEW (CTRATA KASZA) (SFV)	11:240						
FV12 SFVKA	TUNION NECROSIS FACTOR SOLUBLE RELEVIOR PACCOR	-	97 -91						
PVTJA CAPVI		CAN THE COURT OF THE AIM MOS. STATEMENT NEW PERPESVIRUS 41	86.93	505-543					
PVIER EBV	PROBABLE DNA PACKAGING PROTEIN		176.200						
PVTER RCMVA		ISH VIRUS) (CCV)	35-71						
PVTER HSVII			57.93						
PVX SENDS	X PROTEIN		55.13						
YIS ADEM	HYPOTHETICAL 10 4 AU EALLY TRUICIN	MANY CHEFAR YIRUS (SOUTH-AFRICAN ISOLATE) (MSV)	36.54						Į
PY IOX MSVS	HYPOTHETICAL 10 F RO PROJETH		65:12						
PYICK WOV	INVOINE TICAL TO KID PROTEIN .	KTICLE 35V)	3.5						
PY119 53V1	HYPOTHETICAL 11 9 KD PROTEIN		19-61						
PYIIK PASV	HYPOTHETICAL 119 KD PROTEIN (OUT VI)	CIBAIN SAIII	33.63						
PYIIK ROTSI	IIIYPOTHETICAL II KD PROTEIN IN SE	Total ANA CELL CON DAMAGE VIRILE ISTRAIN AUSTRALIA) (TYDV)	23:62						
PYLIK TYDVA	_	A I TOCH A PUA CAL IS DENICA MICH EAR POLYHEDROSIS VIRUS (ACAINPY)	101-59						
PYICK NOVAC	HYPOTHETICAL IS I KD PROTEIN IN S	GINEOLOGICS VIRILS: INE PARTICLE 55VI	161.00						
PYINK SSVI	HYPOTICE IN CALL IS U. R.D. P. COLE IN CO.	THE POLIDATIS VIRUS LIKE PARTICLE 55VI	139-167						
PY TOX SSVI	DIVIDITIES AT A STANDARD TO SELECT LOSS OF STANDARD TO SELECT STANDARD	MAIZE STREAK VIRUS (NICERLAN ISOLATE) (MSV)	122-135						
PY2IK MSVN	-1		94-137						
AVOOR IA	DOCAMENTAL STATE PROTEIN (OR) 21	A POLYMEDROSIS VIRUS (ACIANPY)	П						
TO STATE OF THE PARTY OF THE PA	LUNGATIETETAL AS 9 KD PROTEIN (OA)	SULFOLOBUS VIRUS-LIKE PARTICLE SSVI		×3.58					
MANUEL BOWNE	HYPOTHETICAL BANGIII ONFILI PROTE		X					Ţ	
TANA TIENES	HYPOTHETICAL 21,7 KD PROTEIN IN D		200-244			Ţ			
	AVECTOR FICAL BS KD PROTEIN IN D	=	-						
מינים מינים	ı		7						
THE COURT	1	BOVING COLOMAVIAUS							
200	HAPPING TICAL PROTEIN DI NUCLEOCAPSID ORU (1088)			3			Ī		
MAN COM	HYPOTHETICAL PROTEIN IN MUCLEOCAPSID ON! (ION!)		Ţ	77.163					
	LYPOTHETICAL PROTEIN IN NUCLEOCAPSED DRD (10AL)	T-	21.74	137-165					
			87.18						
VIII (17.74)	BLOUZ MOTERN	EPSTEIN-BALLI VIRUS (STRAIN B95-6) (MUNIAM NEWELSVIRUS 4)		71,77				١	
VOS CONV	HYPOTHETICAL 33 KD PROTEIN OR	CONDUCTINA YELLOW MOTTLE VIRUS (COTNO)		K E					
PYCE COYMV		COMMETTING YELLOW MOTTLE VIIIUS (CUTMY)							
24.474	HYPOTIGETICAL 13 KD PROTEIN (OF	POTATO VIRUS X (STRAIN XC) (PVX)							

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TABLE XV RESPIRATORY SYNCYTIAL VIRUS DP107 F2 REGION ANALOG CARBOXY TRUNCATIONS

X-YTS-Z X-YTSV-Z X-YTSVI-Z X-YTSVIT-Z X-YTSVITI-Z X-YTSVITIE-Z X-YTSVITIEL-Z X-YTSVITIELS-Z X-YTSVITIELSN-Z X-YTSVITIELSNI-Z X-YTSVITIELSNIK-Z X-YTSVITIELSNIKE-Z X-YTSVITIELSNIKEN-Z X-YTSVITIELSNIKENK-Z X-YTSVITIELSNIKENKC-Z X-YTSVITIELSNIKENKCN-Z X-YTSVITIELSNIKENKCNG-Z X-YTSVITIELSNIKENKCNGT-Z X-YTSVITIELSNIKENKCNGTD-Z X-YTSVITIELSNIKENKCNGTDA-Z X-YTSVITIELSNIKENKCNGTDAK-Z X-YTSVITIELSNIKENKCNGTDAKV-Z X-YTSVITIELSNIKENKCNGTDAKVK-Z X-YTSVITIELSNIKENKCNGTDAKVKL-Z X-YTSVITIELSNIKENKCNGTDAKVKLI-Z X-YTSVITIELSNIKENKCNGTDAKVKLIK-Z X-YTSVITIELSNIKENKCNGTDAKVKLIKQ-Z X-YTSVITIELSNIKENKCNGTDAKVKLIKQE-Z X-YTSVITIELSNIKENKCNGTDAKVKLIKOEL-Z X-YTSVITIELSNIKENKCNGTDAKVKLIKQELD-Z X-YTSVITIELSNIKENKCNGTDAKVKLIKQELDK-Z X-YTSVITIELSNIKENKCNGTDAKVKLIKQELDKY-Z 25 X-YTSVITIELSNIKENKCNGTDAKVKLIKQELDKYK-Z X-YTSVITIELSNIKENKCNGTDAKVKLIKQELDKYKN-Z X-YTSVITIELSNIKENKCNGTDAKVKLIKQELDKYKNA-Z X-YTSVITIELSNIKENKCNGTDAKVKLIKQELDKYKNAV-Z X-YTSVITIELSNIKENKCNGTDAKVKLIKQELDKYKNAVT-Z X-YTSVITIELSNIKENKCNGTDAKVKLIKQELDKYKNAVTE-Z X-YTSVITIELSNIKENKCNGTDAKVKLIKQELDKYKNAVTEL-Z X-YTSVITIELSNIKENKCNGTDAKVKLIKQELDKYKNAVTELQ-Z X-YTSVITIELSNIKENKCNGTDAKVKLIKQELDKYKNAVTELQL-Z X-YTSVITIELSNIKENKCNGTDAKVKLIKQELDKYKNAVTELQLL-Z X-YTSVITIELSNIKENKCNGTDAKVKLIKQELDKYKNAVTELQLLM-Z X-YTSVITIELSNIKENKCNGTDAKVKLIKQELDKYKNAVTELQLLMQ-Z X-YTSVITIELSNIKENKCNGTDAKVKLIKQELDKYKNAVTELQLLMQS-Z X-YTSVITIELSNIKENKCNGTDAKVKLIKQELDKYKNAVTELQLLMQST-Z

The one letter amino acid code is used.

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Additionally,

"X" may represent an amino group, a hydrophobic group, including but not limited to carbobenzoxyl, dansyl, or T-butyloxycarbonyl; an acetyl group; a 9-fluorenylmethoxy-carbonyl (FMOC) group; a macromolecular carrier group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.

"Z" may represent a carboxyl group; an amido group; a T-butyloxycarbonyl group; a macromolecular carrier group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.

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TABLE XVI RESPIRATORY SYNCYTIAL VIRUS F2 DP178/DP107 REGION ANALOG AMINO TRUNCATIONS

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X-OST-Z
                                                X-MQST-Z
                                               X-LMOST-Z
 5
                                              X-LLMOST-Z
                                             X-QLLMQST-Z
                                            X-LQLLMQST-Z
                                           X-ELQLLMQST-Z
                                          X-TELQLLMQST-Z
                                         X-VTELOLLMOST-Z
                                        X-AVTELQLLMQST-Z
10
                                       X-NAVTELQLLMQST-Z
                                      X-KNAVTELQLLMQST-Z
                                    X-YKNAVTELQLLMOST-Z
                                   X-KYKNAVTELQLLMQST-Z
                                  X-DKYKNAVTELQLLMQST-Z
                                 X-LDKYKNAVTELQLLMQST-Z
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15
                              X-KQELDKYKNAVTELQLLMQST-Z
                             X-IKQELDKYKNAVTELQLLMQST-Z
                            X-LIKQELDKYKNAVTELQLLMQST-Z
                           X-KLIKQELDKYKNAVTELQLLMQST-Z
                          X-VKLIKQELDKYKNAVTELOLLMOST-Z
                         X-KVKLIKQELDKYKNAVTELQLLMQST-Z
                        X-AKVKLIKQELDKYKNAVTELQLLMQST-Z
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                       X-DAKVKLIKOELDKYKNAVTELOLLMQST-Z
                      X-TDAKVKLIKOELDKYKNAVTELQLLMQST-Z
                     X-GTDAKVKLIKOELDKYKNAVTELQLLMQST-Z
                    X-NGTDAKVKLIKQELDKYKNAVTELQLLMQST-Z
                   X-CNGTDAKVKLIKQELDKYKNAVTELQLLMQST-Z
                  X-KCNGTDAKVKLIKQELDKYKNAVTELQLLMQST-Z
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              X-IKENKCNGTDAKVKLIKQELDKYKNAVTELQLLMQST-Z
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            X-SNIKENKCNGTDAKVKLIKQELDKYKNAVTELQLLMQST-Z
           X-LSNIKENKCNGTDAKVKLIKQELDKYKNAVTELQLLMQST-Z
          X-ELSNIKENKCNGTDAKVKLIKQELDKYKNAVTELQLLMQST-Z
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       X-ITIELSNIKENKCNGTDAKVKLIKQELDKYKNAVTELQLLMQST-Z
      X-VITIELSNIKENKCNGTDAKVKLIKQELDKYKNAVTELQLLMQST-Z
     X-SVITIELSNIKENKCNGTDAKVKLIKQELDKYKNAVTELQLLMQST-Z
    X-TSVITIELSNIKENKCNGTDAKVKLIKQELDKYKNAVTELQLLMQST-Z
```

The one letter amino acid code is used.

35 Additionally,

"X" may represent an amino group, a hydrophobic group, including but not limited to carbobenzoxyl, dansyl, or T-butyloxycarbonyl; an acetyl group; a 9-fluorenylmethoxy-carbonyl (FMOC) group; a macromolecular carrier group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.

"Z" may represent a carboxyl group; an amido group; a T-butyloxycarbonyl group; a macromolecular carrier group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.

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TABLE XVII RESPIRATORY SYNCYTIAL VIRUS F1 DP178 REGION ANALOG CARBOXY TRUNCATIONS

X-FYD-Z X-FYDP-Z X-FYDPL-Z 5 X-FYDPLV-Z X-FYDPLVF-Z X-FYDPLVFP-Z X-FYDPLVFPS-Z X-FYDPLVFPSD-Z X-FYDPLVFPSDE-Z X-FYDPLVFPSDEF-Z X-FYDPLVFPSDEFD-Z X-FYDPLVFPSDEFDA-Z X-FYDPLVFPSDEFDAS-Z X-FYDPLVFPSDEFDASI-Z X-FYDPLVFPSDEFDASIS-Z X-FYDPLVFPSDEFDASISO-Z X-FYDPLVFPSDEFDASISOV-Z X-FYDPLVFPSDEFDASISQVN-Z 15 X-FYDPLVFPSDEFDASISQVNE-Z X-FYDPLVFPSDEFDASISQVNEK-Z X-FYDPLVFPSDEFDASISOVNEKI-Z X-FYDPLVFPSDEFDASISQVNEKIN-Z X-FYDPLVFPSDEFDASISOVNEKINQ-Z X-FYDPLVFPSDEFDASISOVNEKINQS-Z X-FYDPLVFPSDEFDASISQVNEKINQSL-Z X-FYDPLVFPSDEFDASISQVNEKINQSLA-Z X-FYDPLVFPSDEFDASISQVNEKINQSLAF-Z X-FYDPLVFPSDEFDASISQVNEKINQSLAFI-Z X-FYDPLVFPSDEFDASISQVNEKINQSLAFIR-Z X-FYDPLVFPSDEFDASISQVNEKINQSLAFIRK-Z X-FYDPLVFPSDEFDASISQVNEKINQSLAFIRKS-Z X-FYDPLVFPSDEFDASISQVNEKINQSLAFIRKSD-Z X-FYDPLVFPSDEFDASISQVNEKINQSLAFIRKSDE-Z 25 X-FYDPLVFPSDEFDASISQVNEKINQSLAFIRKSDEL-Z X-FYDPLVFPSDEFDASISQVNEKINQSLAFIRKSDELL-Z

The one letter amino acid code is used.

Additionally,
"X" may represent an amino group, a hydrophobic group,
including but not limited to carbobenzoxyl, dansyl, or
T-butyloxycarbonyl; an acetyl group; a 9fluorenylmethoxy-carbonyl (FMOC) group; a
macromolecular carrier group including but not limited
to lipid-fatty acid conjugates, polyethylene glycol,
or carbohydrates.

"Z" may represent a carboxyl group; an amido group; a 35 T-butyloxycarbonyl group; a macromolecular carrier

group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.

TABLE XVIII RESPIRATORY SYNCYTIAL VIRUS F1 DP178 REGION ANALOG AMINO TRUNCATIONS

X-DELL-Z X-SDELL-Z X-KSDELL-Z 5 X-RKSDELL-2 X-IRKSDELL-Z X-FIRKSDELL-Z X-AFIRKSDELL-Z X-LAFIRKSDELL-Z X-SLAFIRKSDELL-Z X-QSLAFIRKSDELL-Z 10 X-NOSLAFIRKSDELL-Z X-INQSLAFIRKSDELL-Z X-KINOSLAFIRKSDELL-Z X-EKINQSLAFIRKSDELL-Z X-NEKINOSLAFIRKSDELL-Z X-VNEKINQSLAFIRKSDELL-Z X-OVNEKINOSLAFIRKSDELL-Z X-SOVNEKINOSLAFIRKSDELL-Z 15 X-ISOVNEKINOSLAFIRKSDELL-2 X-SISQVNEKINQSLAFIRKSDELL-Z X-ASISQVNEKINQSLAFIRKSDELL-Z X-DASISQVNEKINQSLAFIRKSDELL-Z X-FDASISQVNEKINQSLAFIRKSDELL-Z X-EFDASISQVNEKINQSLAFIRKSDELL-Z X-DEFDASISQVNEKINQSLAFIRKSDELL-Z 20 X-SDEFDASISQVNEKINQSLAFIRKSDELL-Z X-PSDEFDASISQVNEKINQSLAFIRKSDELL-Z X-FPSDEFDASISQVNEKINQSLAFIRKSDELL-Z X-VFPSDEFDASISQVNEKINQSLAFIRKSDELL-Z X-LVFPSDEFDASISQVNEKINQSLAFIRKSDELL-Z X-PLVFPSDEFDASISQVNEKINQSLAFIRKSDELL-Z X-DPLVFPSDEFDASISQVNEKINQSLAFIRKSDELL-Z X-YDPLVFPSDEFDASISQVNEKINQSLAFIRKSDELL-Z

The one letter amino acid code is used.

Additionally,
"X" may represent an amino group, a hydrophobic group,
including but not limited to carbobenzoxyl, dansyl, or
T-butyloxycarbonyl; an acetyl group; a 9fluorenylmethoxy-carbonyl (FMOC) group; a
macromolecular carrier group including but not limited
to lipid-fatty acid conjugates, polyethylene glycol,
or carbohydrates.

"Z" may represent a carboxyl group; an amido group; a T-butyloxycarbonyl group; a macromolecular carrier group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.

TABLE XIX HUMAN PARAINFLUENZA VIRUS 3 F1 REGION DP178 ANALOG CARBOXY TRUNCATIONS

X-ITL-Z X-ITLN-Z X-ITLNN-Z X-ITLNNS-Z X-ITLNNSV-Z X-ITLNNSVA-Z X-TTLNNSVAL-Z X-ITLNNSVALD-Z X-ITLNNSVALDP-Z X-ITLNNSVALDPI-Z X-ITLNNSVALDPID-Z X-ITLNNSVALDPIDI-Z X-ITLNNSVALDPIDIS-Z X-ITLNNSVALDPIDISI-Z X-ITLNNSVALDPIDISIE-Z X-ITLNNSVALDPIDISIEL-Z X-TTINNSVALDPIDISIELN-Z X-ITLNNSVALDPIDISIELNK-Z X-ITLNNSVALDPIDISIELNKA-Z X-ITLNNSVALDPIDISIELNKAK-Z X-ITLNNSVALDPIDISIELNKAKS-Z X-ITLNNSVALDPIDISIELNKAKSD-Z X-ITLNNSVALDPIDISIELNKAKSDL-Z X-ITLNNSVALDPIDISIELNKAKSDLE-Z X-ITLNNSVALDPIDISIELNKAKSDLEE-Z X-ITLNNSVALDPIDISIELNKAKSDLEES-Z 20 X-ITLNNSVALDPIDISIELNKAKSDLEESK-Z X-ITLNNSVALDPIDISIELNKAKSDLEESKE-Z X-ITLNNSVALDPIDISIELNKAKSDLEESKEW-Z X-ITLNNSVALDPIDISIELNKAKSDLEESKEWI-Z X-ITLNNSVALDPIDISIELNKAKSDLEESKEWIR-Z

The one letter amino acid code is used.

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X-ITLNNSVALDPIDISIELNKAKSDLEESKEWIRR-Z X-ITLNNSVALDPIDISIELNKAKSDLEESKEWIRRS-Z

Additionally,
"X" may represent an amino group, a hydrophobic group,
including but not limited to carbobenzoxyl, dansyl, or
T-butyloxycarbonyl; an acetyl group; a 9fluorenylmethoxy-carbonyl (FMOC) group; a
macromolecular carrier group including but not limited
to lipid-fatty acid conjugates, polyethylene glycol,
or carbohydrates.

"Z" may represent a carboxyl group; an amido group; a T-butyloxycarbonyl group; a macromolecular carrier group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.

TABLE XX HUMAN PARAINFLUENZA VIRUS 3 F1 REGION DP178 ANALOG AMINO TRUNCATIONS

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X-RRS-Z
                                  X-IRRS-Z
                                 X-WIRRS-Z
5
                                X-EWIRRS-Z
                                X-KEWIRRS-Z
                              X-SKEWIRRS-Z
                             X-ESKEWIRRS-Z
                            X-EESKEWIRRS-Z
                            X-LEESKEWIRRS-Z
                          X-DLEESKEWIRRS-Z
10
                         X-SDLEESKEWIRRS-Z
                        X-KSDLEESKEWIRRS-Z
                       X-AKSDLEESKEWIRRS-Z
                      X-KAKSDLEESKEWIRRS-Z
                     X-NKAKSDLEESKEWIRRS-Z
                    X-LNKAKSDLEESKEWIRRS-Z
                   X-ELNKAKSDLEESKEWIRRS-Z
                  X-IELNKAKSDLEESKEWIRRS-Z
15
                 X-SIELNKAKSDLEESKEWIRRS-2
                X-ISIELNKAKSDLEESKEWIRRS-Z
               X-DISIELNKAKSDLEESKEWIRRS-Z
              X-IDISIELNKAKSDLEESKEWIRRS-Z
             X-PIDISIELNKAKSDLEESKEWIRRS-Z
            X-DPIDISIELNKAKSDLEESKEWIRRS-Z
           X-LDPIDISIELNKAKSDLEESKEWIRRS-Z
20
          X-ALDPIDISIELNKAKSDLEESKEWIRRS-Z
         X-VALDPIDISIELNKAKSDLEESKEWIRRS-Z
        X-SVALDPIDISIELNKAKSDLEESKEWIRRS-Z
       X-NSVALDPIDISIELNKAKSDLEESKEWIRRS-Z
      X-NNSVALDPIDISIELNKAKSDLEESKEWIRRS-Z
     X-LNNSVALDPIDISIELNKAKSDLEESKEWIRRS-Z
    X-TLNNSVALDPIDISIELNKAKSDLEESKEWIRRS-Z
25
```

The one letter amino acid code is used.

Additionally,
"X" may represent an amino group, a hydrophobic group,
including but not limited to carbobenzoxyl, dansyl, or
T-butyloxycarbonyl; an acetyl group; a 9fluorenylmethoxy-carbonyl (FMOC) group; a
macromolecular carrier group including but not limited
to lipid-fatty acid conjugates, polyethylene glycol,
or carbohydrates.

"Z" may represent a carboxyl group; an amido group; a T-butyloxycarbonyl group; a macromolecular carrier group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.

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TABLE XXI HUMAN PARAINFLUENZA VIRUS 3 F1 REGION DP107 ANALOG CARBOXY TRUNCATIONS

X-ALG-Z

X-ALGV-2

X-ALGVA-Z

X-ALGVAT-Z

X-ALGVATS-Z

X-ALGVATSA-Z

X-ALGVATSAQ-Z

X-ALGVATSAQI-Z

X-ALGVATSAQIT-Z

X-ALGVATSAQITA-Z

X-ALGVATSAQITAA-Z

X-ALGVATSAQITAAV-Z

X-ALGVATSAQITAAVA-Z

X-ALGVATSAQITAAVAL-Z

X-ALGVATSAQITAAVALV-Z

X-ALGVATSAQITAAVALVE-Z X-ALGVATSAQITAAVALVEA-Z

X-ALGVATSAQITAAVALVEAK-Z

X-ALGVATSAQITAAVALVEAKQ-Z

X-ALGVATSAQITAAVALVEAKQA-Z X-ALGVATSAQITAAVALVEAKQAR-Z

X-ALGVATSAQITAAVALVEAKQARS-Z

X-ALGVATSAQITAAVALVEAKQARSD-Z X-ALGVATSAQITAAVALVEAKQARSDI-Z

X-ALGVATSAQITAAVALVEAKQARSDIE-Z

X-ALGVATSAQITAAVALVEAKQARSDIEK-Z

20

X-ALGVATSAQITAAVALVEAKQARSDIEKL-Z

X-ALGVATSAQITAAVALVEAKQARSDIEKLK-Z X-ALGVATSAQITAAVALVEAKQARSDIEKLKE-Z

X-ALGVATSAQITAAVALVEAKQARSDIEKLKEA-Z

X-ALGVATSAQITAAVALVEAKQARSDIEKLKEAI-Z

X-ALGVATSAQITAAVALVEAKQARSDIEKLKEAIR-Z

25 The one letter amino acid code is used.

Additionally, "X" may represent an amino group, a hydrophobic group, including but not limited to carbobenzoxyl, dansyl, or

T-butyloxycarbonyl; an acetyl group; a 9fluorenylmethoxy-carbonyl (FMOC) group; a

macromolecular carrier group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.

"Z" may represent a carboxyl group; an amido group; a T-butyloxycarbonyl group; a macromolecular carrier group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.

TABLE XXII HUMAN PARAINFLUENZA VIRUS 3 F1 REGION DP107 ANALOG AMINO TRUNCATIONS

```
X-IRD-Z
                                  X-AIRD-Z
                                 X-EAIRD-Z
                                X-KEAIRD-Z
                               X-LKEAIRD-Z
                              X-KLKEAIRD-Z
                             X-EKLKEAIRD-Z
                            X-IEKLKEAIRD-Z
                           X-DIEKLKEAIRD-Z
                          X-SDIEKLKEAIRD-Z
10
                         X-RSDIEKLKEAIRD-Z
                        X-ARSDIEKLKEAIRD-Z
                       X-OARSDIEKLKEAIRD-Z
                      X-KQARSDIEKLKEAIRD-Z
                     X-AKQARSDIEKLKEAIRD-Z
                    X-EAKQARSDIEKLKEAIRD-Z
                   X-VEAKQARSDIEKLKEAIRD-Z
15
                  X-LVEAKQARSDIEKLKEAIRD-Z
                 X-ALVEAKOARSDIEKLKEAIRD-Z
                X-VALVEAKOARSDIEKLKEAIRD-Z
               X-AVALVEAKOARSDIEKLKEAIRD-Z
              X-AAVALVEAKQARSDIEKLKEAIRD-Z
             X-TAAVALVEAKQARSDIEKLKEAIRD-Z
            X-ITAAVALVEAKQARSDIEKLKEAIRD-Z
           X-QITAAVALVEAKQARSDIEKLKEAIRD-Z
20
          X-AQITAAVALVEAKQARSDIEKLKEAIRD-Z
         X-SAQITAAVALVEAKQARSDIEKLKEAIRD-Z
        X-TSAQITAAVALVEAKQARSDIEKLKEAIRD-Z
       X-ATSAQITAAVALVEAKQARSDIEKLKEAIRD-Z
      X-VATSAQITAAVALVEAKQARSDIEKLKEAIRD-Z
     X-GVATSAQITAAVALVEAKQARSDIEKLKEAIRD-Z
    X-LGVATSAQITAAVALVEAKQARSDIEKLKEAIRD-Z
25
```

The one letter amino acid code is used.

Additionally,

"X" may represent an amino group, a hydrophobic group, including but not limited to carbobenzoxyl, dansyl, or T-butyloxycarbonyl; an acetyl group; a 9-fluorenylmethoxy-carbonyl (FMOC) group; a macromolecular carrier group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.

"Z" may represent a carboxyl group; an amido group; a T-butyloxycarbonyl group; a macromolecular carrier group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.

TABLE XXIII REPRESENTATIVE DP107/DP178 ANALOG ANTIVIRAL PEPTIDES

Anti-Respiratory syncytial virus peptides

- X-TSVITIELSNIKENKCNGTDAKVKLIKQELDKYKN-Z
- X-SVITIELSNIKENKCNGTDAKVKLIKQELDKYKNA-Z
- 5 X-VITIELSNIKENKCNGTDAKVKLIKQELDKYKNAV-Z
 - X-VAVSKVLHLEGEVNKIALLSTNKAVVSLSNGVS-Z
 - X-AVSKVLHLEGEVNKIALLSTNKAVVSLSNGVSV-Z
 - X-VSKVLHLEGEVNKIALLSTNKAVVSLSNGVSVL-Z
 - X-SKVLHLEGEVNKIALLSTNKAVVSLSNGVSVLT-Z
 - X-KVLHLEGEVNKIALLSTNKAVVSLSNGVSVLTS-Z
 - X-LEGEVNKIALLSTNKAVVSLSNGVSVLTSKVLD-Z X-GEVNKIALLSTNKAVVSLSNGVSVLTSKVLDLK-Z
- 10 X-EVNKIALLSTNKAVVSLSNGVSVLTSKVLDLKN-2
 - x-vnkiallstnkavvslsngvsvltskvldlkny-z
 - X-NKIALLSTNKAVVSLSNGVSVLTSKVLDLKNYI-Z
 - X-KIALLSTNKAVVSLSNGVSVLTSKVLDLKNYID-Z
 - X-IALLSTNKAVVSLSNGVSVLTSKVLDLKNYIDK-Z
 - X-ALLSTNKAVVSLSNGVSVLTSKVLDLKNYIDKO-Z
 - X-VAVSKVLHLEGEVNKIALLSTNKAVVSLSNGVS-Z
 - 5 X-AVSKVLHLEGEVNKIALLSTNKAVVSLSNGVSV-Z
- X-VSKVLHLEGEVNKIALLSTNKAVVSLSNGVSVL-Z
 - X-SKVLHLEGEVNKIALLSTNKAVVSLSNGVSVLT-Z
 - X-KVLHLEGEVNKIALLSTNKAVVSLSNGVSVLTS-Z
 - X-LEGEVNKIALLSTNKAVVSLSNGVSVLTSKVLD-Z
 - X-GEVNKIALLSTNKAVVSLSNGVSVLTSKVLDLK-Z
 - X-EVNKIALLSTNKAVVSLSNGVSVLTSKVLDLKN-Z
- X-VNKIALLSTNKAVVSLSNGVSVLTSKVLDLKNY-Z
 - X-NKIALLSTNKAVVSLSNGVSVLTSKVLDLKNYI-Z
 - X-KIALLSTNKAVVSLSNGVSVLTSKVLDLKNYID-2
 - X-IALLSTNKAVVSLSNGVSVLTSKVLDLKNYIDK-Z
 - X-ALLSTNKAVVSLSNGVSVLTSKVLDLKNYIDKQ-Z

Anti-human parainfluenza virus 3 peptides

- 25 X-TLNNSVALDPIDISIELNKAKSDLEESKEWIRRSN-Z
 - X-LNNSVALDPIDISIELNKAKSDLEESKEWIRRSNQ-Z
 - X-NNSVALDPIDISIELNKAKSDLEESKEWIRRSNQK-Z
 - X-NSVALDPIDISIELNKAKSDLEESKEWIRRSNQKL-Z
 - X-SVALDPIDISIELNKAKSDLEESKEWIRRSNQKLD-Z
 - X-VALDPIDISIELNKAKSDLEESKEWIRRSNQKLDS-Z
 - X-ALDPIDISIELNKAKSDLEESKEWIRRSNQKLDSI-Z
- X-LDPIDISIELNKAKSDLEESKEWIRRSNQKLDSIG-Z
 - X-DPIDISIELNKAKSDLEESKEWIRRSNQKLDSIGN-Z
 - X-PIDISIELNKAKSDLEESKEWIRRSNQKLDSIGNW-Z X-IDISIELNKAKSDLEESKEWIRRSNQKLDSIGNWH-Z
 - X-IDISIELNKAKSDLEESKEWIRRSNQKLDSIGNWHQ-Z
 - X-ISIELNKAKSDLEESKEWIRRSNQKLDSIGNWHQS-Z
 - X-SIELNKAKSDLEESKEWIRRSNQKLDSIGNWHQSS-Z
 - X-IELNKAKSDLEESKEWIRRSNQKLDSIGNWHQSST-Z
- 35 X-ELNKAKSDLEESKEWIRRSNQKLDSIGNWHQSSTT-Z
- X-TAAVALVEAKQARSDIEKLKEAIRDTNKAVQSVQS-Z

- X-AVALVEAKQARSDIEKLKEAIRDTNKAVQSVQSSI-Z
 X-LVEAKQARSDIEKLKEAIRDTNKAVQSVQSSIGNL-Z
 X-VEAKQARSDIEKLKEAIRDTNKAVQSVQSSIGNLI-Z
 X-EAKQARSDIEKLKEAIRDTNKAVQSVQSSIGNLIV-Z
 X-AKQARSDIEKLKEAIRDTNKAVQSVQSSIGNLIVA-Z
 X-KQARSDIEKLKEAIRDTNKAVQSVQSSIGNLIVAIK-Z
 X-QARSDIEKLKEAIRDTNKAVQSVQSSIGNLIVAIK-Z
 X-ARSDIEKLKEAIRDTNKAVQSVQSSIGNLIVAIKS-Z
 X-RSDIEKLKEAIRDTNKAVQSVQSSIGNLIVAIKSV-Z
 X-SDIEKLKEAIRDTNKAVQSVQSSIGNLIVAIKSVQ-Z
 X-KLKEAIRDTNKAVQSVQSSIGNLIVAIKSVQDYVN-Z
 X-LKEAIRDTNKAVQSVQSSIGNLIVAIKSVQDYVNK-Z
 X-AIRDTNKAVQSVQSSIGNLIVAIKSVQDYVNK-Z
- Anti-simian immunodeficiency virus peptides
 - X-WQEWERKVDFLEENITALLEEAQIQQEKNMYELQK-Z
 X-QEWERKVDFLEENITALLEEAQIQQEKNMYELQKL-Z
 X-EWERKVDFLEENITALLEEAQIQQEKNMYELQKLN-Z
 X-WERKVDFLEENITALLEEAQIQQEKNMYELQKLNS-Z
 X-ERKVDFLEENITALLEEAQIQQEKNMYELQKLNSWD-Z
 X-RKVDFLEENITALLEEAQIQQEKNMYELQKLNSWDV-Z
 X-VDFLEENITALLEEAQIQQEKNMYELQKLNSWDVF-Z
 X-VDFLEENITALLEEAQIQQEKNMYELQKLNSWDVF-Z
 X-DFLEENITALLEEAQIQQEKNMYELQKLNSWDVFG-Z
 X-FLEENITALLEEAQIQQEKNMYELQKLNSWDVFG-Z

Anti-measles virus peptides

X-LHRIDLGPPISLERLDVGTNLGNAIAKLEAKELL-Z
X-HRIDLGPPISLERLDVGTNLGNAIAKLEAKELLE-Z
X-RIDLGPPISLERLDVGTNLGNAIAKLEAKELLES-Z
X-IDLGPPISLERLDVGTNLGNAIAKLEAKELLESSD-Z
X-DLGPPISLERLDVGTNLGNAIAKLEAKELLESSD-Z
X-LGPPISLERLDVGTNLGNAIAKLEAKELLESSDQ-Z
X-GPPISLERLDVGTNLGNAIAKLEAKELLESSDQIL-Z
X-PPISLERLDVGTNLGNAIAKLEAKELLESSDQIL-Z
X-PISLERLDVGTNLGNAIAKLEAKELLESSDQILR-Z
X-SLERLDVGTNLGNAIAKLEAKELLESSDQILRSM-Z
X-LERLDVGTNLGNAIAKLEAKELLESSDQILRSMK-Z

The one letter amino acid code is used.

Additionally,
"X" may represent an amino group, a hydrophobic group, including but not limited to carbobenzoxyl, dansyl, or T-butyloxycarbonyl; an acetyl group; a 9-fluorenylmethoxy-carbonyl (FMOC) group; a macromolecular carrier group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.

"Z" may represent a carboxyl group; an amido group; a T-butyloxycarbonyl group; a macromolecular carrier group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.

5.4. SYNTHESIS OF PEPTIDES

The peptides of the invention may be synthesized or prepared by techniques well known in the art. See, for example, Creighton, 1983, Proteins: Structures and Molecular Principles, W.H. Freeman and Co., NY, which is incorporated herein by reference in its entirety. Short peptides, for example, can be synthesized on a solid support or in solution. Longer peptides may be made using recombinant DNA techniques. 10 Here, the nucleotide sequences encoding the peptides of the invention may be synthesized, and/or cloned, and expressed according to techniques well known to those of ordinary skill in the art. See, for example, Sambrook, et al., 1989, Molecular Cloning, A 15 Laboratory Manual, Vols. 1-3, Cold Spring Harbor Press, NY.

The peptides of the invention may alternatively be synthesized such that one or more of the bonds which link the amino acid residues of the peptides are 20 non-peptide bonds. These alternative non-peptide bonds may be formed by utilizing reactions well known to those in the art, and may include, but are not limited to imino, ester, hydrazide, semicarbazide, and azo bonds, to name but a few. In yet another 25 embodiment of the invention, peptides comprising the sequences described above may be synthesized with additional chemical groups present at their amino and/or carboxy termini, such that, for example, the stability, bioavailability, and/or inhibitory activity 30 of the peptides is enhanced. For example, hydrophobic groups such as carbobenzoxyl, dansyl, or tbutyloxycarbonyl groups, may be added to the peptides' amino termini. Likewise, an acetyl group or a 9fluorenylmethoxy-carbonyl group may be placed at the 35 peptides' amino termini. (See "X" in Tables I to IV,

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above.) Additionally, the hydrophobic group, tbutyloxycarbonyl, or an amido group may be added to the peptides' carboxy termini. (See "Z" in Tables I to IV, above.)

Further, the peptides of the invention may be synthesized such that their steric configuration is altered. For example, the D-isomer of one or more of the amino acid residues of the peptide may be used, rather than the usual L-isomer.

Still further, at least one of the amino acid residues of the peptides of the invention may be substituted by one of the well known non-naturally occurring amino acid residues. Alterations such as these may serve to increase the stability, bioavailability and/or inhibitory action of the peptides of the invention.

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Any of the peptides described above may, additionally, have a macromolecular carrier group covalently attached to their amino and/or carboxy termini. Such macromolecular carrier groups may include, for example, lipid-fatty acid conjugates, polyethylene glycol, carbohydrates or additional peptides. "X", in Tables I to IV, above, may therefore additionally represent any of the above macromolecular carrier groups covalently attached to the amino terminus of a peptide, with an additional 25 peptide group being preferred. Likewise, "Z", in Tables I to IV, may additionally represent any of the macromolecular carrier groups described above.

ASSAYS FOR ANTI-MEMBRANE FUSION ACTIVITY 30 5.5. Described herein, are methods for ability of a compound, such as the peptides of the invention, to inhibit membrane fusion events. Specifically, assays for cell fusion events are described in Section 5.5.1,

below, and assays for antiviral activity are described in Section 5.5.2, below.

5.5.1 ASSAYS FOR CELL FUSION EVENTS

Assays for cell fusion events are well known to those of skill in the art, and may be used in conjunction, for example, with the peptides of the invention to test the peptides' antifusogenic capabilities.

vitro. Such an assay may comprise culturing cells which, in the absence of any treatment would undergo an observable level of syncytial formation. For example, uninfected cells may be incubated in the presence of cells chronically infected with a virus that induces cell fusion. Such viruses may include, but are not limited to, HIV, SIV, or respiratory syncytial virus.

For the assay, cells are incubated in the presence of a peptide to be assayed. For each peptide, a range of peptide concentrations may be tested. This range should include a control culture wherein no peptide has been added.

Standard conditions for culturing cells, well known to those of ordinary skill in the art, are used. After incubation for an appropriate period (24 hours at 37°C, for example) the culture is examined microscopically for the presence of multinucleated giant cells, which are indicative of cell fusion and syncytial formation. Well known stains, such as crystal violet stain, may be used to facilitate the visualization of syncytial formation.

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5.5.2 ASSAYS FOR ANTIVIRAL ACTIVITY

The antiviral activity exhibited by the peptides of the invention may be measured, for example, by

easily performed in vitro assays, such as those described below, which can test the peptides' ability to inhibit syncytia formation, or their ability to inhibit infection by cell-free virus. Using these assays, such parameters as the relative antiviral activity of the peptides, exhibit against a given strain of virus and/or the strain specific inhibitory activity of the peptide can be determined.

A cell fusion assay may be utilized to test the peptides' ability to inhibit viral-induced, such as 10 HIV-induced, syncytia formation in vitro. Such an assay may comprise culturing uninfected cells in the presence of cells chronically infected with a syncytial-inducing virus and a peptide to be assayed. For each peptide, a range of peptide concentrations 15 may be tested. This range should include a control culture wherein no peptide has been added. Standard conditions for culturing, well known to those of ordinary skill in the art, are used. After incubation for an appropriate period (24 hours at 37°C, for 20 example) the culture is examined microscopically for the presence of multinucleated giant cells, which are indicative of cell fusion and syncytia formation. Well known stains, such as crystal violet stain, may be used to facilitate syncytial visualization. Taking HIV as an example, such an assay would comprise CD-4+ cells (such as Molt or CEM cells, for example) cultured in the presence of chronically HIV-infected cells and a peptide to be assayed.

Other well known characteristics of viral infection may also be assayed to test a peptide's antiviral capabilities. Once again taking HIV as an example, a reverse transcriptase (RT) assay may be utilized to test the peptides' ability to inhibit infection of CD-4⁺ cells by cell-free HIV. Such an assay may comprise culturing an appropriate

concentration (i.e., TCID₅₀) of virus and CD-4+ cells in the presence of the peptide to be tested. Culture conditions well known to those in the art are used. As above, a range of peptide concentrations may be used, in addition to a control culture wherein no peptide has been added. After incubation for an appropriate period (e.g., 7 days) of culturing, a cell-free supernatant is prepared, using standard procedures, and tested for the present of RT activity as a measure of successful infection. The RT activity may be tested using standard techniques such as those described by, for example, Goff et al. (Goff, S. et al., 1981, J. Virol. 38:239-248) and/or Willey et al. (Willey, R. et al., 1988, J. Virol. 62:139-147). These references are incorporated herein by reference 15 in their entirety.

Standard methods which are well-known to those of skill in the art may be utilized for assaying nonretroviral activity. See, for example, Pringle et al. (Pringle, C.R. et al., 1985, J. Medical Virology 17:377-386) for a discussion of respiratory syncytial 20 virus and parainfluenza virus activity assay techniques. Further, see, for example, "Zinsser Microbiology", 1988, Joklik, W.K. et al., eds., Appleton & Lange, Norwalk, CT, 19th ed., for a general 25 review of such techniques. These references are incorporated by reference herein in their entirety. In addition, the Examples presented below, in Sections 17, 18, 26 and 27 each provide additional assays for the testing of a compound's antiviral capability.

In vivo assays may also be utilized to test, for example, the antiviral activity of the peptides of the invention. To test for anti-HIV activity, for example, the in vivo model described in Barnett et al. (Barnett, S.W. et al., 1994, Science 266:642-646) may be used.

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Additionally, anti-RSV activity can be assayed in vivo via well known mouse models. For example, RSV can be administered intranasally to mice of various inbred strains. Virus replicates in lungs of all strains, but the highest titers are obtained in P/N, C57L/N and DBA/2N mice. Infection of BALB/c mice produces an asymptomatic bronchiolitis characterized by lymphocytic infiltrates and pulmonary virus titers of 10⁴ to 10⁵ pfu/g of lung tissue (Taylor, G. et al., 1984, Infect. Immun. 43:649-655).

Cotton rat models of RSV are also well known.

Virus replicates to high titer in the nose and lungs of the cotton rat but produces few if any signs of inflammation.

5.6. USES OF THE PEPTIDES OF THE INVENTION

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The peptides of the invention may be utilized as antifusogenic or antiviral compounds, or as compounds which modulate intracellular processes involving coiled coil peptide structures. Further, such peptides may be used to identify agents which exhibit antifusogenic, antiviral or intracellular modulatory activity. Still further, the peptides of the invention may be utilized as organism or viral type/subtype-specific diagnostic tools.

The antifusogenic capability of the peptides of the invention may additionally be utilized to inhibit or treat/ameliorate symptoms caused by processes involving membrane fusion events. Such events may include, for example, virus transmission via cell-cell fusion, abnormal neurotransmitter exchange via cell-fusion, and sperm-egg fusion. Further, the peptides of the invention may be used to inhibit free viral, such as retroviral, particularly HIV, transmission to uninfected cells wherein such viral infection involves membrane fusion events or involves fusion of a viral

structure with a cell membrane. Among the intracellular disorders involving coiled coil peptides structures which may be ameliorated by the peptides of the invention are disorders involving, for example, bacterial toxins.

With respect to antiviral activity, the viruses whose transmission may be inhibited by the peptides of the invention include, but are not limited to all strains of the viruses listed above, in Tables V through VII, and IX through XIV.

These viruses include, for example, human retroviruses, particularly HIV-1 and HIV-2 and the human T-lymphocyte viruses (HTLV-I and II). The non-human retroviruses whose transmission may be inhibited by the peptides of the invention include, but are not limited to bovine leukosis virus, feline sarcoma and leukemia viruses, simian immunodeficiency, sarcoma and leukemia viruses, and sheep progress pneumonia viruses.

Non retroviral viruses whose transmission may be inhibited by the peptides of the invention include, but are not limited to human respiratory syncytial virus, canine distemper virus, newcastle disease virus, human parainfluenza virus, influenza viruses, measles viruses, Epstein-Barr viruses, hepatitis B viruses, and simian Mason-Pfizer viruses.

Non enveloped viruses whose transmission may be inhibited by the peptides of the invention include, but are not limited to picornaviruses such as polio viruses, hepatitis A virus, enterovirus, echoviruses and coxsackie viruses, papovaviruses such as papilloma virus, parvoviruses, adenoviruses and reoviruses.

As discussed more fully, below, in Section 5.5.1 and in the Example presented, below, in Section 8, DP107, DP178, DP107 analog and DP178 analog peptides form non-covalent protein-protein interactions which

are required for normal activity of the virus. Thus, the peptides of the invention may also be utilized as components in assays for the identification of compounds that interfere with such protein-protein interactions and may, therefore, act as antiviral agents. These assays are discussed, below, in Section 5.5.1.

As demonstrated in the Example presented below in Section 6, the antiviral activity of the peptides of the invention may show a pronounced type and subtype 10 specificity, i.e., specific peptides may be effective in inhibiting the activity of only specific viruses. This feature of the invention presents many advantages. One such advantage, for example, lies in the field of diagnostics, wherein one can use the 15 antiviral specificity of the peptide of the invention to ascertain the identity of a viral isolate. With respect to HIV, one may easily determine whether a viral isolate consists of an HIV-1 or HIV-2 strain. For example, uninfected CD-4+ cells may be co-infected 20 with an isolate which has been identified as containing HIV the DP178 (SEQ ID:1) peptide, after which the retroviral activity of cell supernatants may be assayed, using, for example, the techniques described above in Section 5.2. Those isolates whose 25 retroviral activity is completely or nearly completely inhibited contain HIV-1. Those isolates whose viral activity is unchanged or only reduced by a small amount, may be considered to not contain HIV-1. Such an isolate may then be treated with one or more of the 30 other DP178 peptides of the invention, and subsequently be tested for its viral activity in order to determine the identify of the viral isolate. DP107 and DP178 analogs of the invention may also be utilized in a diagnostic capacity specific to the type 35 and subtype of virus or organism in which the specific

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peptide sequence is found. A diagnostic procedure as described, above, for DP178, may be used in conjunction with the DP107/DP178 analog of interest.

5.5.1. SCREENING ASSAYS

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As demonstrated in the Example presented in Section 8, below, DP107 and DP178 portions of the TM protein gp41 form non-covalent protein-protein interactions. As is also demonstrated, the maintenance of such interactions is necessary for normal viral infectivity. Thus, compounds which bind DP107, bind DP178, and/or act to disrupt normal DP107/DP178 protein-protein interactions may act as antifusogenic, antiviral or cellular modulatory agents. Described below are assays for the identification of such compounds. Note that, while, for ease and clarity of discussion, DP107 and DP178 peptides will be used as components of the assays described, but it is to be understood that any of the DP107 analog or DP178 analog peptides described, 20 above, in Sections 5.1 through 5.3 may also be

utilized as part of these screens for compounds.

Compounds which may be tested for an ability to bind DP107, DP178, and/or disrupt DP107/DP178 interactions, and which therefore, potentially represent antifusogenic, antiviral or intracellular modulatory compounds, include, but are not limited to, peptides made of D- and/or L-configuration amino acids (in, for example, the form of random peptide libraries; see Lam, K.S. et al., 1991, Nature 354:82-84), phosphopeptides (in, for example, the form of random or partially degenerate, directed phosphopeptide libraries; see, for example, Songyang, Z. et al., 1993, Cell 72:767-778), antibodies, and small organic or inorganic molecules. Synthetic compounds, natural products, and other sources of

potentially effective materials may be screened in a variety of ways, as described in this Section.

The compounds, antibodies, or other molecules identified may be tested, for example, for an ability to inhibit cell fusion or viral activity, utilizing, for example, assays such as those described, above, in Section 5.5.

Among the peptides which may be tested are soluble peptides comprising DP107 and/or DP178 domains, and peptides comprising DP107 and/or DP178 domains having one or more mutations within one or both of the domains, such as the M41-P peptide described, below, in the Example presented in Section 8, which contains a isoleucine to proline mutation within the DP178 sequence.

In one embodiment of such screening methods is a method for identifying a compound to be tested for antiviral ability comprising:

- (a) exposing at least one compound to a peptide comprising a DP107 peptide for a time sufficient to allow binding of the compound to the DP107 peptide;
 - (b) removing non-bound compounds; and
 - (c) determining the presence of the compound bound to the DP107 peptide,
- thereby identifying an agent to be tested for antiviral ability.

In a second embodiment of such screening methods is a method for identifying a compound to be tested for antiviral ability comprising:

- (a) exposing at least one compound to a peptide comprising a DP178 peptide for a time sufficient to allow binding of the compound to the DP178 peptide;
 - (b) removing non-bound compounds; and

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(c) determining the presence of the compound bound to the DP178 peptide, thereby identifying an agent to be tested for antiviral ability.

One method utilizing these types of approaches that may be pursued in the isolation of such DP107binding or DP178-binding compounds is an assay which would include the attachment of either the DP107 or the DP178 peptide to a solid matrix, such as, for example, agarose or plastic beads, microtiter plate 10 wells, petri dishes, or membranes composed of, for example, nylon or nitrocellulose. In such an assay system, either the DP107 or DP178 protein may be anchored onto a solid surface, and the compound, or test substance, which is not anchored, is labeled, 15 either directly or indirectly. In practice, microtiter plates are conveniently utilized. anchored component may be immobilized by non-covalent or covalent attachments. Non-covalent attachment may be accomplished simply by coating the solid surface 20 with a solution of the protein and drying.

Alternatively, an immobilized antibody, preferably a monoclonal antibody, specific for the protein may be used to anchor the protein to the solid surface. The surfaces may be prepared in advance and stored.

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In order to conduct the assay, the labeled compound is added to the coated surface containing the anchored DP107 or DP178 peptide. After the reaction is complete, unreacted components are removed (e.g., by washing) under conditions such that any complexes formed will remain immobilized on the solid surface. The detection of complexes anchored on the solid surface can be accomplished in a number of ways. Where the compound is pre-labeled, the detection of label immobilized on the surface indicates that

complexes were formed. Where the labeled component is not pre-labeled, an indirect label can be used to detect complexes anchored on the surface; <u>e.g.</u>, using a labeled antibody specific for the compound (the antibody, in turn, may be directly labeled or indirectly labeled with a labeled anti-Ig antibody).

Alternatively, such an assay can be conducted in a liquid phase, the reaction products separated from unreacted components, and complexes detected; e.g., using an immobilized antibody specific for DP107 or DP178, whichever is appropriate for the given assay, or ab antibody specific for the compound, i.e., the test substance, in order to anchor any complexes formed in solution, and a labeled antibody specific for the other member of the complex to detect anchored complexes.

By utilizing procedures such as this, large numbers of types of molecules may be simultaneously screened for DP107 or DP178-binding capability, and thus potential antiviral activity.

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Further, compounds may be screened for an ability to inhibit the formation of or, alternatively, disrupt DP107/DP178 complexes. Such compounds may then be tested for antifusogenic, antiviral or intercellular modulatory capability. For ease of description, DP107 and DP178 will be referred to as "binding partners." Compounds that disrupt such interactions may exhibit antiviral activity. Such compounds may include, but are not limited to molecules such as antibodies, peptides, and the like described above.

The basic principle of the assay systems used to identify compounds that interfere with the interaction between the DP107 and DP178 peptides involves preparing a reaction mixture containing peptides under conditions and for a time sufficient to allow the two peptides to interact and bind, thus forming a complex.

In order to test a compound for disruptive activity, the reaction is conducted in the presence and absence of the test compound, i.e., the test compound may be initially included in the reaction mixture, or added at a time subsequent to the addition of one of the binding partners; controls are incubated without the test compound or with a placebo. The formation of any complexes between the binding partners is then detected. The formation of a complex in the control reaction, but not in the reaction mixture containing the test compound indicates that the compound interferes with the interaction of the DP107 and DP178 peptides.

The assay for compounds that interfere with the interaction of the binding partners can be conducted 15 in a heterogeneous or homogeneous format. Heterogeneous assays involve anchoring one of the binding partners onto a solid phase and detecting complexes anchored on the solid phase at the end of the reaction. In homogeneous assays, the entire 20 reaction is carried out in a liquid phase. In either approach, the order of addition of reactants can be varied to obtain different information about the compounds being tested. For example, test compounds that interfere with the interaction between the binding partners, e.g., by competition, can be identified by conducting the reaction in the presence of the test substance; i.e., by adding the test substance to the reaction mixture prior to or simultaneously with the binding partners. On the other hand, test compounds that disrupt preformed complexes, e.g. compounds with higher binding constants that displace one of the binding partners from the complex, can be tested by adding the test compound to the reaction mixture after complexes have

been formed. The various formats are described briefly below.

In a heterogeneous assay system, one binding partner, e.g., either the DP107 or DP178 peptide, is anchored onto a solid surface, and its binding partner, which is not anchored, is labeled, either directly or indirectly. In practice, microtiter plates are conveniently utilized. The anchored species may be immobilized by non-covalent or covalent attachments. Non-covalent attachment may be accomplished simply by coating the solid surface with a solution of the protein and drying. Alternatively, an immobilized antibody specific for the protein may be used to anchor the protein to the solid surface. The surfaces may be prepared in advance and stored.

In order to conduct the assay, the binding partner of the immobilized species is added to the coated surface with or without the test compound. After the reaction is complete, unreacted components are removed (e.g., by washing) and any complexes formed will remain immobilized on the solid surface. The detection of complexes anchored on the solid surface can be accomplished in a number of ways. Where the binding partner was pre-labeled, the detection of label immobilized on the surface indicates that complexes were formed. Where the binding partner is not pre-labeled, an indirect label can be used to detect complexes anchored on the surface; e.g., using a labeled antibody specific for the binding partner (the antibody, in turn, may be directly labeled or indirectly labeled with a labeled anti-Ig antibody). Depending upon the order of addition of reaction components, test compounds which inhibit complex formation or which disrupt preformed complexes can be detected.

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Alternatively, the reaction can be conducted in a liquid phase in the presence or absence of the test compound, the reaction products separated from unreacted components, and complexes detected; e.g., using an immobilized antibody specific for one binding partner to anchor any complexes formed in solution, and a labeled antibody specific for the other binding partner to detect anchored complexes. Again, depending upon the order of addition of reactants to the liquid phase, test compounds which inhibit complex or which disrupt preformed complexes can be identified.

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In an alternate embodiment of the invention, a homogeneous assay can be used. In this approach, a preformed complex of the DP107 and DP178 peptides is prepared in which one of the binding partners is labeled, but the signal generated by the label is quenched due to complex formation (see, e.g., U.S. Patent No. 4,109,496 by Rubenstein which utilizes this approach for immunoassays). The addition of a test substance that competes with and displaces one of the binding partners from the preformed complex will result in the generation of a signal above background. In this way, test substances which disrupt DP-107/DP-178 protein-protein interaction can be identified.

In an alternative screening assay, test compounds may be assayed for the their ability to disrupt a DP178/DP107 interaction, as measured immunometrically using an antibody specifically reactive to a DP107/DP178 complex (i.e., an antibody that recognizes neither DP107 nor DP178 individually). Such an assay acts as a competition assay, and is based on techniques well known to those of skill in the art.

The above competition assay may be described, by way of example, and not by way of limitation, by using the DP178 and M41 Δ 178 peptides and by assaying test

compounds for the disruption of the complexes formed by these two peptides by immunometrically visualizing DP178/M41\(\Delta\)178 complexes via the human recombinant Fab, Fab-d, as described, below, in the Example presented in Section 8. M41\(\Delta\)178 is a maltose binding fusion protein containing a gp41 region having its DP178 domain deleted, and is described, below, in the Example presented in Section 8.

Utilizing such an assay, M41∆178 may be immobilized onto solid supports such as microtiter wells. A series of dilutions of a test compound may 10 then be added to each $M41\Delta178$ -containing well in the presence of a constant concentration of DP-178 peptide. After incubation, at, for example, room temperature for one hour, unbound DP-178 and test compound are removed from the wells and wells are then 15 incubated with the DP178/M41A178-specific Fab-d antibody. After incubation and washing, unbound Fab-d is removed from the plates and bound Fab-d is quantitated. A no-inhibitor control should also be 20 conducted. Test compounds showing an ability to disrupt DP178/M41∆178 complex formation are identified by their concentration-dependent decrease in the level of Fab-d binding.

A variation of such an assay may be utilized to perform a rapid, high-throughput binding assay which is capable of directly measuring DP178 binding to M41\text{\text{M41}}78 for the determination of binding constants of the ligand of inhibitory constants for competitors of DP178 binding.

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Such an assay takes advantage of accepted radioligand and receptor binding principles. (See, for example, Yamamura, H.I. et al., 1985, "Neurotransmitter Receptor Binding", 2nd ed., Raven Press, NY.) As above, M41\Delta178 is immobilized onto a solid support such as a microtiter well. DP178

binding to M41 Δ 178 is then quantitated by measuring the fraction of DP178 that is bound as ¹²⁵I-DP178 and calculating the total amount bound using a value for specific activity (dpm/ μ g peptide) determined for each labeled DP178 preparation. Specific binding to M41 Δ 178 is defined as the difference of the binding of the labeled DP178 preparation in the microtiter wells (totals) and the binding in identical wells containing, in addition, excess unlabeled DP178 (nonspecifics).

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5.5 PHARMACEUTICAL FORMULATIONS, DOSAGES AND MODES OF ADMINISTRATION

The peptides of the invention may be administered using techniques well known to those in the art.

Preferably, agents are formulated and administered systemically. Techniques for formulation and administration may be found in "Remington's Pharmaceutical Sciences", 18th ed., 1990, Mack Publishing Co., Easton, PA. Suitable routes may include oral, rectal, transmucosal, or intestinal administration; parenteral delivery, including intramuscular, subcutaneous, intramedullary injections, as well as, intrathecal, direct

intraventricular, intravenous, intraperitoneal,
intranasal, or intraocular injections, just to name a
few. For injection, the agents of the invention may
be formulated in aqueous solutions, preferably in
physiologically compatible buffers such as Hanks'
solution, Ringer's solution, or physiological saline

30 buffer. For such transmucosal administration, penetrants appropriate to the barrier to be permeated are used in the formulation. Such penetrants are generally known in the art.

In instances wherein intracellular administration of the peptides of the invention or other inhibitory

agents is preferred, techniques well known to those of ordinary skill in the art may be utilized. For example, such agents may be encapsulated into liposomes, then administered as described above. Liposomes are spherical lipid bilayers with aqueous interiors. All molecules present in an aqueous solution at the time of liposome formation are incorporated into the aqueous interior. The liposomal contents are both protected from the external microenvironment and, because liposomes fuse with cell membranes, are effectively delivered into the cell cytoplasm. Additionally, due to their hydrophobicity, when small molecules are to be administered, direct intracellular administration may be achieved.

Nucleotide sequences encoding the peptides of the 15 invention which are to be intracellularly administered may be expressed in cells of interest, using techniques well known to those of skill in the art. For example, expression vectors derived from viruses such as retroviruses, vaccinia viruses, adeno-20 associated viruses, herpes viruses, or bovine papilloma viruses, may be used for delivery and expression of such nucleotide sequences into the targeted cell population. Methods for the construction of such vectors and expression constructs 25 are well known. See, for example, Sambrook et al., 1989, Molecular Cloning, A Laboratory Manual, Cold Spring Harbor Press, Cold Spring Harbor NY, and Ausubel et al., 1989, Current Protocols in Molecular Biology, Greene Publishing Associates and Wiley 30 Interscience, NY.

With respect to HIV, peptides of the invention, particularly DP107 and DP178, may be used as therapeutics in the treatment of AIDS. In addition, the peptides may be used as prophylactic measures in previously uninfected individuals after acute exposure

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to an HIV virus. Examples of such prophylactic use of the peptides may include, but are not limited to. prevention of virus transmission from mother to infant and other settings where the likelihood of HIV transmission exists, such as, for example, accidents in health care settings wherein workers are exposed to HIV-containing blood products. The successful use of such treatments do not rely upon the generation of a host immune response directed against such peptides.

Effective dosages of the peptides of the invention to be administered may be determined through procedures well known to those in the art which address such parameters as biological half-life, bioavailability, and toxicity. Given the data presented below in Section 6, DP178, for example, may prove efficacious in vivo at doses required to achieve circulating levels of about 1 to about 10 ng per ml of peptide.

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A therapeutically effective dose refers to that amount of the compound sufficient to result in amelioration of symptoms or a prolongation of survival in a patient. Toxicity and therapeutic efficacy of such compounds can be determined by standard pharmaceutical procedures in cell cultures or experimental animals, e.g., for determining the LD50 (the dose lethal to 50% of the population) and the ED50 (the dose therapeutically effective in 50% of the population). The dose ratio between toxic and therapeutic effects is the therapeutic index and it can be expressed as the ratio LD₅₀/ED₅₀. Compounds which exhibit large therapeutic indices are preferred. The data obtained from these cell culture assays and animal studies can be used in formulating a range of dosage for use in humans. The dosage of such compounds lies preferably within a range of 35 circulating concentrations that include the ED50 with

little or no toxicity. The dosage may vary within this range depending upon the dosage form employed and the route of administration utilized. For any compound used in the method of the invention, the therapeutically effective dose can be estimated initially from cell culture assays. A dose may be formulated in animal models to achieve a circulating plasma concentration range that includes the ICm (e.g., the concentration of the test compound which achieves a half-maximal inhibition of the fusogenic event, such as a half-maximal inhibition of viral infection relative to the amount of the event in the absence of the test compound) as determined in cell culture. Such information can be used to more accurately determine useful doses in humans. Levels in plasma may be measured, for example, by high performance liquid chromatography (HPLC).

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The peptides of the invention may, further, serve the role of a prophylactic vaccine, wherein the host raises antibodies against the peptides of the invention, which then serve to neutralize HIV viruses by, for example, inhibiting further HIV infection.

Administration of the peptides of the invention as a prophylactic vaccine, therefore, would comprise administering to a host a concentration of peptides effective in raising an immune response which is sufficient to neutralize HIV, by, for example, inhibiting HIV ability to infect cells. The exact concentration will depend upon the specific peptide to be administered, but may be determined by using standard techniques for assaying the development of an immune response which are well known to those of ordinary skill in the art. The peptides to be used as vaccines are usually administered intramuscularly.

The peptides may be formulated with a suitable adjuvant in order to enhance the immunological

response. Such adjuvants may include, but are not limited to mineral gels such as aluminum hydroxide; surface active substances such as lysolecithin, pluronic polyols, polyanions; other peptides; oil emulsions; and potentially useful human adjuvants such as BCG and Corynebacterium parvum. Many methods may be used to introduce the vaccine formulations described here. These methods include but are not limited to oral, intradermal, intramuscular, intraperitoneal, intravenous, subcutaneous, and intranasal routes.

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Alternatively, an effective concentration of polyclonal or monoclonal antibodies raised against the peptides of the invention may be administered to a host so that no uninfected cells become infected by HIV. The exact concentration of such antibodies will vary according to each specific antibody preparation, but may be determined using standard techniques well known to those of ordinary skill in the art.

Administration of the antibodies may be accomplished using a variety of techniques, including, but not limited to those described in this section.

For all such treatments described above, the exact formulation, route of administration and dosage can be chosen by the individual physician in view of the patient's condition. (See e.g. Fingl et al., 1975, in "The Pharmacological Basis of Therapeutics", Ch. 1 pl).

It should be noted that the attending physician would know how to and when to terminate, interrupt, or adjust administration due to toxicity, or to organ dysfunctions. Conversely, the attending physician would also know to adjust treatment to higher levels if the clinical response were not adequate (precluding toxicity). The magnitude of an administrated dose in the management of the oncogenic disorder of interest

will vary with the severity of the condition to be treated and the route of administration. The dose and perhaps dose frequency, will also vary according to the age, body weight, and response of the individual patient. A program comparable to that discussed above may be used in veterinary medicine.

Use of pharmaceutically acceptable carriers to formulate the compounds herein disclosed for the practice of the invention into dosages suitable for systemic administration is within the scope of the invention. With proper choice of carrier and suitable manufacturing practice, the compositions of the present invention, in particular, those formulated as solutions, may be administered parenterally, such as by intravenous injection. The compounds can be formulated readily using pharmaceutically acceptable carriers well known in the art into dosages suitable for oral administration. Such carriers enable the compounds of the invention to be formulated as tablets, pills, capsules, liquids, gels, syrups, slurries, suspensions and the like, for oral ingestion by a patient to be treated.

pharmaceutical compositions suitable for use in the present invention include compositions wherein the active ingredients are contained in an effective amount to achieve its intended purpose. Determination of the effective amounts is well within the capability of those skilled in the art, especially in light of the detailed disclosure provided herein.

In addition to the active ingredients, these pharmaceutical compositions may contain suitable pharmaceutically acceptable carriers comprising excipients and auxiliaries which facilitate processing of the active compounds into preparations which can be used pharmaceutically. The preparations formulated

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for oral administration may be in the form of tablets, dragees, capsules, or solutions.

The pharmaceutical compositions of the present invention may be manufactured in a manner that is itself known, e.g., by means of conventional mixing, dissolving, granulating, dragee-making, levigating, emulsifying, encapsulating, entrapping or lyophilizing processes.

Pharmaceutical formulations for parenteral administration include aqueous solutions of the active compounds in water-soluble form. Additionally, suspensions of the active compounds may be prepared as appropriate oily injection suspensions. Suitable lipophilic solvents or vehicles include fatty oils such as sesame oil, or synthetic fatty acid esters, such as ethyl oleate or triglycerides, or liposomes. Aqueous injection suspensions may contain substances which increase the viscosity of the suspension, such as sodium carboxymethyl cellulose, sorbitol, or dextran. Optionally, the suspension may also contain suitable stabilizers or agents which increase the solubility of the compounds to allow for the preparation of highly concentrated solutions.

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pharmaceutical preparations for oral use can be obtained by combining the active compounds with solid excipient, optionally grinding a resulting mixture, and processing the mixture of granules, after adding suitable auxiliaries, if desired, to obtain tablets or dragee cores. Suitable excipients are, in particular, fillers such as sugars, including lactose, sucrose, mannitol, or sorbitol; cellulose preparations such as, for example, maize starch, wheat starch, rice starch, potato starch, gelatin, gum tragacanth, methyl cellulose, hydroxypropylmethyl-cellulose, sodium carboxymethylcellulose, and/or polyvinylpyrrolidone (PVP). If desired, disintegrating agents may be

added, such as the cross-linked polyvinyl pyrrolidone, agar, or alginic acid or a salt thereof such as sodium alginate.

Dragee cores are provided with suitable coatings. For this purpose, concentrated sugar solutions may be used, which may optionally contain gum arabic, talc, polyvinyl pyrrolidone, carbopol gel, polyethylene glycol, and/or titanium dioxide, lacquer solutions, and suitable organic solvents or solvent mixtures. Dyestuffs or pigments may be added to the tablets or dragee coatings for identification or to characterize different combinations of active compound doses.

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pharmaceutical preparations which can be used orally include push-fit capsules made of gelatin, as well as soft, sealed capsules made of gelatin and a plasticizer, such as glycerol or sorbitol. The push-fit capsules can contain the active ingredients in admixture with filler such as lactose, binders such as starches, and/or lubricants such as talc or magnesium stearate and, optionally, stabilizers. In soft capsules, the active compounds may be dissolved or suspended in suitable liquids, such as fatty oils, liquid paraffin, or liquid polyethylene glycols. In addition, stabilizers may be added.

6. EXAMPLE: DP178 (SEQ ID:1) IS A POTENT INHIBITOR OF HIV-1 INFECTION

In this example, DP178 (SEQ ID:1) is shown to be a potent inhibitor of HIV-1 mediated CD-4⁺ cell-cell fusion and infection by cell free virus. In the fusion assay, this peptide completely blocks virus induced syncytia formation at concentrations of from 1-10 ng/ml. In the infectivity assay the inhibitory concentration is somewhat higher, blocking infection at 90ng/ml. It is further shown that DP178 (SEQ ID:1) shows that the antiviral activity of DP178 (SEQ ID:1)

is highly specific for HIV-1. Additionally, a synthetic peptide, DP-185 (SEQ ID:3), representing a HIV-1-derived DP178 homolog is also found to block HIV-1-mediated syncytia formation.

6.1. MATERIALS AND METHODS

6.1.1. PEPTIDE SYNTHESIS

Peptides were synthesized using Fast Moc chemistry on an Applied Biosystems Model 431A peptide 10 synthesizer. Generally, unless otherwise noted, the peptides contained amidated carboxy termini and acetylated amino termini. Amidated peptides were prepared using Rink resin (Advanced Chemtech) while peptides containing free carboxy termini were 15 synthesized on Wang (p-alkoxy-benzyl-alcohol) resin (Bachem). First residues were double coupled to the appropriate resin and subsequent residues were single coupled. Each coupling step was followed by acetic anhydride capping. Peptides were cleaved from the 20 resin by treatment with trifluoracetic acid (TFA) (10ml), H₂O (0.5ml), thioanisole (0.5ml), ethanedithiol (0.25ml), and crystalline phenol (0.75g). Purification was carried out by reverse phase HPLC. Approximately 50mg samples of crude peptide were 25 chromatographed on a Waters Delta Pak C18 column (19mm x 30cm, 15µ spherical) with a linear gradient; H₂O/acetonitrile 0.1% TFA. Lyophilized peptides were stored desiccated and peptide solutions were made in water at about 1mg/ml. Electrospray mass spectrometry 30 vielded the following results: DP178 (SEQ ID:1):4491.87 (calculated 4491.94); DP-180 (SEQ ID:2):4491.45 (calculated 4491.94); DP-185 (SEQ ID:3):not done (calculated 4546.97).

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6.1.2. <u>VIRUS</u>

The HIV-1 virus was obtained from R. Gallo (Popovic, M. et al., 1984, Science 224:497-508) and propagated in CEM cells cultured in RPMI 1640 containing 10% fetal calf serum. Supernatant from the infected CEM cells was passed through a 0.2 m filter and the infectious titer estimated in a microinfectivity assay using the AA5 cell line to support virus replication. For this purpose, 25µl of serial diluted virus was added to 75µl AA5 cells at a concentration of 2 x 105/ml in a 96-well microtitre plate. Each virus dilution was tested in triplicate. Cells were cultured for eight days by addition of fresh medium every other day. On day 8 post infection, supernatant samples were tested for virus replication as evidenced by reverse transcriptase activity released to the supernatant. The $TCID_{50}$ was calculated according to the Reed and Muench formula (Reed, L.J. et al., 1938, Am. J. Hyg. 27:493-497). 20 The titer of the HIV-1 and HIV-1 stocks used for these studies, as measured on the AA5 cell line, was approximately 1.4 x 10^6 and 3.8 x 10^4 TCID₅₀/ml, respectively.

6.1.3. CELL FUSION ASSAY

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Approximately 7 x 10⁴ Molt cells were incubated with 1 x 10⁴ CEM cells chronically infected with the HIV-1_{LAI} virus in 96-well plates (one-half area cluster plates; Costar, Cambridge, MA) in a final volume of 100µl culture medium as previously described (Matthews, T.J. et al., 1987, Proc. Natl. Acad. Sci. USA 84: 5424-5428). Peptide inhibitors were added in a volume of 10µl and the cell mixtures were incubated for 24 hr. at 37°C. At that time, multinucleated giant cells were estimated by microscopic examination

at a 40x magnification which allowed visualization of the entire well in a single field.

6.1.4. CELL FREE VIRUS INFECTION ASSAY

Synthetic peptides were incubated at 37°C with either 247 TCID₅₀ (for experiment depicted in FIG. 2), or 62 TCID₅₀ (for experiment depicted in FIG.3) units of HIV-1_{LAI} virus or 25 TCID₅₀ units of HIV-2_{NHZ} and CEM CD4⁺ cells at peptide concentrations of 0, 0.04, 0.4, 4.0, and 40µg/ml for 7 days. The resulting reverse transcriptase (RT) activity in counts per minute was determined using the assay described, below, in Section 6.1.5. See, Reed, L.J. et al., 1938, Am. J. Hyg. 27: 493-497 for an explanation of TCID₅₀ calculations.

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6.1.5. REVERSE TRANSCRIPTASE ASSAY

The micro-reverse transcriptase (RT) assay was adapted from Goff et al. (Goff, S. et al., 1981, J. Virol. 38:239-248) and Willey et al. (Willey, R. et 20 al., 1988, J. Virol. 62:139-147). Supernatants from virus/cell cultures are adjusted to 1% Triton-X100. A 10µl sample of supernatant was added to 50µl of RT cocktail in a 96-well U-bottom microtitre plate and the samples incubated at 37°C for 90 min. 25 cocktail contained 75mM KCl, 2mM dithiothreitol, 5mM MgCl₂, 5µg/ml poly A (Pharmacia, cat. No. 27-4110-01), 0.25 units/ml oligo dT (Pharmacia, cat. No. 27-7858-01), 0.05% NP40, 50mM Tris-HCl, pH 7.8, 0.5μM nonradioactive dTTP, and $10\mu\text{Ci/ml}$ $^{12}\text{P-dTTP}$ (Amersham, cat. 30 No. PB.10167).

After the incubation period, $40\mu l$ of reaction mixture was applied to a Schleicher and Schuell (S+S) NA45 membrane (or DE81 paper) saturated in 2 x SSC buffer (0.3M NaCl and 0.003M sodium citrate) held in a S+S Minifold over one sheet of GB003 (S+S) filter

paper, with partial vacuum applied. Each well of the minifold was washed four times with 200µl 2xSSC, under full vacuum. The membrane was removed from the minifold and washed 2 more times in a pyrex dish with an excess of 2xSSC. Finally, the membrane was drained on absorbent paper, placed on Whatman #3 paper, covered with Saran wrap, and exposed to film overnight at -70°C.

6.2. RESULTS

6.2.1. PEPTIDE INHIBITION OF INFECTED CELL-INDUCED SYNCYTIA FORMATION

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The initial screen for antiviral activity assayed peptides' ability to block syncytium formation induced by overnight co-cultivation of uninfected Molt4 cells 15 with chronically HIV-1 infected CEM cells. results of several such experiments are presented herein. In the first of these experiments, serial DP178 (SEQ ID:1) peptide concentrations between 10µg/ml and 12.5ng/ml were tested for blockade of the 20 cell fusion process. For these experiments, CEM cells chronically infected with either HIV-1LAI, HIV-1MN, HIV-1gp, or HIV-1gp; virus were cocultivated overnight with uninfected Molt 4 cells. The results (FIG. 4) show that DP178 (SEQ ID:1) afforded complete protection 25 against each of the HIV-1 isolates down to the lowest concentration of DP178 (SEQ ID:1) used. For HIVLAI inhibition, the lowest concentration tested was 12.5ng/ml; for all other HIV-1 viruses, the lowest concentration of DP178 (SEQ ID:1) used in this study 30 was 100ng/ml. A second peptide, DP-180 (SEQ ID:2), containing the same amino acid residues as DP178 (SEQ ID:1) but arranged in a random order exhibited no evidence of anti-fusogenic activity even at the high concentration of $40\mu g/ml$ (FIG. 4). These observations 35 indicate that the inhibitory effect of DP178 (SEQ

ID:1) is primary sequence-specific and not related to non-specific peptide/protein interactions. The actual endpoint (i.e., the lowest effective inhibitory concentration) of DP178 inhibitory action is within the range of 1-10 ng/ml.

The next series of experiments involved the preparation and testing of a DP178 (SEQ ID:1) homolog for its ability to inhibit HIV-1-induced syncytia formation. As shown in FIG. 1, the sequence of DP-185 (SEQ ID:3) is slightly different from DP178 (SEQ ID:1) in that its primary sequence is taken from the HIV-1_{SF2} isolate and contains several amino acid differences relative to DP178 (SEQ ID:1) near the N terminus. As shown in FIG. 4, DP-185 (SEQ ID:3), exhibits inhibitory activity even at 312.5ng/ml, the lowest concentration tested.

The next series of experiments involved a comparison of DP178 (SEQ ID:1) HIV-1 and HIV-2 inhibitory activity. As shown in FIG. 5, DP178 (SEQ ID:1) blocked HIV-1-mediated syncytia formation at 20 peptide concentrations below lng/ml. DP178 (SEQ ID:1) failed, however, to block HIV-2 mediated syncytia formation at concentrations as high as 10µg/ml. This striking 4 log selectivity of DP178 (SEQ ID:1) as an inhibitor of HIV-1-mediated cell fusion demonstrates 25 an unexpected HIV-1 specificity in the action of DP178 (SEQ ID:1). DP178 (SEQ ID:1) inhibition of HIV-1mediated cell fusion, but the peptide's inability to inhibit HIV-2 medicated cell fusion in the same cell type at the concentrations tested provides further 30 evidence for the high degree of selectivity associated with the antiviral action of DP178 (SEQ ID:1).

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6.2.2. PEPTIDE INHIBITION OF INFECTION BY CELL-FREE VIRUS

DP178 (SEQ ID:1) was next tested for its ability to block CD-4* CEM cell infection by cell free HIV-1 virus. The results, shown in FIG. 2, are from an 5 experiment in which DP178 (SEQ ID:1) was assayed for its ability to block infection of CEM cells by an HIV-1[A] isolate. Included in the experiment were three control peptides, DP-116 (SEQ ID:9), DP-125 (SEQ ID:8), and DP-118 (SEQ ID:10). DP-116 (SEQ ID:9) 10 represents a peptide previously shown to be inactive using this assay, and DP-125 (SEQ ID:8; Wild, C. et al., 1992, Proc. Natl. Acad, Sci. USA 89:10,537) and DP-118 (SEQ ID:10) are peptides which have previously been shown to be active in this assay. Each 15 concentration (0, 0.04, 0.4, 4, and $40\mu g/ml$) of peptide was incubated with 247 TCID₅₀ units of HIV-1, AT virus and CEM cells. After 7 days of culture, cellfree supernatant was tested for the presence of RT activity as a measure of successful infection. 20 results, shown in FIG. 2, demonstrate that DP178 (SEQ ID:1) inhibited the de novo infection process mediated by the HIV-1 viral isolate at concentrations as low as 90ng/ml (IC50=90ng/ml). In contrast, the two positive control peptides, DP-125 (SEQ: ID:8) and DP-118 (SEQ 25 ID:10), had over 60-fold higher IC50 concentrations of approximately $5\mu g/ml$.

In a separate experiment, the HIV-1 and HIV-2 inhibitory action of DP178 (SEQ ID:1) was tested with CEM cells and either HIV-1_{LAI} or HIV-2_{NHZ}. 62 TCID₅₀

30 HIV-1_{LAI} or 25 GCID₅₀ HIV-2_{NHZ} were used in these experiments, and were incubated for 7 days. As may be seen in FIG. 3, DP178 (SEQ ID:1) inhibited HIV-1 infection with an IC50 of about 31ng/ml. In contrast, DP178 (SEQ ID:1) exhibited a much higher IC50 for HIV-35 2_{NHZ}, thus making DP178 (SEQ ID:1) two logs more potent

as a HIV-1 inhibitor than a HIV-2 inhibitor. This finding is consistent with the results of the fusion inhibition assays described, above, in Section 6.2.1, and further supports a significant level of selectivity (i.e., for HIV-1 over HIV-2).

7. EXAMPLE: THE HIV-1 INHIBITOR, DP178 (SEO ID:1) IS NON-CYTOTOXIC

In this Example, the 36 amino acid synthetic peptide inhibitor DP178 (SEQ ID:1) is shown to be non-cytotoxic to cells in culture, even at the highest peptide concentrations (40µg/ml) tested.

7.1. MATERIALS AND METHODS

Cell proliferation and toxicity assay:

15 Approximately 3.8x10⁵ CEM cells for each peptide concentration were incubated for 3 days at 37°C in T25 flasks. Peptides tested were DP178 (SEQ ID:1) and DP-116 (SEQ ID:9), as described in FIG. 1. Peptides were synthesized as described, above, in Section 6.1. The concentrations of each peptide used were 0, 2.5, 10, and 40µg/ml. Cell counts were taken at incubation times of 0, 24, 48, and 72 hours.

7.2. RESULTS

ID:1) exhibited any cytotoxic effects was assessed by assaying the peptide's effects on the proliferation and viability of cells in culture. CEM cells were incubated in the presence of varying concentrations of DP178 (SEQ ID:1), and DP-116 (SEQ ID:9), a peptide previously shown to be ineffective as a HIV inhibitor (Wild, C. et al., 1992, Proc. Natl. Acad. Sci. USA 89:10,537-10,541). Additionally, cells were incubated in the absence of either peptide.

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The results of the cytotoxicity study demonstrate that DP178 (SEQ ID:1) exhibits no cytotoxic effects on cells in culture. As can be seen, below, in Table XXIV, even the proliferation and viability characteristics of cells cultured for 3 days in the presence of the highest concentration of DP178 (SEQ ID:1) tested (40µg/ml) do not significantly differ from the DP-116 (SEQ ID:9) or the no-peptide controls. The cell proliferation data is also represented in graphic form in FIG. 6. As was demonstrated in the 10 Working Example presented above in Section 6, DP178 (SEQ ID:1) completely inhibits HIV-1 mediated syncytia formation at peptide concentrations between 1 and 10ng/ml, and completely inhibits cell-free viral infection at concentrations of at least 90ng/ml. 15 Thus, this study demonstrates that even at peptide concentrations greater than 3 log higher than the HIV inhibitory dose, DP178 (SEQ ID:1) exhibits no cytotoxic effects.

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TABLE XXIV

% Viability
at time (hours)

5	<u>Peptide</u>	Peptide Concentration µg/ml	0	24	48	72
	DP178 (SEQ ID:1)	40	98	97	95	97
10		10	98	97	98	98
10		2.5	98	93	96	96
	DP116 (SEQ ID:9)	40	98	95	98	97
15		10	98	95	93	98
		2.5	98	96	98	99
20	No Peptide	0	98	97	99	98

8. EXAMPLE: THE INTERACTION OF DP178 AND DP107
Soluble recombinant forms of gp41 used in the
example described below provide evidence that the
DP178 peptide associates with a distal site on gp41
whose interactive structure is influenced by the DP107
leucine zipper motif. A single mutation disrupting
the coiled-coil structure of the leucine zipper domain
transformed the soluble recombinant gp41 protein from
an inactive to an active inhibitor of HIV-1 fusion.
This transformation may result from liberation of the
potent DP178 domain from a molecular clasp with the
leucine zipper, DP107, determinant. The results also
indicate that the anti-HIV activity of various gp41
derivatives (peptides and recombinant proteins) may be

due to their ability to form complexes with viral gp41 and interfere with its fusogenic process.

8.1. MATERIALS AND METHODS

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8.1.1. CONSTRUCTION OF FUSION PROTEINS AND GP41 MUTANTS

Construction of fusion proteins and mutants shown in FIG. 7 was accomplished as follows: the DNA sequence corresponding to the extracellular domain of 10 gp41 (540-686) was cloned into the Xmn I site of the expression vector pMal-p2 (New England Biolab) to give The gp41 sequence was amplified from pgtat (Malim et al., 1988, Nature 355: 181-183) by using polymerase chain reaction (PCR) with upstream primer 15 5'-ATGACGCTGACGGTACAGGCC-3' (primer A) and downstream primer 5'-TGACTAAGCTTAATACCACAGCCAATTTGTTAT-3' (primer B). M41-P was constructed by using the T7-Gen in vitro mutagenesis kit from United States Biochemicals (USB) following the supplier's 20 instructions. The mutagenic primer (5'-GGAGCTGCTTGGGGCCCCAGAC-3') introduces an Ile to Pro mutation in M41 at position 578. M41 Δ 107, from which the DP-107 region has been deleted, was made using a deletion mutagenic primer 5'-

- 25 CCAAATCCCCAGGAGCTGCTCGAGCTGCACTATACCAGAC-3 (primer C) following the USB T7-Gen mutagenesis protocol.

 M41Δ178, from which the DP-178 region has been deleted, was made by cloning the DNA fragment corresponding to gp41 amino acids 540-642 into the
- 30 Xmn I site of pMal-p2. Primer A and 5'ATAGCTTCTAGATTAATTGTTAATTTCTCTGTCCC-3' (primer D) were
 used in the PCR with the template pgtat to generate
 the inserted DNA fragments. M41-P was used as the
 template with primer A and D in PCR to generate M41-
- 35 PA178. All inserted sequences and mutated residues

were checked by restriction enzyme analysis and confirmed by DNA sequencing.

8.1.2. PURIFICATION AND CHARACTERIZATION OF FUSION PROTEINS

The fusion proteins were purified according to the protocol described in the manufacturer's brochure of protein fusion and purification systems from New England Biolabs (NEB). Fusion proteins (10 ng) were analyzed by electrophoresis on 8% SDS polyacrylamide 10 gels. Western blotting analysis was performed as described by Sambrook et al., 1989, Molecular Cloning: A Laboratory Manual, 2d Ed, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, Ch. 18, pp. 64-75. An HIV-1 positive serum diluted 1000-fold, 15 or a human Fab derived from repertoire cloning was used to react with the fusion proteins. The second antibody was HRP-conjugated goat antihuman Fab. An ECL Western blotting detection system (Amersham) was used to detect the bound antibody. A detailed 20 protocol for this detection system was provided by the manufacturer. Rainbow molecular weight markers (Amersham) were used to estimate the size of fusion proteins.

25 8.1.3. CELL FUSION ASSAYS FOR ANTI-HIV ACTIVITY
Cell fusion assays were performed as previously
described (Matthews et al., 1987, Proc. Natl. Acad.
Sci. USA 84: 5424-5481). CEM cells (7 X 10⁴) were
incubated with HIV-1_{mB} chronically infected CEM cells
30 (10⁴) in 96-well flat-bottomed half-area plates
(Costar) in 100 μl culture medium. Peptide and fusion
proteins at various concentrations in 10 μl culture
medium were incubated with the cell mixtures at 37°C
for 24 hours. Multinucleated syncytia were estimated
35 with microscopic examination. Both M41 and M41-P did

not show cytotoxicity at the concentrations tested and shown in FIG. 8.

Inhibition of HIV-1 induced cell-cell fusion activity was carried out in the presence of 10 nM DP178 and various concentrations of M41\text{\Delta}178 or M41-P\text{\Delta}178 as indicated in FIG. 9. There was no observable syncytia in the presence of 10 nM DP178. No peptide or fusion protein was added in the control samples.

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8.1.4. ELISA ANALYSIS OF DP178 BINDING TO THE LEUCINE ZIPPER MOTIF OF GP41

The amino acid sequence of DP178 used is: YTSLIHSLIEESQNQQEKNEQELLELDKWASLWNWF. For enzyme linked immunoassay (ELISA), M41\Delta178 or M41-P\Delta178 (5 μg/ml) in 0.1M NaHCO, pH 8.6, were coated on 96 wells 15 Linbro ELISA plates (Flow Lab, Inc.) overnight. well was washed three times with distilled water then blocked with 3% bovine serum albumin (BSA) for 2 hours. After blocking, peptides with 0.5% BSA in TBST (40 mM Tris-HCl pH7.5, 150 mM NaCl, 0.05% Tween 20) 20 were added to the ELISA plates and incubated at room temperature for 1 hour. After washing three times with TBST, Fab-d was added at a concentration of 10 ng/ml with 0.5% BSA in TBST. The plates were washed three times with TBST after incubation at room 25 temperature for 1 hour. Horse radish peroxidase (HRP) conjugated goat antihuman Fab antiserum at a 2000 fold dilution in TBST with 0.5% BSA was added to each well and incubated at room temperature for 45 minutes. plates were then washed four times with TBST. The 30 peroxidase substrate o-phenylene diamine (2.5 mg/ml) and 0.15% H2O2 were added to develop the color. reaction was stopped with an equal volume of 4.5 N H,SO4 after incubation at room temperature for 10 minutes. The optical density of the stopped reaction 35 mixture was measured with a micro plate reader

(Molecular Design) at 490 nm. Results are shown in FIG. 10.

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8.2. RESULTS

8.2.1. THE EXPRESSION AND CHARACTERIZATION OF THE ECTODOMAIN OF qp41

As a step toward understanding the roles of the two helical regions in gp41 structure and function, the ectodomain of gp41 was expressed as a maltose binding fusion protein (M41) (FIG. 7). The fusogenic 10 peptide sequence at the N-terminal of gp41 was omitted from this recombinant protein and its derivatives to improve solubility. The maltose binding protein facilitated purification of the fusion proteins under relatively mild, non-denaturing conditions. Because 15 the M41 soluble recombinant gp41 was not glycosylated, lacked several regions of the transmembrane protein (i.e., the fusion peptide, the membrane spanning, and the cytoplasmic domains), and was expressed in the absence of gp120, it was not expected to precisely 20 reflect the structure of native gp41 on HIV-1 virions. Nevertheless, purified M41 folded in a manner that preserved certain discontinuous epitopes as evidenced by reactivity with human monoclonal antibodies, 98-6, 126-6, and 50-69, previously shown to bind 25 conformational epitopes on native gp41 expressed in eukaryotic cells (Xu et al., 1991, J. Virol. 65: 4832-4838; Chen, 1994, J. Virol. 68:2002-2010). Thus, at least certain regions of native gp41 defined by these antibodies appear to be reproduced in the recombinant 30 fusion protein M41. Furthermore, M41 reacted with a human recombinant Fab (Fab-d) that recognizes a conformational epitope on gp41 and binds HIV-1 virions as well as HIV-1 infected cells but not uninfected cells as analyzed by FACS. Deletion of either helix 35 motif, i.e., DP107 or DP178, of the M41 fusion protein

eliminated reactivity with Fab-d. These results indicate that both helical regions, separated by 60 amino acids in the primary sequence, are required to maintain the Fab-d epitope.

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8.2.2. ANTI-HIV ACTIVITY OF THE RECOMBINANT ECTODOMAIN OF GP41

The wild type M41 fusion protein was tested for anti-HIV-1 activity. As explained, supra, synthetic peptides corresponding to the leucine zipper (DP107) and the C-terminal putative helix (DP178) show potent anti-HIV activity. Despite inclusion of both these regions, the recombinant M41 protein did not affect HIV-1 induced membrane fusion at concentrations as high as 50 µM (Table XXV, below).

TABLE XXV							
DISRUPTION OF	_			OF			

20		<u>DP107</u>	DP178	<u>M41</u>	<u>M41-P</u>	<u>Μ41-ΡΔ178</u>
	Cell fusion (IC ₉₀)	l μM	1 nM	>50 μM	83 nM	>50 μM
25	Fab-D binding (k _D)	-	-	3.5x10°	2.5x10 ⁴	-
	HIV infectiv- ity (IC ₃₀)	1 μΜ	80 nM	> 16 μM	66 nM	>8 μM

The affinity constants of Fab-d binding to the fusion proteins were determined using a protocol described by B. Friguet et al., 1985, J. Immunol. Method. 77:305-319.

^{- =} No detectable binding of Fab-d to the fusion proteins.

Antiviral Infectivity Assays. 20 μ l of serially diluted virus stock was incubated for 60 minutes at ambient temperature with 20 μ l of the indicated

concentration of purified recombinant fusion protein in RPMI 1640 containing 10% fetal bovine serum and antibiotics in a 96-well microtiter plate. 20 μ l of CEM4 cells at 6 x 10⁵ cells/ml were added to each well, and cultures were incubated at 37°C in a humidified CO₂ incubator. Cells were cultured for 9 days by the addition of fresh medium every 2 to 3 days. On days 5, 7, and 9 postinfection, supernatant samples were assayed for reverse transcriptase (RT) activity, as described below, to monitor viral replication. The 50% tissue culture infectious dose (TCID₃₀) was calculated for each condition according to the formula of Reed & Muench, 1937, Am. J. Hyg. 27:493-497. RT activity was determined by a modification of the published methods of Goff et al., 1981, J. Virol. 38:239-248 and Willey et al., 1988, J. Virol. 62:139-147 as described in Chen et al., 1993, AIDS Res. Human Retroviruses 9:1079-1086.

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Surprisingly, a single amino acid substitution, proline in place of isoleucine in the middle of the leucine zipper motif, yielded a fusion protein (M41-P) which did exhibit antiviral activity (Table XXV and 15 Fig. 8). As seen in Table XXV, M41-P blocked syncytia formation by 90% at approximately 85 nM and neutralized HIV-1mm infection by 90% at approximately 70 nM concentrations. The anti-HIV-1 activity of M41-P appeared to be mediated by the C-terminal helical sequence since deletion of that region from M41-P yielded an inactive fusion protein, M41-PΔ178 (Table XXV). This interpretation was reinforced by experiments demonstrating that a truncated fusion protein lacking the DP178 sequence, M41\Delta178, abrogated the potent anti-fusion activity of the DP178 peptide in a concentration-dependent manner (FIG. 9). The same truncated fusion protein containing the proline mutation disrupting the leucine zipper, M41-PA178, was not active in similar competition experiments (FIG. 30 9). The results indicate that the DP178 peptide associates with a second site on gp41 whose interactive structure is dependent on a wild type leucine zipper sequence. A similar interaction may occur within the wild type fusion protein, M41, and act to form an intramolecular clasp which sequesters

the DP178 region, making it unavailable for anti-viral activity.

A specific association between these two domains is also indicated by other human monoclonal Fab-d studies. For example, Fab-d failed to bind either the DP178 peptide or the fusion protein M41Δ178, but its epitope was reconstituted by simply mixing these two reagents together (FIG. 10). Again, the proline mutation in the leucine zipper domain of the fusion protein, M41-PΔ178, failed to reconstitute the epitope in similar mixing experiments.

9. EXAMPLE: METHOD FOR COMPUTER-ASSISTED IDENTIFICATION OF DP107-LIKE AND DP178-LIKE SEQUENCES

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A number of known coiled-coil sequences have been 15 well described in the literature and contain heptad repeat positioning for each amino acid. Coiled-coil nomenclature labels each of seven amino acids of a heptad repeat A through G, with amino acids A and D 20 tending to be hydrophobic positions. Amino acids E and G tend to be charged. These four positions (A, D, E, and G) form the amphipathic backbone structure of a monomeric alpha-helix. The backbones of two or more amphipathic helices interact with each other to form 25 di-, tri-, tetrameric, etc., coiled-coil structures. In order to begin to design computer search motifs, a series of well characterized coiled coils were chosen including yeast transcription factor GCN4, Influenza Virus hemagglutinin loop 36, and human proto-oncogenes 30 c-Myc, c-Fos, and c-Jun. For each peptide sequence, a strict homology for the A and D positions, and a list of the amino acids which could be excluded for the B, C, E, F, and G positions (because they are not observed in these positions) was determined. Motifs 35 were tailored to the DP107 and DP178 sequences by

deducing the most likely possibilities for heptad positioning of the amino acids of HIV-1 Bru DP-107, which is known to have coiled-coil structure, and HIV-1 Bru DP178, which is still structurally undefined. The analysis of each of the sequences is contained in FIG. 12. For example, the motif for GCN4 was designed as follows:

- The only amino acids (using standard single letter amino acid codes) found in the A or D positions of GCN4 were [LMNV].
- 2. All amino acids were found at B, C, E, F, and G positions except {CFGIMPTW}.
 - 3. The PESEARCH motif would, therefore, be written as follows:
 - [LMNV]-{CFGIMPTW}(2)-[LMNV]-{CFGIMPTW}(3)-
- 15 [LMNV]-{CFGIMPTW}(2)-[LMNV]-{CFGIMPTW}(3)-
 - $[LMNV] \{CFGIMPTW\} (2) [LMNV] \{CFGIMPTW\} (3) -$
 - [LMNV]-{CFGIMPTW}(2)-[LMNV]-{CFGIMPTW}(3)

position either L, M, N, or V must occur; at positions
B and C (the next two positions) accept everything
except C, F, G, I, M, P, T, or W; at the D position
either L, M, N, or V must occur; at positions E, F,
and G (the next 3 positions) accept everything except
C, F, G, I, M, P, T, or W." This statement is
contained four times in a 28-mer motif and five times
in a 35-mer motif. The basic motif key then would be:
[LMNV]-{CFGIMPTW}. The motif keys for the remaining
well described coiled-coil sequences are summarized in
FIG. 12.

The motif design for DP107 and DP178 was slightly different than the 28-mer model sequences described above due to the fact that heptad repeat positions are not defined and the peptides are both longer than 28 residues. FIG. 13 illustrates several possible

sequence alignments for both DP107 and DP178 and also includes motif designs based on 28-mer, 35-mer, and full-length peptides. Notice that only slight differences occur in the motifs as the peptides are lengthened. Generally, lengthening the base peptide results in a less stringent motif. This is very useful in broadening the possibilities for identifying DP107-or DP-178-like primary amino acid sequences referred to in this document as "hits".

In addition to making highly specific motifs for each type peptide sequence to be searched, it is also 10 possible to make "hybrid" motifs. These motifs are made by "crossing" two or more very stringent motifs to make a new search algorithm which will find not only both "parent" motif sequences but also any peptide sequences which have similarities to one, the other, or both "parents". For example, in FIG. 14 the "parent" sequence of GCN4 is crossed with each of the possible "parent" motifs of DP-107. Now the hybrid motif must contain all of the amino acids found in the A and D positions of both parents, and exclude all of 20 the amino acids not found in either parent at the other positions. The resulting hybrid from crossing GCN4 or [LMNV]{CFGIMPTW} and DP107 (28-mer with the first L in the D position) or [ILQT]{CDFIMPST}, is [ILMNQTV]{CFIMPT}. Notice that now only two basic 25 hybrid motifs exist which cover both framing possibilities, as well as all peptide lengths of the parent DP-107 molecule. FIG. 15 represents the "hybridizations" of GCN4 with DP-178. FIG. 16 represents the "hybridizations" of DP107 and DP178. It is important to keep in mind that the represented motifs, both parent and hybrid, are motif keys and not the depiction of the full-length motif needed to actually do the computer search.

Hybridizations can be performed on any combination of two or more motifs. FIG. 17 summarizes several three-motif hybridizations including GCN4, DP107 (both frames), and DP178 (also both frames). Notice that the resulting motifs are now becoming much more similar to each other. fact, the first and third hybrid motifs are actually subsets of the second and fourth hybrid motifs respectively. This means that the first and third hybrid motifs are slightly more stringent than the second and fourth. It should also be noted that with 10 only minor changes in these four motifs, or by hybridizing them, a single motif could be obtained which would find all of the sequences. However, it should be remembered that stringency is also reduced. Finally, the most broad-spectrum and least-stringent 15 hybrid motif is described in FIG. 18 which summarizes the hybridization of GCN4, DP107 (both frames), DP178 (both frames), c-Fos, c-Jun, c-Myc, and Flu loop 36.

A special set of motifs was designed based on the 20 fact that DP-178 is located only approximately ten amino acids upstream of the transmembrane spanning region of gp41 and just C-terminal to a proline which separates DP107 and DP178. It has been postulated that DP178 may be an amphipathic helix when membrane 25 associated, and that the proline might aid in the initiation of the helix formation. The same arrangement was observed in Respiratory Syncytial Virus; however, the DP178-like region in this virus also had a leucine zipper just C-terminal to the proline. Therefore, N-terminal proline-leucine zipper motifs were designed to analyze whether any other viruses might contain this same pattern. The motifs are summarized in FIG. 19.

The PC/Gene protein database contains 5879 viral

amino acid sequences (library file PVIRUSES; CD-ROM

release 11.0). Of these, 1092 are viral enveloped or glycoprotein sequences (library file PVIRUSE1).

Tables V through XIV contain lists of protein sequence names and motif hit locations for all the motifs searched.

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10. EXAMPLE: COMPUTER-ASSISTED IDENTIFICATION OF DP107 AND DP178-LIKE SEQUENCES IN HUMAN IMMUNODEFICIENCY VIRUS

FIG. 20 represents search results for HIV-1 BRU 10 isolate gp41 (PC/Gene protein sequence PENV_HV1BR). Notice that the hybrid motif which crosses DP-107 and DP-178 (named 107x178x4; the same motif as found in FIG. 16 found three hits including amino acids 550-599, 636-688, and 796-823. These areas include DP-107 15 plus eight N-terminal and four C-terminal amino acids; DP178 plus seven N-terminal and ten C-terminal amino acids; and an area inside the transmembrane region (cytoplasmic). FIG. 20 also contains the results obtained from searching with the motif named ALLMOTI5, 20 for which the key is found in FIG. 17 ({CDGHP} {CFP}x5). This motif also found three hits including DP107 (amino acids 510-599), DP178 (615-717), and a cytoplasmic region (772-841). These hits overlap the hits found by the motif 107x178x4 with considerable 25 additional sequences on both the amino and carboxy termini. This is not surprising in that 107x178x4 is a subset of the ALLMOTI5 hybrid motif. Importantly, even though the stringency of ALLMOTI5 is considerably less than 107x178x4, it still selectively identifies the DP107 and DP178 regions of gp41 shown to contain sequences for inhibitory peptides of HIV-1. results of these two motif searches are summarized in Table V under the PC/Gene protein sequence name PENV HV1BR. The proline-leucine zipper motifs also gave 35 several hits in HIV-1 BRU including 503-525 which is

at the very C-terminus of gp120, just upstream of the cleavage site (P7LZIPC and P12LZIPC); and 735-768 in the cytoplasmic domain of gp41 (P23LZIPC). These results are found in Tables VIII, IX, and X under the same sequence name as mentioned above. Notice that the only area of HIV-1 BRU which is predicted by the Lupas algorithm to contain a coiled-coil region, is from amino acids 635-670. This begins eight amino acids N-terminal to the start and ends eight amino acids N-terminal to the end of DP178. DP107, despite the fact that it is a known coiled coil, is not predicted to contain a coiled-coil region using the Lupas method.

11. EXAMPLE: COMPUTER-ASSISTED IDENTIFICATION OF DP107-LIKE AND DP178-LIKE SEQUENCES IN HUMAN RESPIRATORY SYNCYTIAL VIRUS

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FIG. 21 represents search results for Human Respiratory Syncytial Virus (RSV; Strain A2) fusion glycoprotein F1 (PC/Gene protein sequence name PVGLF_ 20 HRSVA). Motif 107x178x4 finds three hits including amino acids 152-202, 213-243, and 488-515. The arrangement of these hits is similar to what is found in HIV-1 except that the motif finds two regions with similarities to DP-178, one just downstream of what 25 would be called the DP107 region or amino acids 213-243, and one just upstream of the transmembrane region (also similar to DP178) or amino acids 488-515. Motif ALLMOTI5 also finds three areas including amino acids 116-202, 267-302, and 506-549. The proline-leucine 30 zipper motifs also gave several hits including amino acids 205-221 and 265-287 (P1LZIPC 265-280, P12LZIPC), and 484-513 (P7LZIPC and P12LZIPC 484-506, P23LZIPC). Notice that the PLZIP motifs also identify regions which share location similarities with DP-178 of HIV-35 1.

12. EXAMPLE: COMPUTER-ASSISTED IDENTIFICATION OF DP107-LIKE AND DP178-LIKE SEQUENCES IN SIMIAN IMMUNODEFICIENCY VIRUS

Motif hits for Simian immunodeficiency Virus qp41 (AGM3 isolate; PC/Gene protein sequence name 5 PENV_SIVAG) are shown in FIG. 22. Motif 107x178x4 finds three hits including amino acids 566-593, 597-624, and 703-730. The first two hits only have three amino acids between them and could probably be combined into one hit from 566-624 which would 10 represent a DP107-like hit. Amino acids 703 to 730 would then represent a DP178-like hit. ALLMOTI5 also finds three hits including amino acids 556-628 (DP107like), 651-699 (DP178-like), and 808-852 which represents the transmembrane spanning region. SIV 15 also has one region from 655-692 with a high propensity to form a coiled coil as predicted by the Lupas algorithm. Both 107x178x4 and ALLMOTI5 motifs find the same region. SIV does not have any PLZIP motif hits in gp41.

The identification of DP178/DP107 analogs for a second SIV isolate (MM251) is demonstrated in the Example presented, below, in Section 19.

13. EXAMPLE: COMPUTER-ASSISTED IDENTIFICATION OF DP107-LIKE AND DP178 LIKE SEQUENCES IN CANINE DISTEMPER VIRUS

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Canine Distemper Virus (strain Onderstepoort) fusion glycoprotein F1 (PC/Gene Protein sequence name PVGLF_CDVO) has regions similar to Human RSV which are predicted to be DP107-like and DP178-like (FIG. 23). Motif 107x178x4 highlights one area just C-terminal to the fusion peptide at amino acids 252-293. Amino acids 252-286 are also predicted to be coiled coil using the Lupas algorithm. Almost 100 amino acids C-terminal to the first region is a DP178-like area at residues 340-367. ALLMOTI5 highlights three areas of

interest including: amino acids 228-297, which completely overlaps both the Lupas prediction and the DP107-like 107x178x4 hit; residues 340-381, which overlaps the second 107x178x4 hit; and amino acids 568-602, which is DP178-like in that it is located just N-terminal to the transmembrane region. It also overlaps another region (residues 570-602) predicted by the Lupas method to have a high propensity to form a coiled coil. Several PLZIP motifs successfully identified areas of interest including P6 and P12LZIPC which highlight residues 336-357 and 336-361 respectively; P1 and P12LZIPC which find residues 398-414; and P12 and P23LZIPC which find residues 562-589 and 562-592 respectively.

14. EXAMPLE: COMPUTER-ASSISTED IDENTIFICATION OF DP107-LIKE AND DP178-LIKE SEQUENCES IN NEWCASTLE DISEASE VIRUS

pige. 24 shows the motif hits found in Newcastle Disease Virus (strain Australia-Victoria/32; PC Gene protein sequence name PVGLF_NDVA). Motif 107x178x4 finds two areas including a DP107-like hit at amino acids 151-178 and a DP178-like hit at residues 426-512. ALLMOTIS finds three areas including residues 117-182, 231-272, and 426-512. The hits from 426-512 include a region which is predicted by the Lupas method to have a high coiled-coil propensity (460-503). The PLZIP motifs identify only one region of interest at amino acids 273-289 (P1 and 12LZIPC).

30 15. EXAMPLE: COMPUTER-ASSISTED IDENTIFICATION
OF DP107-LIKE AND DP178-LIKE
SEQUENCES IN HUMAN PARAINFLUENZA VIRUS

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Both motifs 107x178x4 and ALLMOTI5 exhibit
DP107-like hits in the same region, 115-182 and 117182 respectively, of Human Parainfluenza Virus (strain
NIH 47885; PC/Gene protein sequence name PVGLF_p13H4;

(FIG. 25). In addition, the two motifs have a DP178-like hit just slightly C-terminal at amino acids 207-241. Both motifs also have DP178-like hits nearer the transmembrane region including amino acids 457-497 and 462-512 respectively. Several PLZIP motif hits are also observed including 283-303 (P5LZIPC), 283-310 (P12LZIPC), 453-474 (P6LZIPC), and 453-481 (P23LZIPC). The Lupas algorithm predicts that amino acids 122-176 may have a propensity to form a coiled-coil.

16. EXAMPLE: COMPUTER-ASSISTED IDENTIFICATION OF DP107-LIKE AND DP178-LIKE SEQUENCES OF INFLUENZA A VIRUS

rig. 26 illustrates the Lupas prediction for a coiled coil in Influenza A Virus (strain A/Aichi/2/68) at residues 379-436, as well as the motif hits for 107x178x4 at amino acids 387-453, and for ALLMOTI5 at residues 380-456. Residues 383-471 (38-125 of HA2) were shown by Carr and Kim to be an extended coiled coil when under acidic pH (Carr and Kim, 1993, Cell 73: 823-832). The Lupas algorithm predicts a coiled-coil at residues 379-436. All three methods successfully predicted the region shown to actually have coiled-coil structure; however, ALLMOTI5 predicted the greatest portion of the 88 residue stretch.

17. EXAMPLE: POTENTIAL RESPIRATORY SYNCYTIAL VIRUS DP178/DP107 ANALOGS: CD AND ANTIVIRAL CHARACTERIZATION

syncytial virus (RSV) peptides identified by utilizing the computer-assisted search motifs described in the Examples presented in Sections 9 and 11, above, were tested for anti-RSV activity. Additionally, circular dichroism (CD) structural analyses were conducted on the peptides, as discussed below. It is demonstrated

that several of the identified peptides exhibit potent antiviral capability. Additionally, it is shown that several of these peptides exhibit a substantial helical character.

17.1 MATERIALS AND METHODS

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Structural analyses: The CD spectra were measured in a 10mM sodium phosphate, 150mM sodium chloride, pH 7.0, buffer at approximately 10mM concentrations, using a 1 cm pathlength cell on a Jobin/Yvon Autodichrograph Mark V CD spectrophotometer. Peptides were synthesized according to the methods described, above, in Section 6.1. Peptide concentrations were determined from A₂₀₀ using Edlehoch's method (1967, Biochemistry 6:1948).

Anti-RSV antiviral activity assays: The assay utilized herein tested the ability of the peptides to disrupt the ability of HEp2 cells acutely infected with RSV (i.e., cells which are infected with a multiplicity of infection of greater than 2) to fuse and cause syncytial formation on a monolayer of uninfected an uninfected line of Hep-2 cells. The lower the observed level of fusion, the greater the antiviral activity of the peptide was determined to be.

Uninfected confluent monolayers of Hep-2 cells were grown in microtiter wells in 3% EMEM (Eagle Minimum Essential Medium w/o L-glutamine [Bio Whittaker Cat. No. 12-125F], with fetal bovine serum [FBS; which had been heat inactivated for 30 minutes at 56°C; Bio Whittaker Cat. No. 14-501F) supplemented at 3%, antibiotics (penicillin/streptomycin; Bio Whittaker Cat. No. 17-602E) added at 1%, and glutamine added at 1%.

To prepare Hep2 cells for addition to uninfected cells, cultures of acutely infected Hep2 cells were

washed with DPBS (Dulbecco's Phosphate Buffered Saline W/o calcium or magnesium; Bio Whittaker Cat. No. 17-512F) and cell monolayers were removed with Versene (1:5000; Gibco Life Technologies Cat. No. 15040-017). The cells were spun 10 minutes and resuspended in 3% FBS. Cell counts were performed using a hemacytometer. Persistent cells were added to the uninfected Hep-2 cells.

The antiviral assay was conducted by, first, removing all media from the wells containing uninfected Hep-2 cells, then adding peptides (at the dilutions described below) in 3% EMEM, and 100 acutely RSV-infected Hep2 cells per well. Wells were then incubated at 37°C for 48 hours.

checked for fusion centers, media was removed from the wells, followed by addition, to each well, of either crystal Violet stain or XTT. With respect to Crystal Violet, approximately 50µl 0.25% Crystal Violet stain in methanol were added to each well. The wells were rinsed immediately, to remove excess stain, and were allowed to dry. The number of syncytia per well were then counted, using a dissecting microscope.

With respect to XTT (2,3-bis[2-Methoxy-4-nitro-5-sulfophenyl]-2H-tetrazolium-5-carboxyanilide inner salt), 50µl XTT (1mg/ml in RPMI buffered with 100mM HEPES, pH 7.2-7.4, plus 5% DMSO) were added to each well. The OD₄₅₀₄₉₀ was measured (after blanking against growth medium without cells or reagents, and against reagents) according to standard procedures.

Peptides: The peptides characterized in the
study presented herein were:
1) peptides T-142 to T-155 and T-575, as shown in FIG.
27A, and peptides T-22 to T-27, T-68, T-334 and T-371

to T-375 and T-575, as shown in FIG. 27B;

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2) peptides T-120 to T-141 and T-576, as shown in FIG. 27B, and peptides T-12, T-13, T-15, T-19, T-28 to T-30, T-66, T-69, T-70 and T-576, as shown in FIG. 27D; and

3) peptides T-67 and T-104 to T-119 and T-384, as shown in FIG. 28A, and peptides T-71, T-613 to T-617, T-662 to T-676 and T-730, as shown in FIG. 28B.

The peptides of group 1 represent portions of the RSV F2 protein DP178/107-like region. The peptides of group 2 represent portions of the RSV F1 protein DP107-like region. The peptides of groups 3 represent portions of the RSV F1 protein DP178-like region.

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Each peptide was tested at 2-fold serial dilutions ranging from $100\mu g/ml$ to approximately 100ng/ml. For each of the assays, a well containing no peptide was also used. The IC₅₀ data for each peptide represents the average of several experiments conducted utilizing that peptide.

17.2 RESULTS

The data summarized in FIGS. 27A-B and 28A-B represent antiviral and structural information obtained from peptides derived from the RSV F2 DP178/DP107-like F2 region (FIG. 27A-B), the RSV F1 DP-107-like region (FIG. 27C-D) and the RSV DP178-like F2 region (FIG. 28A-B).

As shown in FIGS. 27A-D, a number of the RSV DP178/DP107-like peptides exhibited a detectable level of antiviral activity. Peptides from the RSV DP178/DP107-like F2 region (FIG. 27A-B), for example, T-142 to T-145 and T-334 purfied peptides, exhibited detectable levels of antiviral activity, as evidenced by their IC₅₀ values. Further, a number of RSV F1 DP107-like peptides (FIG. 27C-D) exhibited a sizable level of antiviral activity as purified peptides, including, for example, peptides T-124 to T-127, T-

131, T-135 and T-137 to T-139, as demonstrated by their low IC₅₀ values. In addition, CD analysis FIG. 27A, 27C) reveals that many of the peptides exhibit some detectable level of helical structure.

The results summarized in FIG. 28A-B demonstrate that a number of DP178-like purified peptides exhibit a range of potent anti-viral activity. These peptides include, for example, T-67, T-104, T-105 and T-107 to T-119, as listed in FIG. 28A, and T-665 to T-669 and T-671 to T-673, as listed in FIG. 28B. In addition, some of the DP178-like peptides exhibited some level of helicity.

Thus, the computer assisted searches described, hereinabove, successfully identified viral peptide domains that represent highly promising anti-RSV antiviral compounds.

18. EXAMPLE: POTENTIAL HUMAN PARAINFLUENZA VIRUS TYPE 3 DP178/DP107 ANALOGS: CD AND ANTIVIRAL CHARACTERIZATION

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- In the Example presented herein, human parainfluenza virus type 3 (HPIV3) peptides identified by utilizing the computer-assisted search motifs described in the Examples presented in Sections 9 and 15, above, were tested for anti-HPIV3 activity.
- 25 Additionally, circular dichroism (CD) structural analyses were conducted on the peptides, as discussed below. It is demonstrated that several of the identified peptides exhibit potent antiviral capability. Additionally, it is shown that several of
- 30 these peptides exhibit a substantial helical character.

18.1 MATERIALS AND METHODS

<u>Structural analyses</u>: Structural analyses

35 consisted of circular dichroism (CD) studies. The CD

spectra were measured in a 10mM sodium phosphate, 150mM sodium chloride, pH 7.0, buffer at approximately 10mM concentrations, using a 1 cm pathlength cell on a Jobin/Yvon Autodichrograph Mark V CD spectrophotometer. Peptide concentrations were determined from A_{210} using Edlehoch's method (1967, Biochemistry $\underline{6}$:1948).

Anti-HPIV3 antiviral activity assays: The assay utilized herein tested the ability of the peptides to disrupt the ability of Hep2 cells chronically infected with HPIV3 to fuse and cause syncytial formation on a monolayer of an uninfected line of CV-1W cells. The more potent the lower the observed level of fusion, the greater the antiviral activity of the peptide.

Uninfected confluent monolayers of CV-1W cells

were grown in microtiter wells in 3% EMEM (Eagle

Minimum Essential Medium w/o L-glutamine [Bio

Whittaker Cat. No. 12-125F], with fetal bovine serum

[FBS; which had been heat inactivated for 30 minutes

at 56°C; Bio Whittaker Cat. No. 14-501F) supplemented

at 3%, antibiotics/antimycotics (Gibco BRL Life

Technologies Cat. No. 15040-017) added at 1%, and

glutamine added at 1%.

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To prepare Hep2 cells for addition to uninfected cells, cultures of chronically infected Hep2 cells were washed with DPBS (Dulbecco's Phosphate Buffered Saline w/o calcium or magnesium; Bio Whittaker Cat. No. 17-512F) and cell monolayers were removed with Versene (1:5000; Gibco Life Technologies Cat. No. 15040-017). The cells were spun 10 minutes and resuspended in 3% FBS. Cell counts were performed using a hemacytometer. Persistent cells were added to the uninfected CV-1W cells.

The antiviral assay was conducted by, first, removing all media from the wells containing uninfected CV-1W cells, then adding peptides (at the

dilutions described below) in 3% EMEM, and 500 chronically HPIV3-infected Hep2 cells per well. Wells were then incubated at 37°C for 24 hours.

On day 2, after cells in control wells were checked for fusion centers, media was removed from the wells, followed by addition, to each well, of approximately 50µl 0.25% Crystal Violet stain in methanol. Wells were rinsed immediately, to remove excess stain and were then allowed to dry. The number of syncytia per well were then counted, using a dissecting microscope.

Alternatively, instead of Crystal Violet analysis, cells were assayed with XTT, as described, avove, in Section 17.1.

Peptides: The peptides characterized in the
study presented herein were:

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- Peptides 157 to 188, as shown in FIG. 29A, and peptides T-38 to T-40, T-42 to T-46 and T-582, as shown in FIG. 29B. These peptides are derived from the DP107 region of the HPIV3 F1 fusion protein (represented by HPF3 107, as shown in FIG. 29A); and
- Peptides 189 to 210, as shown in FIG. 30A, and T269, T-626, T-383 and T-577 to T-579, as shown in
 FIG. 30B. These peptides are primarily derived
 from the DP178 region of the HPIV3 F1 fusion
 protein (represented by HPF3 178, as shown in
 FIG. 30A). Peptide T-626 contains two mutated
 amino acid resides (represented by a shaded
 background). Additionally, peptide T-577
 represents F1 amino acids 65-100, T-578
 represents F1 amino acids 207-242 and T-579
 represents F1 amino acids 273-309.

Each peptide was tested at 2-fold serial dilutions ranging from 500µg/ml to approximately

500ng/ml. For each of the assays, a well containing no peptide was also used.

18.2 RESULTS

The data summarized in FIGS. 29A-B and 30A-B represent antiviral and structural information obtained from peptides derived from the HPIV3 fusion protein DP107-like region (FIG. 29A-B) and the HPIV3 fusion protein DP178-like region (FIG. 30A-B).

As shown in FIG. 29A-B, a number of the HPIV3

DP107-like peptides exhibited potent levels of
antiviral activity. These peptides include, for
example, peptides T-40, T-172 to T-175, T-178, T-184
and T-185.

that a number of the DP178-like peptides tested exhibit a range of anti-viral activity. These peptides include, for example, peptides 194 to 211, as evidenced by their low IC₅₀ values. In fact, peptides 201 to 205 exhibit IC₅₀ values in the nanogram/ml range. In addition, many of the DP178-like peptides exhibited some level of helicity.

Thus, the computer assisted searches described, hereinabove, have successfully identified viral peptide domains that represent highly promising anti-HPIV3 antiviral compounds.

19. EXAMPLE: COMPUTER-ASSISTED IDENTIFICATION OF DP178/DP107 ANALOGS IN SIMIAN IMMUNODEFICIENCY VIRUS

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FIG. 31 represents search results for SIV isolate MM251 (PC/Gene® protein sequence PENV_SIVM2). Both 107x178x4 and ALLMOTI5 search motifs identified two regions with similarities to DP107 and/or DP178.

The peptide regions found by 107x178x4 were

located at amino acid residues 156-215 and 277-289.

The peptide regions found by ALLMOTI5 were located at

amino acid residues 156-219 and 245-286. Both motifs, therefore, identify similar regions.

Interestingly, the first SIV peptide region (i.e., from amino acid residue 156 to approximately amino acid residue 219) correlates with a DP107 region, while the second region identified (i.e., from approximately amino acid residue 245 to approximately amino acid residue 289) correlates with the DP178 region of HIV. In fact, an alignment of SIV isolate MM251 and HIV isolate BRU, followed by a selection of the best peptide matches for HIV DP107 and DP178, reveals that the best matches are found within the peptide regions identified by the 107x178x4 and ALLMOTI5 search motifs.

region at amino acid residues 242-282 is predicted by the Lupas program. This is similar to the observation in HIV in which the coiled-coil is predicted by the Lupas program to be in the DP178 rather than in the DP107 region. It is possible, therefore, that SIV may be similar to HIV in that it may contain a coiled-coil structure in the DP107 region, despite such a structure being missed by the Lupas algorithm.

Likewise, it may be that the region corresponding to a DP178 analog in SIV may exhibit an undefined structure, despite the Lupas program's prediction of a coiled-coil structure.

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20. EXAMPLE: COMPUTER-ASSISTED IDENTIFICATION OF DP178/DP107 ANALOGS IN EPSTEIN-BARR VIRUS

The results presented herein describe the identification of DP178/DP107 analogs within two different Epstein-Barr Virus proteins. Epstein-Barr is a human herpes virus which is the causative agent of, for example, infectious mononucleosis (IM), and is also associated with nasopharyngeal carcinomas (NPC), Burkitt's lymphoma and other diseases. The virus predominantly exists in the latent form and is activated by a variety of stimuli.

FIG. 32 depicts the search motif results for the Epstein-Barr Virus (Strain B95-8; PC/Gene® protein sequence PVGLB_EBV) glycoprotein gp110 precursor (gp115). The 107x178x4 motif identified two regions of interest, namely the regions covered by amino acid residues 95-122 and 631-658. One PZIP region was identified at amino acid residue 732-752 which is most likely a cytoplasmic region of the protein. The Lupas algorithm predicts a coiled-coil structure for amino acids 657-684. No ALLMOTI5 regions were identified.

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FIG. 33 depicts the search motif results for the Zebra (or EB1) trans-activator protein (BZLF1) of the above-identified Epstein-Barr virus. This protein is a transcription factor which represents the primary mediator of viral reactivation. It is a member of the b-ZIP family of transcription factors and shares significant homology with the basic DNA-binding and dimerization domains of the cellular oncogenes c-fos and C/EBP. The Zebra protein functions as a homodimer.

Search results domonstrate that the Zebra protein exhibits a single region which is predicted to be either of DP107 or DP178 similarity, and is found between the known DNA binding and dimerization regions of the protein. Specifically, this region is located

at amino acid residues 193-220, as shown in FIG. 33. The Lupas program predicted no coiled-coil regions.

21. EXAMPLE: COMPUTER-ASSISTED IDENTIFICATION OF DP178/DP107 ANALOGS IN MEASLES VIRUS

FIG. 34 illustrates the motif search results for the fusion protein F1 of measles virus, strain Edmonston (PC Gene® protein sequence PVGLF_MEASE), successfully identifying DP178/DP107 analogs.

The 107x178x4 motif identifies a single region at
amino acid residues 228-262. The ALLMOTIS search
motif identifies three regions, including amino acid
residues 116-184, 228-269 and 452-500. Three regions
containing proline residues followed by a leucine
zipper-like sequence were found beginning at proline
residues 214, 286 and 451.

The Lupas program identified two regions it predicted had potential for coiled-coil structure, which include amino acid residues 141-172 and 444-483.

20 22. EXAMPLE: COMPUTER-ASSISTED IDENTIFICATION OF DP178/DP107 ANALOGS IN HEPATITIS B VIRUS

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FIG. 35 depicts the results of a PZIP motif search conducted on the Hepatitis B virus subtype AYW. Two regions of interest within the major surface antigen precursor S protein were identified. The first lies just C-terminal to the proposed fusion peptide of the major surface antigen (Hbs) which is found at amino acid residues 174-191. The second region is located at amino acid residues 233-267. The Lupas program predicts no coiled-coil repeat regions.

In order to test the potential anti-HBV antiviral activity of these D178/DP107 analog regions, peptides derived from area around the analog regions are synthesized, as shown in FIG. 52A-B. These peptides represent one amino acid peptide "walks" through the

putative DP178/DP107 analog regions. The peptides are synthesized according to standard Fmoc chemistry on Rinkamide MBHA resins to provide for carboxy terminal blockade (Chang, C.D. and Meinhofer, J., 1978, Int. J. Pept. Protein Res. 11:246-249; Fields, G.B. and Noble, R.L., 1990, Int. J. Pept. Protein Res. 35:161-214). Follwing complete synthesis, the peptide aminoterminus is blocked through automated acetylation and the peptide is cleaved with trifluoroacetic acid (TFA) and the appropriate scavengers (King, D.S. et al., 1990, Int. J. Pept. Res. 36:255-266). After cleavage, the peptide is precipitated with ether and dried under vacuum for 24 hours.

The anti-HBV activity of the peptides is tested by utilizing standard assays to determine the test peptide concentration required to cause an acceptable (e.g., 90%) decrease in the amount of viral progeny formed by cells exposed to an HBV viral inoculum. Candidate antivial peptides are further characterized in model systems such as wood chuck tissue culture and animal sytems, prior to testing on humans.

23. EXAMPLE: COMPUTER-ASSISTED IDENTIFICATION OF DP178/DP107 ANALOGS IN SIMIAN MASON-PFIZER MONKEY VIRUS

The results depicted herein illustrate the results of search motifs conducted on the Simian Mason-Pfizer monkey virus. The motifs reveal DP178/DP107 analogs within the enveloped (TM) protein GP20, as shown in FIG. 36.

The 107x178x4 motifs identifies a region at amino acid residues 422-470. The ALLMOTIS finds a region at amino acid residues 408-474. The Lupas program predicted a coiled-coil structure a amino acids 424-459.

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24. EXAMPLE: COMPUTER-ASSISTED IDENTIFICATION OF DP178/DP107 ANALOGS IN BACTERIAL PROTEINS

The results presented herein demonstrate the identification of DP178/DP107 analogs corresponding to sequences present in proteins of a variety of bacterial species.

FIG. 37 depicts the search motif results for the Pseudomonas aeruginosa fimbrial protein (Pilin). Two regions were identified by motifs 107x178x4 and ALLMOTI5. The regions located at amino acid residues 30-67 and 80-144 were identified by the 107x178x4 motif. The regions at amino acid residues 30-68 and 80-125 were identified by the ALLMOTI5.

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Pseudomonas gonorrhoeae fimbrial protein (Pilin). A single region was identified by both the 107x178x4 and the ALLMOTI5 motifs. The region located at amino acid residues 66-97 was identified by the 107x178x4 motif. The region located at amino acid residues 66-125 were identified by the ALLMOTI5 search motif. No coiled-coil regions were predicted by the Lupas program.

FIG. 39 depicts the search motif results for the Hemophilus Influenza fimbrial protein (Pilin). A single region was identified by both the 107x178x4 and the ALLMOTI5 motifs. The region located at amino acid residues 102-129 was identified by the 107x178x4 motif. The region located at amino acid residues 102-148 were identified by the ALLMOTI5 search motif. No coiled-coil regions were predicted by the Lupas program.

FIG. 40 depicts the search motif results for the Staphylococcus aureus toxic shock syndrome Hemophilus Influenza fimbrial protein (Pilin). A single region was identified by both the 107x178x4 and the ALLMOTI5 motifs. The region located at amino acid residues 102-129 was identified by the 107x178x4 motif. The

region located at amino acid residues 102-148 were identified by the ALLMOTI5 search motif. No coiled-coil regions were predicted by the Lupas program.

FIG. 41 summarizes the motif search results conducted on the Staphylococcus aureus enterotoxin Type E protein. These results demonstrate the successful identification of DP178/DP107 analogs corresponding to peptide sequences within this protein, as described below.

The ALLMOTI5 motif identified a region at amino acid residues 22-27. The 107x178x4 motif identified two regions, with the first at amino acid residues 26-69 and the second at 88-115. A P12LZIPC motif search identified two regions, at amino acid residues 163-181 and 230-250.

The Lupas program predicted a region with a high propensity for coiling at amino acid residues 25-54. This sequence is completely contained within the first region identified by both ALLMOTI5 and 107x178x4 motifs.

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FIG. 42 depicts the search motif results conducted on a second Staphylococcus aureus toxin, enterotoxin A. Two regions were identified by the ALLMOTI5 motif, at amino acid residues 22-70 and amino acid residues 164-205. The 107x178x4 motif found two regions, the first at amino acid residues 26-69 and the second at amino acid residues 165-192. A P23LZIPC motif search revealed a region at amino acid residues 216-250. No coiled-coil regions were predicted by the Lupas program.

FIG. 43 shows the motif search results conducted on the E. coli heat labile enterotoxin A protein, demonstrating that identification of DP178/DP107 analogs corresponding to peptides located within this protein. Two regions were identified by the ALLMOTI5 motif, with the first residing at amino acid residues

55-115, and the second residing at amino acid residues 216-254. The 107x178x4 motif identified a single region at amino acid residues 78-105. No coiled-coil regions were predicted by the Lupas program.

25. EXAMPLE: COMPUTER-ASSISTED IDENTIFICATION OF DP178/DP107 ANALOGS WITHIN VARIOUS HUMAN PROTEINS

The results presented herein demonstrate the identification of DP178/DP107 analogs corresponding to peptide sequences present within several different human proteins.

FIG. 44 illustrates the search motif results conducted on the human c-fos oncoprotein. The ALLMOTI5 motif identified a single region at amino acid residues 155-193. The 107x178x4 motif identified one region at amino acid residues 162-193. The Lupas program predicted a region at amino acid residues 148-201 to have coiled-coil structure.

conducted on the human lupus KU autoantigen protein P70. The ALLMOTI5 motif identified a single region at amino acid residues 229-280. The 107x178x4 motif identified one region at amino acid residues 235-292. The Lupas program predicted a region at amino acid residues 232-267 to have coiled-coil structure.

FIG. 46 illustrates the search motif results conducted on the human zinc finger protein 10. The ALLMOTI5 motif identified a single region at amino acid residues 29-81. The 107x178x4 motif identified one region at amino acid residues 29-56. A P23LZIPC motif search found a single region at amino acid residues 420-457. The Lupas program predicted no coiled-coil regions.

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26. EXAMPLE: POTENTIAL MEASLES VIRUS DP178/DP107
ANALOGS: CD AND ANTIVIRAL
CHARACTERIZATION

In the Example presented herein, measles (MeV) virus DP178-like peptides identified by utilizing the computer-assisted search motifs described in the Examples presented in Sections 9 and 21, above, are tested for anti-MeV activity. Additionally, circular dichroism (CD) structural analyses are conducted on the peptides, as discussed below. It is demonstrated that several of the identified peptides exhibit potent antiviral capability. Additionally, it is shown that none of the these peptides exhibit a substantial helical character.

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26.1 MATERIALS AND METHODS

Structural analyses: The CD spectra were measured in a 10mM sodium phosphate, 150mM sodium chloride, pH 7.0, buffer at approximately 10mM concentrations, using a 1 cm pathlength cell on a Jobin/Yvon Autodichrograph Mark V CD spectrophotometer. Peptide concentrations were determined from A_{280} using Edlehoch's method (1967, Biochemistry $\underline{6}$:1948).

assay: The assay utilized herein tested the ability of the peptides to disrupt the ability of Vero cells acutely infected with MeV (i.e., cells which are infected with a multiplicity of infection of 2-3) to fuse and cause syncytial formation on a monolayer of an uninfected line of Vero cells. The more potent the peptide, the lower the observed level of fusion, the greater the antiviral activity of the peptide.

Uninfected confluent monolayers of Vero cells were grown in microtiter wells in 10% FBS EMEM (Eagle Minimum Essential Medium w/o L-glutamine [Bio Whittaker Cat. No. 12-125F], with fetal bovine serum

[FBS; which had been heat inactivated for 30 minutes at 56°C; Bio Whittaker Cat. No. 14-501F) supplemented at 10%, antibiotics/antimycotics (Bio Whittaker Cat. No. 17-602E) added at 1%, and glutamine added at 1%.

To prepare acutely infected Vero cells for addition to the uninfected cells, cultures of acutely infected Vero cells were washed twice with HBSS (Bio Whittaker Cat. No. 10-543F) and cell monolayers were removed with trypsin (Bio Whittaker Cat. No. 17-161E). Once cells detached, media was added, any remaining clumps of cells were dispersed, and hemacytometer cell counts were performed.

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The antiviral assay was conducted by, first, removing all media from the wells containing uninfected Vero cells, then adding peptides (at the dilutions described below) in 10% FBS EMEM, and 50-100 acutely MeV-infected Vero cells per well. Wells were then incubated at 37°C for a maximum of 18 hours.

On day 2, after cells in control wells were checked for fusion centers, media was removed from the wells, followed by addition, to each well, of approximately 50µl 0.25% Crystal Violet stain in methanol. Wells were rinsed twice with water immediately, to remove excess stain and were then allowed to dry. The number of syncytia per well were then counted, using a dissecting microscope.

Anti-MeV antiviral activity plaque reduction assay: The assay utilized herein tested the ability of the peptides to disrupt the ability of MeV to infect permissive, uninfected Vero cells, leading to the infected cells' fusing with uninfected cells to produce syncytia. The lower the observed level of syncytial formation, the greater the antiviral activity of the peptide.

Monolayers of uninfected Vero cells are grown as described above.

The antiviral assay was conducted by, first, removing all media from the wells containing uninfected Vero cells, then adding peptides (at the dilutions described below) in 10% FBS EMEM, and MeV stock virus at a final concentration of 30 plaque forming units (PFU) per well. Wells were then incubated at 37°C for a minimum of 36 hours and a maximum of 48 hours.

On day 2, after cells in control wells were checked for fusion centers, media was removed from the wells, followed by addition, to each well, of approximately 50µl 0.25% Crystal Violet stain in methanol. Wells were rinsed twice with water immediately, to remove excess stain and were then allowed to dry. The number of syncytia per well were then counted, using a dissecting microscope.

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<u>Peptides</u>: The peptides characterized in the study presented herein were peptides T-252A0 to T-256A0, T-257B1/C1, and T-258B1 to T-265B0, and T-266A0 to T-268A0, as shown in FIG. 47. These peptides represent a walk through the DP178-like region of the MeV fusion protein.

Each peptide was tested at 2-fold serial dilutions ranging from $100\mu g/ml$ to approximately 100ng/ml. For each of the assays, a well containing no peptide was also used.

26.2 RESULTS

The data summarized in FIG. 47 represents antiviral and structural information obtained via "peptide walks" through the DP178-like region of the MeV fusion protein.

As shown in FIG. 47, the MeV DP178-like peptides exhibited a range of antiviral activity as crude peptides. Several of these peptides were chosen for purification and further antiviral characterization.

The IC₅₀ values for such peptides were determined, as shown in FIG. 47, and ranged from $1.35\mu g/ml$ (T-257B1/C1) to $0.072\mu g/ml$ (T-265B1). None of the DP178-like peptides showed, by CD analysis, a detectable level of helicity.

Thus, the computer assisted searches described, hereinabove, as in for example, the Example presented in Section 9, for example, successfully identified viral peptide domains that represent highly promising anti-MeV antiviral compounds.

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27. EXAMPLE: POTENTIAL SIV DP178/DP107 ANALOGS: ANTIVIRAL CHARACTERIZATION

In the Example presented herein, simian immunodeficiency virus (SIV) DP178-like peptides

15 identified by utilizing the computer-assisted search motifs described in the Examples presented in Sections 9, 12 and 19, above, were tested for anti-SIV activity. It is demonstrated that several of the identified peptides exhibit potent antiviral capability.

27.1 MATERIALS AND METHODS

Anti-SIV antiviral assays: The assay utilized
herein were as reported in Langolis et al. (Langolis,
25 A.J. et al., 1991, AIDS Research and Human
Retroviruses 7:713-720).

Peptides: The peptides characterized in the study presented herein were peptides T-391 to T-400, as shown in FIG. 48. These peptides represent a walk
through the DP178-like region of the SIV TM protein.

Each peptide was tested at 2-fold serial dilutions ranging from $100\mu g/ml$ to approximately 100ng/ml. For each of the assays, a well containing no peptide was also used.

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27.2 RESULTS

The data summarized in FIG. 48 represents antiviral information obtained via "peptide walks" through the DP178-like region of the SIV TM protein.

As shown in FIG. 48, peptides T-391 to T-400 were tested and exhibited a potent antiviral activity as crude peptides.

Thus, the computer assisted searches described, hereinabove, as in for example, the Example presented in Section 9, for example, successfully identified viral peptide domains that represent highly promising anti-SIV antiviral compounds.

28. EXAMPLE: ANTI-VIRAL ACTIVITY OF DP107 AND DP-178 PEPTIDE TRUNCATIONS AND MUTATIONS

The Example presented in this Section represents a study of the antiviral activity of DP107 and DP178 truncations and mutations. It is demonstrated that several of these DP107 and DP178 modified peptides exhibit substantial antiviral activity.

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28.1 MATERIALS AND METHODS

Anti-HIV assays: The antiviral assays performed
were as those described, above, in Section 6.1.
Assays utilized HIV-1/IIIb and/or HIV-2 NIHZ isolates.
Purified peptides were used, unless otherwise noted in
FIGS. 49A-C.

Peptides: The peptides characterized in the
study presented herein were:

1) FIGS. 49A-C present peptides derived from
the region around and containing the DP178
region of the HIV-1 BRU isolate.
Specifically, this region spanned from gp41
amino acid residue 615 to amino acid residue
717. The peptides listed contain
truncations of this region and/or mutations

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which vary from the DP178 sequence amino acid sequence. Further, certain of the peptides have had amino- and/or carboxy-terminal groups either added or removed, as indicated in the figures; and

2) FIG. 50. presents peptides which represent truncations of DP107 and/or the gp41 region surrounding the DP107 amino acid sequence of HIV-1 BRU isolate. Certain of the peptides are unblocked or biotinylated, as indicated in the figure.

Blocked peptides contained an acyl N-terminus and an amido C-terminus.

28.2 RESULTS

Anti-HIV antiviral data was obtained with the group 1 DP178-derived peptides listed in FIG. 49A-C. The full-length, non-mutant DP178 peptide (referred to in FIG. 49A-C as T20) results shown are for 4ng/ml.

In FIG. 49A, a number of the DP178 truncations exhibited a high level of antiviral activity, as evidenced by their low IC₅₀ values. These include, for example, test peptides T-50, T-624, T-636 to T-641, T-645 to T-650, T-652 to T-654 and T-656. T-50 represents a test peptide which contains a point mutation, as indicated by the residue's shaded background. The HIV-1-derived test peptides exhibited a distinct strain-specific antiviral activity, in that none of the peptides tested on the HIV-2 NIHZ isolate demonstrated appreciable antti-HIV-2 antiviral activity.

Among the peptides listed in FIG. 49B, are test peptides representing the amino (T-4) and carboxy (T-3) terminal halves of DP178 were tested. The amino terminal peptide was not active (IC $_{50}$ >400 μ g/ml) whereas the carboxy terminal peptide showed potent antiviral

activity (IC₅₀= $3\mu g/ml$). A number of additional test peptides also exhibited a high level of antiviral activity. These included, for example, T-61/T-102, T-217 to T-221, T-235, T-381, T-677, T-377, T-590, T-378, T-591, T-271 to T-272, T-611, T-222 to T-223 and T-60/T-224. Certain of the antiviral peptides contain point mutations and/or amino acid residue additions which vary from the DP178 amino acid sequence.

In FIG. 49C, point mutations and/or amino and/or carboxy-terminal modifications are introduced into the DP178 amino acid sequence itself. As shown in the figure, the majority of the test peptides listed exhibit potent antiviral activity.

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Truncations of the DP107 peptide (referred to in IG. 50 as T21) were also produced and tested, as shown in FIG. 50. FIG. 50 also presents data concerning blocked and unblocked peptides which contain additional amino acid residues from the gp41 region in which the DP107 sequence resides. Most of these peptides showed antiviral activity, as evidenced by their low IC50 values.

Thus, the results presented in this Section demonstrate that not only do the full length DP107 and DP178 peptides exhibit potent antiviral activity, but truncations and/or mutant versions of these peptides can also possess substantial antiviral character.

29: EXAMPLE: POTENTIAL EPSTEIN-BARR DP178/DP107 ANALOGS: ANTIVIRAL CHARACTERIZATION

In the Example presented herein, peptides derived
from the Epstein-Barr (EBV) DP-178/DP107 analog region
of the Zebra protein identified, above, in the Example
presented in Section 20 are described and tested for
anti-EBV activity. It is demonstrated that among
these peptides are ones which exhibit potential antiviral activity.

29.1 MATERIALS AND METHODS

Electrophoretic Mobility Shift Assays (EMSA): Briefly, an EBV Zebra protein was synthesized utilizing SP6 RNA polymerase in vitro transcription and wheat germ in vitro translation systems (Promega Corporation recommendations; Butler, E.T. and Chamberlain, M.J., 1984, J. Biol. Chem. 257:5772; Pelham, H.R.B. and Jackson, R.J., 1976, Eur. J. Biochem. 67:247). The in vitro translated Zebra protein was then preincubated with increasing amounts of peptide up to 250 ng/ml prior to the addition of 10,000 to 20,000 c.p.m. of a 32P-labeled Zebra response element DNA fragment. After a 20 minute incubation in the presence of the response element, the reaction was analyzed on a 4% non-denaturing polyacrylamide gel, followed by autoradiography, utilizing standard gel-15 shift procedures. The ability of a test peptide to prevent Zebra homodimer DNA binding was assayed by the peptide's ability to abolish the response element gel migration retardation characteristic of a protein-20 bound nucleic acid molecule.

Peptides: The peptides characterized in this study represent peptide walks through the region containing, and flanked on both sides by, the DP178/DP107 analog region identified in the Example presented in Section 20, above, and shown as shown in FIG. 33. Specifically, the peptide walks covered the region from amino acid residue 173 to amino acid residue 246 of the EBV Zebra protein.

range of concentrations, with 150ng/ml being the lowest concentration at which any of the peptides exerted an inhibitory effect.

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29.2 RESULTS

The EBV Zebra protein transcription factor contains a DP178/DP107 analog region, as demonstrated in the Example presented, above, in Section 20. This protein appears to be the primary factor responsible for the reactivation capability of the virus. A method by which the DNA-binding function of the Zebra virus may be abolished may, therefore, represent an effective antiviral technique. In order to identify potential anti-EBV DP178/DP107 peptides, therefore, peptides derived from the region identified in Section 20, above, were tested for their ability to inhibit Zebra protein DNA binding.

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The test peptides' ability to inhibit Zebra protein DNA binding was assayed via the EMSA assays described, above, in Section 28.1. The data summarized in FIG. 51A-B presents the results of EMSA assays of the listed EBV test peptides. These peptides represent one amino acid "walks" through the region containing, and flanked on both sides by, the DP178/DP107 analog region identified in the Example presented in Section 20, above, and shown as shown in FIG. 33. As shown in FIG. 51A-B, the region from which these peptides are derived lies from EBV Zebra protein amino acid residue 173 to 246. A number of the test peptides which were assayed exhibited an ability to inhibit Zebra protein homodimer DNA binding, including 439, 441, 444 and 445.

Those peptides which exhibit an ability to inhibit Zebra protein DNA binding represent potential anti-EBV antiviral compounds whose ability to inhibit EBV infection can be further characterized.

The present invention is not to be limited in scope by the specific embodiments described which are intended as single illustrations of individual aspects

of the invention, and functionally equivalent methods and components are within the scope of the invention. Indeed, various modifications of the invention, in addition to those shown and described herein will become apparent to those skilled in the art from the foregoing description and accompanying drawings. Such modifications are intended to fall within the scope of the appended claims.

WHAT IS CLAIMED IS:

 An isolated peptide recognized by an ALLMOTI5, 107x178x4 or a PLZIP sequence search motif.

- 2. The peptide of Claim 1 wherein the peptide corresponds to a peptide present in a virus.
- 3. The peptide of Claim 2 in which the virus is 10 HIV-1 or HIV-2.
 - 4. The peptide of Claim 2 in which the virus is a respiratory syncytial virus.
- 5. The peptide of Claim 2 in which the virus is a human parainfluenza virus.
- The peptide of Claim 2 in which the virus is an influenza virus.
 - 7. The peptide of Claim 2 in which the virus is a hepatitis B virus.
- 8. The peptide of Claim 2 wherein the virus is an Epstein-Barr virus.
 - 9. A method for the inhibition of transmission of a virus to a cell, comprising contacting the cell with an effective concentration of a peptide recognized by an ALIMOTIS, 107x178x4 or a PLZIP sequence search motif for an effective period of time so that no infection of the cell by the virus occurs.
- 10. The method of Claim 9 wherein the virus is HIV-1 or HIV-2.

11. The method of Claim 9 wherein the virus is a respiratory syncytial virus.

- 12. The method of Claim 9 wherein the virus is a human parainfluenza virus.
- 13. The method of Claim 9 wherein the virus is an influenza virus.
- 14. The method of Claim 9 in which the virus is a hepatitis B virus.
 - 15. The method of Claim 9 wherein the virus is an Epstein-Barr virus.

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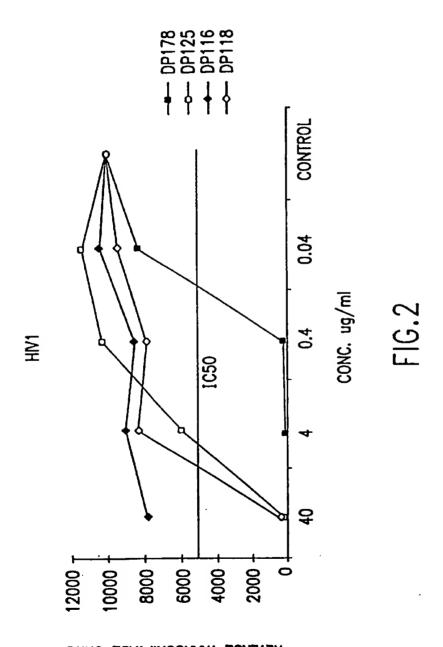
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HIV1LAI	(DP-178; SEQ ID:1)	YTSL 1HSL 1EESQNQQEKNEQELLELDKWASLWNWF
HIV1SF2	(DP-185; SEQ ID:3)	YTNTIYNLLEESQNQQEKNEQELLELDKWASLWNWF
HIV1RF	(SEQ ID:4)	YTGIIYNLLEESQNQQEKNEQELLELDKWANLWNWF
HIVIM	HIV1MN (SEQ ID:5)	YTSL IYSLLEKSQTQQEKNEQELLELDKWASLWNWF
HIV2ROD	HIV2ROD (SEQ ID:6)	LEANISKSLEQAQIQQEKNAYELQKLNSWDIFGNWF
HIVZNIH	HIV2NIHZ (SEQ ID:7)	LEANISQSLEQAQIQQEKNMYELQKLNSWDVFTNWL
0P180	(SEQ 10:2)	SSESFTLLEGWNNWKLQLAEGMLEQINEKHYLEDIS
DP118	(SEQ ID:10)	QOLL DVVKRQQEMLRL TVWGTKNLQARVTA I EKYLKDQ
DP125	(SEQ 10:8)	CGGNNLLRAIEAQQHLLQLTVMGIKQLQARILAVERYLKDC
20118	(SEO 10.9)	SOUTH TOWN

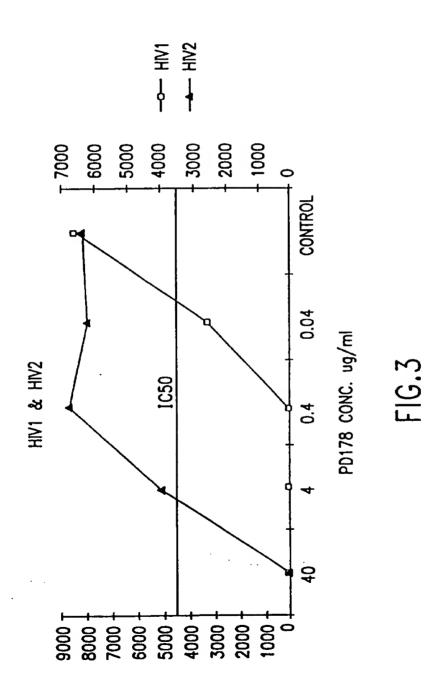
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REVERSE TRANSCRIPTASE UNITS

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HUMDET C	or Sync	<u>y</u> ciu,	WCII.	Concen	ici de l'on	<u> </u>	nl (micro	, , ,	
DP178	10	5	1	0.2	0.1	0.05	0.025	0.0125	Control
Syncylia					_		•	^	· ·
HIVILAL	0	0	0	0	0	0	0	0	67
H]V1MN	0	0	0	0	0	ND	ND	ND	34
HIVIRF	0	0	0	0	0	ND	ND ND	ND ND	65
HIVISF2	0	0	0	0	0	ND	MD	ND	58
DP125	10	5	1	0.2_	0.1	0.05_	0.025	0.0125_	Control
Syncylia									67
HIVILAL	0	0	54	69	80	75	79	82	67
HIVIMN	0	0	30	36	ND	ND	ND	ND	34
HIVIRF	0	0	67	63	ND	ND	ND	ND	65
HIVISF2	0	0	9	6 6	ND	ND	ND	ОN	58
DP116	. 10	5	1	0.2	0.1	0.05	0.025	0.0125	Control
Syncylio	 -								
HIVILAL	75	ND	ND	ND	МD	ND	ND	ND	67
HIVIMN	35	ND	ND	ND	ND	ND	ND	ND	34
HIVIRF	81	ND	ND	ND	ND	ND	ND	ND	65
HJV1SF2	81	ND	ND	ND	ND	ND	ND	ON	58

FIG.4A

DP180	40	20	10_	5_	2.5	1.25	0.625	0.3125	Control
Syncylia HIVILAI	50	>45	>45	>45	>45	>45	>45	>45	58
DP185	40	20	10_	5_	2.5	1.25	0.625	0.3125	Control
Syncylia HIVILAI	0	0	0	0	0	0	0	ND	60

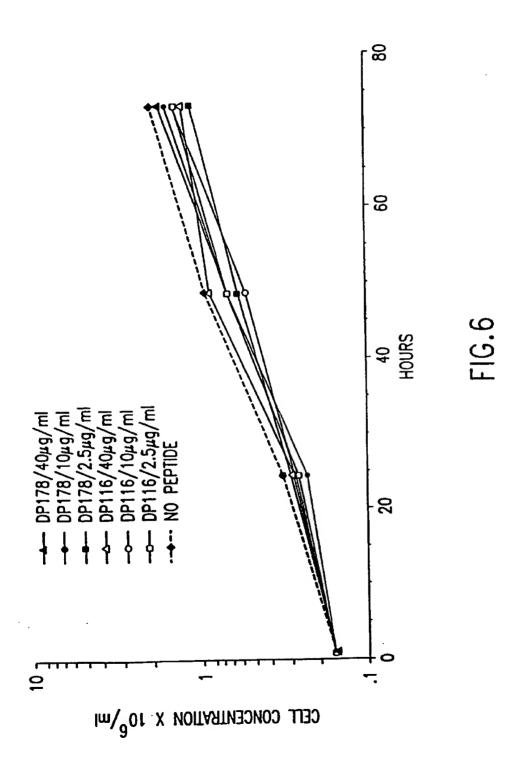
FIG.4B

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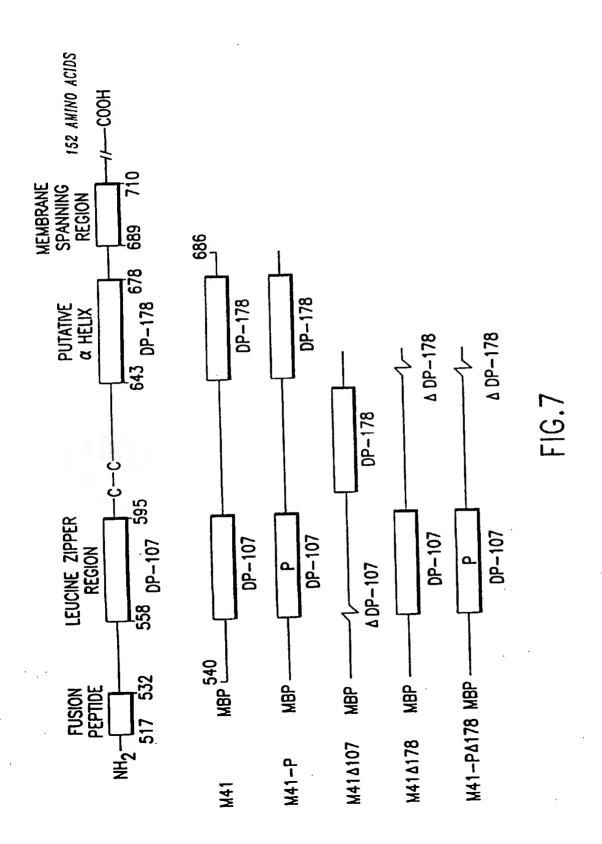
				HIVI					
_	Number	of	Syncyli	io/well:	concer	ntration	in ng/ml	(nanograms/ml)	
OP178	20	10	5	2.5	1.25	0.625	0.3125	Control	
Syncylia HIV1	0	0	0	0	0	14	20	48	
DP116	20	10	5	2.5	1.25	0.625	0.3125	Control	
Syncytio HIV1	ND	48	ND	ND	ND	ND	ND	ND	
HIV2									
	Number	oſ	Syncyt	io/well:	conce	ntration	in μg/ml	(micrograms/ml)	
DP178	20	10	5	2.5	1.25	0.625	0.3125	Control	
Syncylia HIV2	50	54	55	57	63	77	78	76	
DP116	20	10	5	2.5	1.25	0.625	0.3125	Control	
Syncylio HIV2	ND	58	ND	ND	ND	ND	ND	ND	

FIG.5

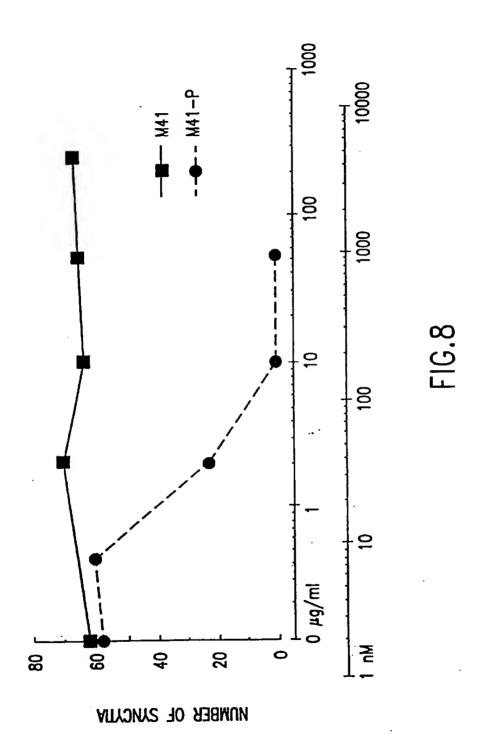
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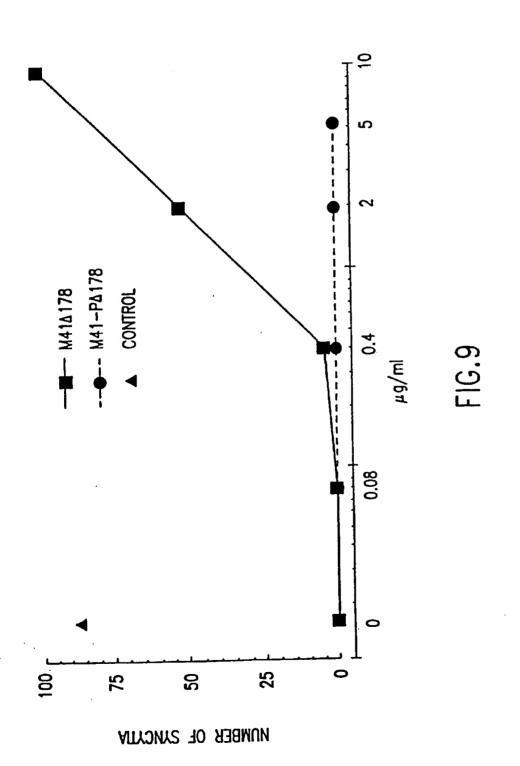
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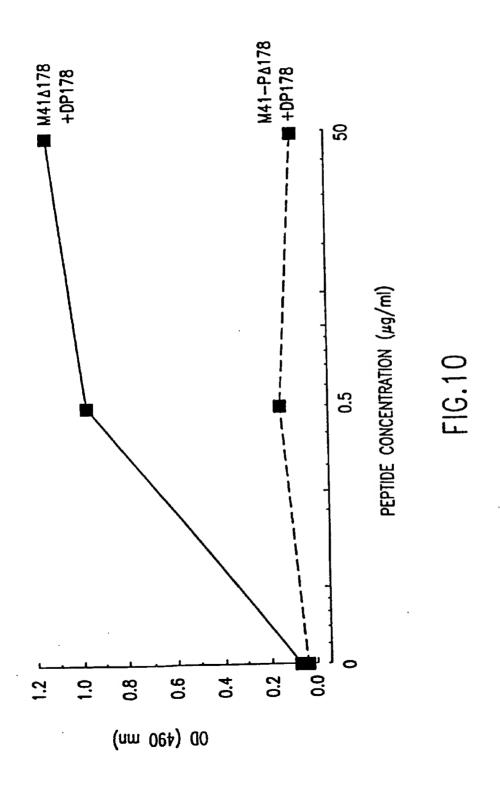
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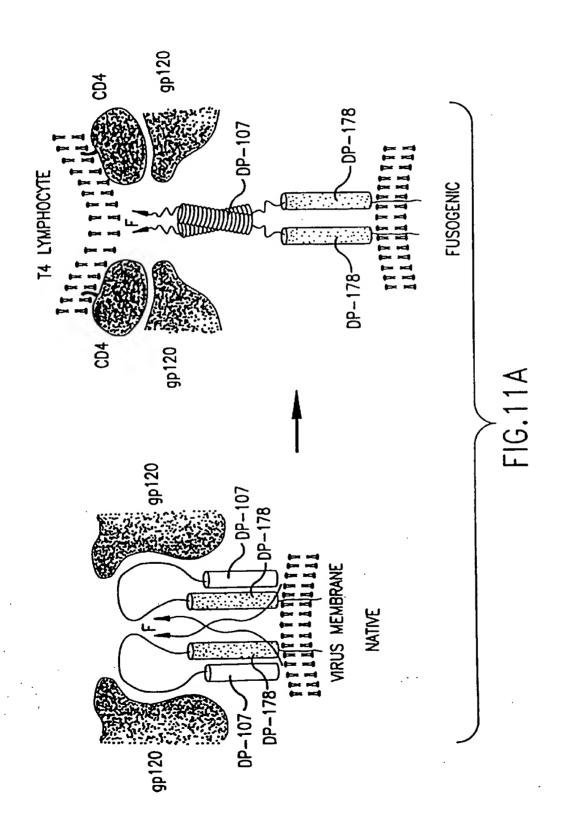
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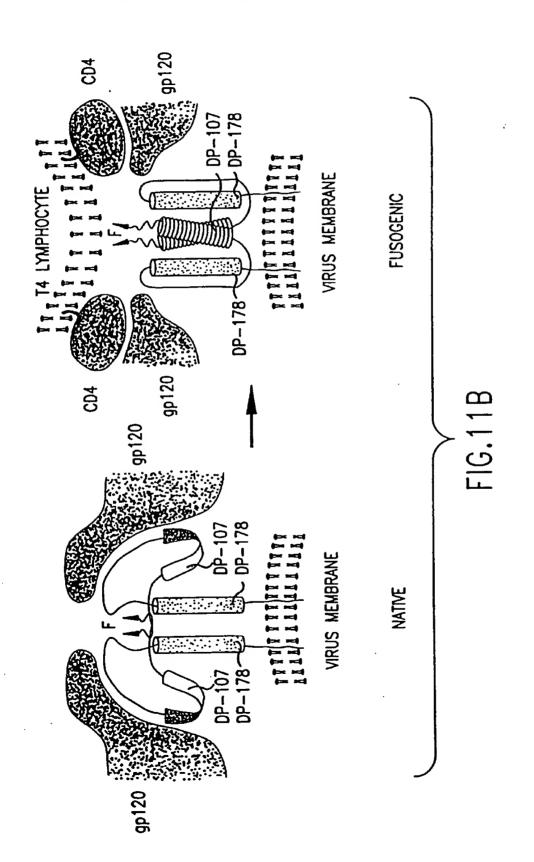
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Motifs		[LMNV] {CFG1MPTW}	[IKLT] {CFGHIMPRWM}	[AILNV] {CDFGHILPVMY}	[ELR] {ACFGMPVMY}	[FILTV] {ACFLIPPTWM}
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FIG. 12

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FIG. 13

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	Parent Hotif	[LMNV] {CFCIMPTW}	[1L01] {GF1WPSTY} [1L01V] {G0F1WPST} [1L01V] {G0F1WPST}	[EKLNOV] {CDFNAPSVY} [[EKLNOV] {CFNAPS} [[EKLNOV] {CFNAPS}
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FIG. 14

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Hybrid Molif			[EKLINOVY] {CFGNPW} [EKLINOVNY] {CFGNP} [EFKLINOVNY] {CFGNP}	EILNOSY] {ACFGWPRYMY} [EILMNOSYY] {CFGWPM} EILNOSMY] {CFGWPRYY} [EILMNOSYMY} {CFGWP} EFILNOSMY] {CFGWPRYY} [EFILMNOSYMY] {CFGWP}
Parent Holif		[LMN] {CFG1MPTW}	[EKLOY] {ACFCAPRYMY} [EKLOMY] {CFCAPRYY} [EFKLOMY] {CFCAPRYY}	ت
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FIG. 15

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Hybrid Holif		ILOTV] {CDFIMPS!} EKLNOV] {CFRAPS} EFKLOMY] {CFGAPRYY} EFILNOSMY] {CFGAPRYY} [EFIKINOSTYMY] {CFAP}	
Parent Motif			[FILTV] {ACFLIAPTWM}
Positions	A 0 A 0 A 0 A 0 A 0		CFHOILE KEFSEVEGRIDOOLEKY
		DP-107 (env_hv1bru)L1=D	FLU LOOP 36 I E K T N E K F H O

FIG. 16

		7872	2-020	(SHEET	18 0
Hybrid Motif		[EFIKLHNOTYMY] {GFUP}	[EFILMACRSTWY] {GFMP}	[EFKLINOVIY] {CFJP]	[EFIKLMNOSVMY] {GFAP}
Porent Wolif		[LIAV] {CFCIAPTIN] [1LOTV] {CDFJAPST} [EFKLOHY] {CFGIAPRYY}	[LLAN] {CCGIMPTM} [LLOTV] {CDFIMPST} [EFILNOSHY] {CFGMPRVY}	[LIMN] {GFGIMPTW} [EKLNOV] {GFKAPS} [EFKLOMY] {GFGKPRVY}	[LMAY] {CFGIMPTW} [EKLNOY] {CFRAPS} [EFILNOSWY] {CFGAPRYY}
		KNYHLENEVARLKKL 1 LLQLIIVWGIKOLOARILAVERYLKDO 1 NOQEKNEQELLELOKWASLWWF	K NY H L E N E V A R L K K L L L O L T V W G I K O L O A R I L A V E R Y L K O O E S O N O O E K N E O E L L E L D K W A S L W N W F		K N Y H L E N E V A R L K K L L O L I V W G I K O L O A R I L A V E R Y L K D O E S O N O O E K N E O E L L E L D K W A S L W N W F
	D A 0 A	<u> </u>	<u> </u>	KNYHLENEVARLKKL LOLTVWGIKOLOARILAVERYLKDO MOOEKNEOELLELDKWASLWWF	o z
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		-0 v			<u> </u>
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	Sequence	14 yeast) env_hvibru)L1=0 env_hvibru)Y1=A	GCN4 (gcn4 yeast) DP-107 (env_hv1bru)L1=D DP-178 (env_hv1bru)Y1=D		GCN4 (gan4 yeast) OP-107 (env_hv1bru)L2=0 OP-178 (env_hv1bru)Y1=0

FIG.17

7872-020 (SHEET 19 OF 63)

Hybrid Molif Parent Holif \blacksquare 35 a > z v - X W W O N env_hv1bru)Y1=A env_hv1bru)L2=0 (env_hv1bru)Y1=0 env_hv1bru)L1=0 (acn4 yeast)

FIG. 18

7872-020 (SHEET 20 OF 63)

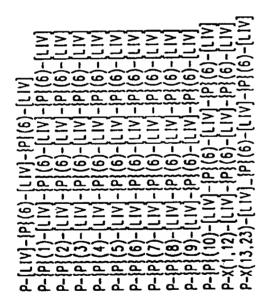


FIG. 19

7872-020 (SHEET 21 OF 63)

Fusion

▼ALLMOTI5▼

Peptide

4107x178x44

v....FLGFLG

A AGSTMGARSM TLTVQARQ ALLSGIYQQQ DP107-NNL

LRAIEAOOHL LOLTYWGIKO LOARILAYER YLKDO-DP107 QLLG * V I WGC

4107x178x44

♥ALLMOTI5♥

LVS Coilcd-Coil

SGKLICT TAVP ▼WNASWS NKSLEQIWNN MTWM *E ◆WDREINN DP178-

YTSLIHSL IEESONOOEK NEOELLELDK* WASLWNWT-DP178 NI

◆Transmembrane Region ◆

TNWLWYIK + IF IMIYGGLYGLRIVFAVLSIY NRVRQGYS + PL

+P23LZIPC+

SFQTHLPTPR GPDR *PEGIEE EGGERDRDRS IRLVNGSLAL IWDDLRSL+ CL

♥ALLMOTI5♥

4107x178x44

F ★SYHRLRDLL LIVTRIVELL GRRGW ★EALKY WWNLLOYWSO

ELKNSAYSLL NAT * ALAVAEG TDRVIEVVQG A * CRAIRHIPR

RIRQGLERIL L

7872-020 (SHEET 22 OF 63)

Fusion

VALLMOTISY

Peptide

★107x178x4◆

V....FLGFL

LGVGSAIAS GVA AVSKYLHL EGEVNICIKSA

+P1&12LZIPC+

LLSTNKAVVS LSNGVSVLTS KVLDLKNYID KQ * LL +PIVNKQ

4107x178x44

SC ASISNIETY I+ EFOOKNNRLLETTREFSVNAGA VITPVSTMLTNSELLSL

+P1&12LZIPC+

♥ALLMOTI5♥

INDM +PI +TNDQ KKLMSNNVQI V+ RQQSYSI+ MS IIKEEVLAYV

VQ♥ LPLYGVID TPCWKLHTSP LCTTNTKEGS NICLTRTDRG WYCDNAGSVS

FFPQAETCKV QSNRVFCDTM NSLTLPSEIN LCNVDIFNPK

YDCKIMTSKT DVSSSVITSL GAIVSCYGKT KCTASNKNRG

IIKTFSNĢCDYVSNKGMDTV SVGNTLYYVN KQEGKSLYVK G

+P7, 12, & 23LZIPC+

4107x178x44

▼ALLMOTI5▼

EPHNFYDPLVF +PSDE +FDASISQVNEKINQSLAF *I+ RKSDELL+

+ Transmembrane Region ◆

HNVNA + GK STTN + IMITTL IIVIIVILLS LIAVGLLLY + C+

KARSTPVTLS KDQLSGINNI AFSN

7872-020 (SHEET 23 OF 63)

Fusion Peptide

♦ALLMOTI5♥ **♦107x178x4**♠

FLGFLG

♥AAGTA MGAAA ◆TALTYOSOHLLAGILOQOKNLLAAY

4107x178x44

EAQ+ QQM +LKLTIWGYKNLNARYTALEKYLEDQARLN+ AWG+ CA

LVS Coilcd-Coil

4107x178x44 YALLMOTISY

WKQVCHTTVP WQWNNRTPDW VNNMT *WLE *WERQISYLEGNIT

4107x178x44

TOLEEARAGEEKNLD * AYOKLSS* WSDFWSW * FDF *SKWLN +ILK

+Transmembrane Region +

IGFLDYLGIIGLRLLYTY + YS + CIARVRQGYS PLSPQIHIHP WKGQPDNAEG

PGEGGDKRKN SSEPWQKESG TAEWKSNWCK RLTNWCSISS IWLYNS

∀ALLMOTI5∀

♥CLTL LVHLRSAFQY IQYGLGELKA AAQEAVVALA RLAQNAGYQIWL♥

ACRSAYRA IINSPRRVRQ GLEGILN

7872-020 (SHEET 24 OF 63)

Fusion

4107x178x44

LVS Coiled-Coil

....FAG

Peptide VALLMOTI5 V

*VVL AGVALGVATA AQITAGIALHQ **SNLNAQAIQ

SLRTSLEOSNKAIEEIREATOETVIA* VOGVODY* VNNEL* VP

VALLMOTISY

4107x178x44

+P6 & 12LZIPC+

AMOHMSCELVGQRLGLRLLRYYTELLSIFGPSLRD +PISA +VEISIQALIYAL

GGEHKILEKLGYSGSD ↑ MIAILESRGIKTKI ▼ THVDLPGKF IILSISY

+P1 & 12LZIPC+

PTLSEVKGVIVHRLEAV SYNIGSQEWYTTVPRYIATNGYLISNFDESSCVFVS

ESAICSONSL YPMSPLLQQC IRGDTSSCAR TLVSGTMGNK FILSKGNIVA

NCASILCKCY STSTIINQSP DKLLTFIASD TCPLVEIDGA TIQVGGRQYP

LVS Coiled-Coil

VALLMOTI5 ▼

+P12 & 23LZIPC+

DMVYEGKVAL G +PAISLD +RL+DVGTNLGNALKKLDDAKYLI+

+ Transmembrane Region +

DSS+ NOILETVR RS+* SFN + FGSLL SYPILSCTAL ALLLLIYCC+

K RRYQQTLKQH TKVDPAFKPD LTGTSKSYVR SL

7872-020 (SHEET 25 OF 63)

Fusion ▼ALLMOTI5▼

Peptide

4107x178x44

▼.....FIGAI IGSVALGVA TAAQITAASA LIQANQNAAN AILRLKESITA

TIEAVHEYTDGLSQLAYA♠ VG KM♥ QQFVNDQFNNTAQELDCIKITQQV

♥ALLMOTI5♥

GVELNLYLTELTTV FGPQITSPAL *TQLTIQALYNAGGNMDYLLTKLGVG

+P1 & 12LZIPC+

LSVST TKGFASALVP KVVTQVGSVI EELDTSYCIE TDLDLYCTRI VTFPMSPGIY

SCLNGNTSAC MYSKTEGALT TPYMTLKGSV IANCKMTTCR CADPPGIISQ

♥ALLMOTI5♥

4107x178x44

NYGEAVSLID RHSCN A VLSLD GITLRLSGEF DATYQKNISI LDSQVIVTG

LVS Coiled-Coil

Trans-

*N LDISTELGNV NNSISNALDK LEESNSKLDK VNVKLTSTSA *LIT* YL

membrane Region +

<u>LTAISLVCGILSLV</u> * <u>LACYLMY</u> * KQKAQQKTLLWLGNNTLGQMRATTKM

7872-020 (SHEET 26 OF 63)

Fusion

♥ ALLMOTI5 ♥

Peptide

↑107x178x4 ↑LVS Coiled-Coil

....FFGGV

◆IG ▼TIALG •YATSAQITAAVALVEAKQARSDIEKLKE

AIRDTNKAVQSVQSSIGNLIVAIKSVQ* DYVNKE** IVPSIARLGCEAAG

VALLMOTISY

4107x178x44

LQLGIALTQH *YSELTNIFGDNIGSLOEKGIKLOGIASLYRTNITEY*

+P5 & 12LZIPC+

IFTTSTVDKYDIYDLLFTESIKVRVIDVDLNDYSITLQVRL +PLLTRLLNTQIYR

VDSISYNI+ QNREWYI+ PLPSHIMTKGAFLGGADVKECIEAFSSYIC

PSDPGFVLNHEMESCLSGNISQCPRTVVKSDIVPRYAFVNGGVVANCITT

TCTCNGIGNRINQPPDQGVKIITHKECNTIGINGMLFNTNKEGTLAFYTP

VALLMOTI5V

4107x178x44

+P6 & 23LZIPC+

NDITLNNSVALD +PIDI +SIELN +KAKSDLEESKEWI+ RRSNOKL+

+ Transmembrane Region +

DSIGNWHOSSTT

+IIIV A LIM IIILEIINVT II +

ILAVKYY R

IQKRNRVDQN DKPYVLTNK

7872-020 (SHEET 27 OF 63)

Fusion
Peptide
.....GLFGAI AGFIENGWEGMIDGWYGFRHQNSEGTG

4107x178x44

♥ALLMOTI5♥

LVS Coiled-Coil

*Q *AADLKST *QAAIDQINGKLNRVIEKTNEKFHQIEKEFSEVEGRIQ

DLEKYVEDTKIDL* WSYNAELLVALENOHTI* DLT▼ DSEMNKLFEKTR

RQLRENAEEMGNGCFKIYHKCDNACIESIRNGTYDHDVYRDEALNNRFQIKG

VELKSGYKDWILWISFAISCFLLCVVLLGFIMWACQRGNIRCNICI

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7872-020 (SHEET 28 OF 63)

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7872-020 (SHEET 29 OF 63)

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7872-020 (SHEET 30 OF 63)

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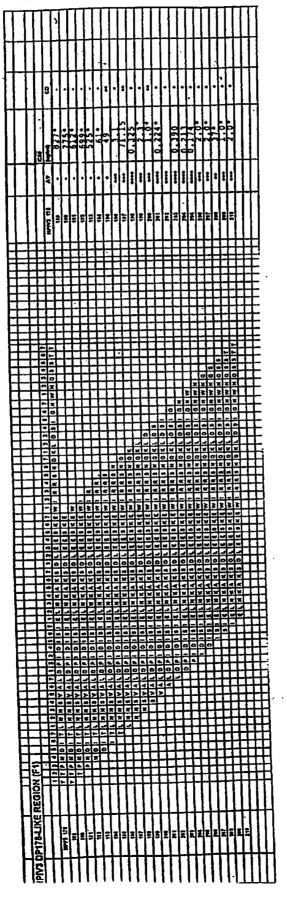
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Fusion

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Peptide

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LLDVVKRQQELLRLTVWGTKNLQTRVTAIEKYLKDQAQL ANAWG CAF

♥ALLMOTI5♥

*LVS Predicted Coiled -Coil

RQVCHTTVPWPNASLTPDW *NND *TWQEWERKVDFLEENITALLEEAQIQQ

↑107x178x4↑

IYIVMLAKLRQGYRPVFSSPPSYFQXTHTQQDPALPTREGKEGDGGEGGGNSSWP

WQIEYIHF

PCT/US95/16733

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MTRRRVLSVVVLLAALACRLGAQTPEQPAPPATTVQPTATRQQTSFPFRVCELSSHGDLFRFSSD

4107x178x44

IQCPSFGTRENHTEGLLMVFKDNIIPYSF *KVRSYTKIVTNILIYNGWYADSVTNRHE*

EKFSVDSY ETDQMDTIYQ CYNAVKMTKD GLTRVYVDRD GVNITVNLKP TGGLANGVRR

YASQTELYDA PGWLIWTYRT RTTVNCLITD MMAKSNSPFD FFVTTTGQTV EMSPFYDGKN

KETFHERADS FHVRTNYKIV DYDNRGTNPQ GERRAFLDKG TYTLSWKLEN RTAYCPLQHW

QTFDSTIATE TGKSIHFVTD EGTSSFVTNT TVGIELPDAF KCIEEQVNKT HEKYEAVQD

RYTKGQEAIT YFITSGGLLL AWLPLTPRSL ATVKNLTELT TPTSSPPSSP SPPAPSAARG

STPAAVLRRR RRDAGNATTP VPPTAPGKSL GTLNNPATVQ IQFAYDSLRR QINRMLGDLA

RAWCLEQKRQ NMVLRELTKI NPTTVMSSIY GKAVAAKRLG DVISVSQCVP VNQATVTLRK

SMRVPGSETM CYSRPLVSFS FINDTKTYEG QLGTDNEIFL TKKMTEVCQA TSQYYFQSGN

107x178x4
EIHVYNDYHH FKTIELDGIA TLQTFISLNT *SLIENIDFASLELYSRDEQRASNVFD *LE*

LVS Predicted Coiled Coil TM Potential
GIFREYNFQAQNIAGLRKDLDNAVSN* GRNQ FVDGLGELMDSLGSVG QSITN

→P12LZIPC →

TM Potential

LVSTVGGLFSSLVSGFISF FK N +PFGGMLILVLVAGVVILVISL+ TRRTRQMS

QQPVQMLYPG IDELAQQHAS GEGPGINPIS KTELQAIMLA LHEQNQEQKR AAQRAAGPSV

ASRALQAARDRFPGLRRRRY HDPETAAALL GEAETEF

PCT/US95/16733

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MMDPNSTSED VKFTPDPYQV PFVQAFDQAT RVYQDLGGPS QAPLPCVLWP VLPEPLPQGQ

*
LTAYHVSTAP TGSWFSAPQP APENAYQAYA APQLFPVSDI TQNQQTNQAG GEAPQPGDNS

TVQTAAAVVF ACPGANQGQQ LADIGVPQPA PVAAPARRTR KPQQPESLEE CDSELEI

@DNA Binding@

<u>↑107x178x4</u> +Dimerization+

@KRY KNRVASRKCRAK ♠FK@ Q

+LLOHYREVAAAKSSENDRLRLLLKO.

MCPSLDVD+ SI IPRTPDVLHE DLLNF

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Fusion

Peptide

♥ALLMOTI5♥

LVS Coiled-Coil

FAG

♥VVLAGAALGVATAAQITAGIALHQSML*NSQAIDNLRASLETTN

QAIEAIRQAGQEMI*LAVQGVQDYINN♥ ELIPSMNQLSCDLIGQKLGLKLLRYYT

+P23LZIPC+

P6,12LZIPC

★107x178x4◆

♥ALLMOTI5♥

EILSLFGPSLRD +PISA +VEISIQALSYALGGDINKV+ LEKLGYSGGDL+

P1,12LZIPC

LGILES

 RGIKARI

▼ THVDTESYFIVLSIAY

 *PTLSEIKGVIVHRLEGV

* SY

NIGSQEWYTTVPKYVATQGYLISNFDESSCTFMPEGTVCSQNALYPMSPLLQECL

RGSTKSCARTLVSGSFGNRFILSQGNLIANCASILCKCYTTGTIINQDPDKILTYIAA

+P23LZIPC÷

+P12LZIPC÷

▼ALLMOTI5 ▼

LVS Coiled-Coil

DHCPVVEVNGVTIQVGSRRYPDAVYLHRIDLGP →P ▼IS*LERLDVGTNLGN

◆Transmembrane Region ◆

AIAKLEDAKELL÷ ESSDOI*L÷ RSMK ◆GLSSTSIVYILI♥ AVCLGGLIGIP

<u>ALICCC</u> ◆ RGRCNKKGEQVGMSRPGLKPDLTGTSKSYVRSL

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Pre S1 and Pre S2
MGQNLSTSNPLGFFPDHQLDPAFRANTANPDWDFNPNKDTWPDANKVGAGAFG
LGFTPPHGGLLGWSPQAQGILQTLPANPPPASTNRQSGRQPTPLSPPLRNTHPQAM
QWNSTTFHQTLQDPRVRGLYFPAGGSSSGTVNPVLTTASPLSSIFSRIGDPALN

Major Surface Antigen (HBs)

Fusion

Peptide

♣P12 & 23LZIPC

MENITSG FLG *PLL VLQAGFFLLTRILTI* PQSLDSWWTSLNFLGGTTVCLG

P12 & 23LZIPC
QNSQSPTSNHSPTSCPPTC *PGYRWMCLRRFIIFLFILLLCLIFLLVLLDYQGML*
PVCPLIPGSSTTSTGPCRTCMTTAQGTSMYPSCCCTKPSDGNCTCIPIPSSWAFGKF

◆ <u>Transmembrane Region</u> ◆
LWEWASARFSWLS ◆ <u>LLVPFVOWFVGLSPTVWLSVI</u> ◆ WMMWYWGPSL

- ◆Transmembrane Region ◆
- YSILSPFLPLLPIFFCLWVYI •

7872-020 (SHEET 43 OF 63)

Fusion

♥ALLMOTI5♥

<u>↑107x178x4</u>

Peptide

*LVS Coiled Coil

AIQLIPLFVG LGI *TTAVSTGAAGLGVS *IT *QYTKLSHQLISDV

OAISSTIODLODOVDSLAEVVLQ* NRRGLDLLTAE A QGGI♥

CLALQEKCCFYANKSGIVRDKIKNLQDDLERRRRQLIDNPFWTSFHG

FLPYVMPLLGPLLCLLLVLSFGPIIFNKLMTFIKHQIESIQAKPIQVHYH

Transmembrane Region

RLEQEDSGGSYLTLT......??????????????????????????

FIG 36

7872-020 (SHEET 44 OF 63)

MKAQKGFTLI ELMIVVAIIG ILAAIAIPQ

- **↑107x178x4↑**
- **♥ALLMOTI5♥**
- **↑ YODYTARTQVTRAVSEVSALKTAAESAILEGKEIVSSA ↑ T**

PK DTQYDIGFT

- <u>↑107x178x4</u>
- **♥**ALLMOTI5**♥**
- **♦♥ESTLLDGSGKSQIQVTDNQDGTVELVATLGKSSGS♦**AIKGAVITVSR**♥**

KNDGV WNCKITKTPT AWKPNYAPAN CPKS

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MNTLQKGFTL IELMIVIAIV GILAAVALPA YQDYTARAQV

SEAILLAEGQ KSAVTEYYLN HGIWP

- **↑107x178x4↑**
- **♥ALLMOTI5♥**
- **♦♥KDNTSAGVASSSSIKGKYVKEVKVENGVVTAT**◆

MNSSNVNKEIQGKKLSLWAKRQDGSVKW♥

FCGQP VTRNAKDDTV TADATGNDGK IDTKHLPSTC RDNFDAS

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MKKTLLGSLI LLAFAGNVQA DINTETSGKV TFFGKVVENT

CKVKTEHKNL SVVLNDVGKN SLSTKVNTAM PTPFTITLQN

CDPTTANGTA NKANKVGLYF Y

- **↑107x178x4↑**
- **▼ALLMOTI5▼**
- **▲ ♥ SWKNVDKENNFTLKNEQTTADYATNVNI ◆**

QLMESNGTKAISVVGKETE

DF MHTNNNGVAL NQTHPNNAHI SGSTQLTTGT NELPLHFIAQ

YYATNKATAG KVQSSVDFQI AYE

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MNKKLLMNFF IVSPLLLATT ATDFTPVP

- **↑107x178x4**◆
- **♥ALLMOTI5♥**
- **♦♥LSSNQIIKTAKASTNDNIKDLLDWYSSGSDTFTNS♦♥**

EVLDNSL GSMRIKNTDG SISLIIFPSP YYSPAFTKGE KV

- **↑107x178x4**◆
- **♦DLNTKRTKKSQHTSEGTYIHFQISGVT♦**

N TEKLPTPIEL PLKVKVHGKD SPLKYG

- *P12LZIPC*
- *PKFDKKQLAISTLDFEIRHQLTQI*

HGLYRSSDKT GGYWKITMND GSTYQSDLSK KFEYNTEKPP

INIDEIKTIE AEIN

F19. 40

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♥ALLMOTI5♥

MKKTAFILLL FIALTLTTSP L ♥VNG

- **★107x178x4★**
- *LVS Predicted Coiled-Coil*
- *S & EKSEEINEKDLRKKSELORNALSNLRQIY* YYNEKAITENKESDD &

OFLENTLL♥ FKG FFTGHPW

- **★107x178x4★**
- **♦YNDLLVDLGSKDATNKYKGKKVDLYGAY♦**

YGYQCAGGTPNKTACMYGGVTLHDN NRLTEEKKVP INLWIDGKQTTV

- *P12LZIPC*
- *PIDKVKTSKKEVTVQELDL* QARHYLHGK FGLYNSDSFGGKVQ

P12LZIPC

RGLIVF HSSEGSTVSY DLFDAQGQY +P DTLLRIYRDN KTINSENLHI+

DLYLYTT

7872-020 (SHEET Y OF 63)

♥ALLMOTI5♥

MKKTAFTLLL FIALTLTTSP L

▼VNGS

↑107x178x4↑

◆EKSEEINEKDLRKKSELQGTALGNLKQIYYYNEKAKTENKESHD ◆ Q▼

FLOHTILFKG FFTDHSWYND LLVDFDSKDI VDKYKGKKVDLYGAYY

GYQC AGGTPNKTAC MYGGVTLHDN NRLTEEKKVPINLWLDGKQNTV

♦107x178x4♦

♥ALLMOTI5♥

P12LZIPC

♣P ♥L ♠ETVKTNKKNVTVOELDLOARRYL♣ QEKYNLYN♠

SDVFDGKVQR♥ GLIVF HTSTE

+P23LZIPC+

PSVNYDLFGAQGQYSNTLLRIYRDNKTINSENMHI DIYLYTS

F1G. 42

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MKNITFIFFILLASPLYANGDRLYRADSRPPDEIKRFRSLMPRGNEYFDRGT

- **♥ALLMOTI5♥**
- **♥QMNINLYDHARGTQTGFVRYDDGYV**
- **4107x178x44**
- **♦STSLSLRSAHLAGOYILSGYSLTIYIVI** ANMFNVNDVISVY♥

SP HPYEQEVSAL GGIPYSQIYG WYRVNFGVID ERLHRNREYR

DRYYRNLNIA PAEDGYRLAG FPPDHQAWRE EPWIHHAPQG

CGDSSRTITG DTCNE

- **♥ALLMOTI5♥**
- **▼ETQNLSTIYLREYQSKVKRQIFSDYQSEVDIYNRIRDEL ▼**

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MMFSGFNADY EASSSRCSSA SPAGDSLSYY HSPADSFSSM

GSPVNAQDFC TDLAVSSANF IPTVTAISTS PDLQWLVQPA

LVSSVAPSQT RAPHPFGVPA PSAGAYSRAG VVKTMTGGRA

LVS Predicted Coiled-Coil

QSIGRRGKVE QLSPEEEEKR RIRRE *RNKMA AAK

↑107x178x4↑

- **♥ALLMOTI5♥**
- **♥CRNRRREL ♠TDTLQAETDQLEDEKSALQTEIANLLKEKEKL♥**

EFILAAH R* PACKIPDDL GFPEEMSVAS LDLTGGLPEV

ATPESEEAFT LPLLNDPEPK PSVEPVKSIS SMELKTEPFD

DFLFPASSRP SGSETARSVP DMDLSGSFYA LPLLNDPEPK

PSVEPVKSIS SMELKTEPFD DFLFPASSRP SGSETARSVP

DMDLSGSFYA GSSSNEPSSD SLSSPTLLAL

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SGWESYYKTEGDEEAEEEQEENLEASGDYKYSGRDSLIFLVDASKA
MFESQSEDELTPFDMSIQCIQSVYISKIISSDRDLLAVVFYGTEKDKNS
VNFKNIYVLQELDNPGAKRILELDQFKGQQGQKRFQDMMGHGSDY
SLSEVLWVCANLFSDVQFKMSHKRIMLFTNEDNPHGNDSAKASRAR
TKAGDLRDTGIFLDLMHLKKPGGFDISLFYRDIISIAEDED

↑107x178x4↑

♥ALLMOTI5♥

LVS Predicted Coiled-Coil

♥LRVH *FEE &SSKLEDLLRKVRAKETRKRALSRLKLKLNKDIV* ISV

GIYNLVQKAL♥ KPPPIKLYRETN♠ EPVKTKTRTFNTSTGGLLLPSDTKR

SQIYGSRQIILEKEETEELKRFDDPGLMLMGFKPLVLLKKHHLRPSLFVYPE ESLVIGSSTLFSALLIKCLEKEVAALCRYTPRRNIPPYFVALVPQEEELDDQK IQVTPPGFQLVFLPFADDKRKMPFTEKIMATPEQVGKMKAIVEKLRFTYRS DSFENPVLQQHFRNLEALALDLME

- *P12LZIPC*
- *PEQAVDLTLPKVEAMNKRL* GSLVDEFKELVYPPDYNPEGKVTKR
 KHDNEGSGSKRPKVEYSEEELKTHISKGTLGKFTVPMLKEACRAYGLKSG
 LKKQELLEALTKHFQD

7872-020 (SHEET 53 OF 63)

GGGALSPQHSAVTQGSIIKNKEGMDAKS

- **★107x178x4**◆
- **♥ALLMOTI5♥**
- **▼**▲LTAWSRTLVTFKDVFVDFTREEWKLLDT AQQIVYRNV
 MLENYKNLVSLGYQLT KPDVILRLEKGEEPWLVEREIHQETHPD
 SETAFEIKSSVSSRSIFKDKQSCDIKMEGMARNDLWYLSLEEVWKCR
 DQLDKYQENPERHLRHQLIHTGEKPYECKECGKSFSRSSHLIGHQKT
 HTGEEPYECKECGKSFSWFSHLVTHQRTHTGDKLYTCNQCGKSFVH
 SSRLIRHQRTHTGHKPYECPECGKSFRQSTHLILHQRTHVRVRPYECN
 ECGKSYSQRSHLVVHHRIHTGLKPFECKDCGKCFSRSSHLYSHQRTH
 TGEKPYECHDCGKSFSQSSALIVHQRIHTGEKPYECCQCGKAFIRKN
 DLIKHQRIHVGAETYKCNQCGIIFSQNS
- *P23LZIPC*
- *PFIVHQIAHTGEQFLTCNQCGTALVNTSNLIGYQTNHI* RENAY

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Domain I: 174P-L-L-V-L-Q-A-G-F-F-L-L-T-R-H-L-T-I-P-Q-S-L-D-S-W-W-T-S-L-N-F-L-G-G-G-T-T-V-C-L-G-Q-N-S-Q-S-P₂₂₀

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J-I-P-L-L-V-L-L-D-Y-Q-G-H-L-P-V-C-P-L-I-P-G-8-8-7-8-7-G-P-C-R-T-C-H-T I-P-L-L-V-L-L-D-Y-Q-G-H-L-P-V-C-P-L-I-P-G-8-8-7-8-7-G-P-C-R-T-C-H-T-T

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Domain II:

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INTERNATIONAL SEARCH REPORT

International application No. PCT/US95/16733

A. CLASSIFICATION OF SUBJECT MATTER IPC(6):C07K 7/04,14/025, 14/16; C12N 9/94, 9/96, 9/98, US CL:530/324; 424/184.1 According to International Patent Classification (IPC) or to both B. FIELDS SEARCHED Minimum documentation searched (classification system follower U.S.: 530/324, 325, 326, 327, 328, 329; 424/184.1, 185.1	national classification and IPC d by classification symbols) , 186.1, 187.1, 188.1
Documentation searched other than minimum documentation to the Electronic data base consulted during the international search (na MEDLINE, AIDSLINE, APS	
C. DOCUMENTS CONSIDERED TO BE RELEVANT	
Category* Citation of document, with indication, where a	ppropriate, of the relevant passages Relevant to claim No.
PROCEEDINGS OF THE NATIONAL OF THE UNITED STATES OF AME 21, issued November 1992, Wild of Inhibitor of Human Immunodefic Correlation Between Solution Strupages 10537-41, see entire documents.	RICA, Volume 89, Number et al, "A Synthetic Peptide ciency Virus Replication: cture and Viral Inhibition",
X Further documents are listed in the continuation of Box	
Special categories of cited documents: 'A" document defining the general state of the art which is not considered to be of particular relevance 'E" curtier document published on or after the interactional filing date "L" document which may throw doubts on priority chain(s) or which is clad to enablish the publication date of enother citation or other special reason (as specified) "O" document referring to an oral disclosure, use, exhibition or other means "P" document published prior to the international filing date but later than	"T" inter-document published offer the increasional filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention. "X" document of particular relevance; the claimed invention cannot be considered acreal or cannot be considered to involve an inventive step when the document is tulent alone. "Y" document of particular subvance; the claimed invention cannot be considered to invelve an inventive step when the document is combined with one or more other such documents, each combination being obvious to a passes skilled in the ext. "A" document member of the same patent family.
Date of the actual completion of the international search	Date of mailing of the international search report 09 APR 1996
28 MARCH 1996 Name and mailing address of the ISA/US Commissioner of Patents and Trademarks Box PCT Washington, D.C. 20231 Facsimile No. (703) 305-3230	Authorized officer () (703) 308-0196

INTERNATIONAL SEARCH REPORT

International application No. PCT/US95/16733

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No
X Y	PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA, Volume 91, Number 26, issued December 1994, Wild et al, "Propensity for a Leucine Zipper-Like Domain of Human Immunodeficiency Virus Type 1 gp41 to Form Oligomers Correlates With a Role in Virus-Induced Fusion Rather Than Assembly of the Glycoprotein Complex", pages 12676-80, see entire document.	1-3, 9 and 10 4-8 and 11-15
X Y	PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA, Volume 81, Number 24, issued December 1984, Collins et al, "Nucleotide Sequence of the Gene Encoding the Fusion (F) Glycoprotein of Human Respiratory Syncytial Virus", pages 7683-87, see pages 7683 and 7685.	1 and 4
X Y	VIROLOGY, Volume 204, Number 2, issued 01 November 1994, Bousse et al, "Regions on the Hemagglutinin-Neuraminidase Proteins of Human Parainfluenza Virus Type-1 and Sendai Virus Important for Membrane Fusion", pages 506-514, see pages 506 and 510-513.	1 and 5 9 and 12
<u>x</u> <u>y</u>	JOURNAL OF VIROLOGY, Volume 67, Number 9, issued September 1993, Wang et al, "Ion Channel Activity of Influenza A Virus M2 Protein: Characterization of the Amantidine Block", pages 5585-94, see pages 5585-86.	1 and 6 9 and 13
X Y	JOURNAL OF VIROLOGY, Volume 67, Number 5, issued May 1993, Lazinski et al, "Relating Structure to Function in the Hepatitis Delta Virus Antigen", pages 2672-80, see pages 2672-73 and 2678.	1 and 7 9 and 14
Р, Ү	JOURNAL OF EXPERIMENTAL MEDICINE, Volume 182, Number 2, issued August 1995, Suzuki et al, "Viral Interleukin 10 (IL-10), the Human Herpes Virus 4 Cellular IL-10 Homologue, Induces Local Anergy to Allogenic and Syngeneic Tumors", pages 477-486, see entire document.	1, 8, 9, and 15